

UNIVERSITY OF CALGARY

Modelling of Antihydrogen Formation and the Commissioning of the

ALPHA Antihydrogen Apparatus

by

Richard Allan Hydomako

A THESIS

SUBMITTED TO THE FACULTY OF GRADUATE STUDIES

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE

DEGREE OF MASTERS OF SCIENCE

DEPARTMENT OF PHYSICS AND ASTRONOMY

CALGARY, ALBERTA

September, 2007

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ISBN: 978-0-494-34223-7

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ISBN: 978-0-494-34223-7

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The undersigned certify that they have read, and recommend to the Faculty of Graduate Studies for acceptance, a thesis entitled “Modelling of Antihydrogen Formation and the Commissioning of the ALPHA Antihydrogen Apparatus” submitted by Richard Allan Hydomako in partial fulfillment of the requirements for the degree of MASTERS OF SCIENCE.

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Abstract

This thesis describes several models of antihydrogen formation as well as the commissioning of the ALPHA antihydrogen during the 2006 Antiproton Decelerator (AD) physics run. Three models are given to describe the short-time production of antihydrogen, including the Simple Temperature Dependant Model, Inverse Velocity Model, and Scaled Inverse Velocity Model. All three models are compared to results from the ATHENA experiment. After an introduction to the ALPHA apparatus and some of the techniques used to produce antihydrogen the commissioning process is described, focusing on the optimization of the antiproton capture, cooling, and manipulation. Also included is an appendix describing in detail the ALPHA data acquisition system as of the end of the 2006 physics run.

Preface

The ALPHA experiment (Antihydrogen Laser PHysics Apparatus¹) represents one of two major international efforts aimed at generating, storing and studying antihydrogen ($\bar{H}$). Based at CERN, where it utilizes the Antiproton Decelerator (AD) facility, ALPHA uses a set of charged particle traps to mix the constituent particles of antihydrogen atoms (antiprotons and positrons), and will attempt to use a magnetic trap to hold the neutral antihydrogen produced by this mixing. This thesis represents a major summary of the first year of ALPHA on-line operation. It includes both a computational section, which attempts to further our understanding of antihydrogen production through models of the data from the precursor ATHENA experiment², and a larger, detailed description of the commissioning of the ALPHA apparatus, including results from its first season of operation.

The first chapter provides an introduction to antihydrogen, including a history of its study and a description of its properties. Chapter two deals with the simulation of antihydrogen production, focusing in particular on the formation rates immediately after mixing of the positrons and antiprotons. The third chapter outlines some of the atomic, particle, and accelerator physics that motivated the design of the ALPHA apparatus and its antiparticle delivery systems. Chapter four describes in detail the ALPHA antihydrogen apparatus, its commissioning, and related results from its first season of operation. Finally, the fifth chapter provides a summary of work to date, an outlook towards the future activities of ALPHA, and a conclusion to the thesis. An appendix is also included that describes in detail the ALPHA data acquisition system with an emphasis on the online display and analysis program.

¹ALPHA website: <http://alpha.web.cern.ch/alpha/>

²ATHENA website: <http://athena.web.cern.ch/athena/>

Papers and Publications

1. M. C. Fujiwara, G. Andresen, W. Bertsche, A. Boston, P. D. Bowe, C. L. Cesar, S. Chapman, M. Charlton, M. Chartier, A. Deutsch, J. Fajans, R. Funakoshi, D. R. Gill, K. Gomberoff, J. S. Hangst, W. N. Hardy, R. S. Hayano, R. Hydomako, M. J. Jenkins, L. V. jørgensen, L. Kurchaninov, N. Madsen, P. Nolan, K. Olchanski, A. Olin, R. D. Page, A. Povilus, F. Robicheaux, E. Sarid, D. M. Silveira, J. W. Storey, R. I. Thompson, D. P. van der Werf, J. S. Wurtele, Y. Yamazaki (ALPHA Collaboration), *Towards Antihydrogen Confinement with the ALPHA antihydrogen Trap*. *Hyperfine Interactions* **172**, 81 (2006).
2. G. Andresen, W. Bertsche, A. Boston, P. D. Bowe, C. L. Cesar, S. Chapman, M. Charlton, M. Chartier, A. Deutsch, J. Fajans, M. C. Fujiwara, R. Funakoshi, D. R. Gill, K. Gomberoff, J. S. Hangst, R. S. Hayano, R. Hydomako, M. J. Jenkins, L. V. Jørgensen, L. Kurchaninov, N. Madsen, P. Nolan, K. Olchanski, A. Olin, A. Povilus, F. Robicheaux, E. Sarid, D. M. Silveira, J. W. Storey, H. H. Telle, R. I. Thompson, D. P. van der Werf, J. S. Wurtele and Y. Yamazaki (ALPHA Collaboration), *Antimatter Plasmas in a Multipole Trap for Antihydrogen*. *Phys. Rev. Lett.* **98**, 023402 (2007).

Acknowledgements

This thesis includes the work of many. Specifically, the design, construction and operation of the ALPHA antihydrogen apparatus was, and continues to be, the occupation of a large number of people. I would like to thank the entire ALPHA collaboration for the excellent opportunity to participate in an exciting project with many great people. Personally, I have learnt a tremendous amount from all involved, not only in regards to experimental physics, but also about being a part of a team and working on a large, complicated, project.

I would like to personally thank Prof. Robert Thompson, who has been an excellent supervisor. Despite being unceasingly busy, he has always found the time to answer all my questions and provide numerous revisions to this thesis.

Likewise, Dr. Makoto Fujiwara has been incredibly supportive and has gone above and beyond to help me along. Even being in another province or country has not stopped or slowed his involvement through the course of my program.

Lastly, I would like to acknowledge the support and encouragement of my parents, William and Marianne Hydomako. Without their continued support and encouragement, none of this would have been possible.

*In loving memory of my Baba,
Alexandria Hydomako (1918–2007)*

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Abbreviations and Symbols

Abbreviation	Description
CERN	European Center for Nuclear Research
PS	Proton Synchrotron
AD	Antiproton Decelerator
ALPHA	Antihydrogen Laser PHysics Apparatus
ATHENA	AnTiHydrEN Apparatus
ATRAP	Antihydrogen TRAP
CPT	The combination of charge (C), parity (P) and time reversal (T) operations
WEP	Weak Equivalence Principle
RF	Radio Frequency
MWPC	Multiwire Proportional Chamber
HVA	High-Voltage Electrode A
HVB	High-Voltage Electrode B
FWHM	Full Width Half Maximum
DAQ	Data Acquisition
MIDAS	Maximum Integration Data Acquisition System
VME	Versa Module Europa (module standard)
ADC	Analog to Digital Converter
FIFO	First In First Out
NIM	Nuclear Instrumentation Module
CASTOR	CERN Advanced STORage
ODB	Online DataBase

Table 0.1: List of Abbreviations

Symbol	Description
p	Proton
$\bar{p}$	Antiproton
e^-	Electron
$e^+(\beta^+)$	Positron
H	Hydrogen
$\bar{H}$	Antihydrogen
$\bar{H}^*$	Excited antihydrogen
Ps	Positronium
Cs	Cesium
Cs^*	Excited Cesium
ν	Neutrino
γ	Gamma ray
$\vec{v}$	Velocity
$\vec{E}$	Electric field
$\vec{B}$	Magnetic field
Φ	Scalar potential
σ	Cross section
Z	Atomic number
e	Fundamental electric charge
ϵ_0	Permittivity of free space
k_B	Boltzmann's constant
$N_{\bar{p}}$	Number of antiprotons
N_e^+	Number of positrons
$n_{\bar{p}}$	Antiproton density
n_e^+	Positron density
$T_{\bar{p}}$	Antiproton temperature
T_e^+	Positron temperature
$R_{\bar{H}}$	Antihydrogen formation rate
τ_c	Antiproton cooling constant
τ_e	Synchrotron cooling constant
η	Antihydrogen temperature scaling parameter
μ	Magnetic dipole moment
ω_c	Cyclotron frequency
ω_z	Axial frequency
ω_m	Magnetron frequency
$m_{\bar{p}}$	Mass of the antiproton
m_e^+	Mass of the positron
$\ln(\Lambda)$	Coulomb logarithm

Table 0.2: List of Symbols

Chapter 1

Introduction

This thesis deals with the study of antihydrogen with numerical simulations and within an experimental apparatus. This first chapter introduces antihydrogen and motivates its study. Several potential measurements using antihydrogen are described, including high-precision tests of *CPT*-violation and gravitational interactions with antimatter. The hypothetical application of antihydrogen as a fuel source for long-range space probes is briefly outlined. Hot (in-flight) antihydrogen production is discussed, along with descriptions of the experiments that observed in-flight antihydrogen. General techniques for the formation of cold (low-energy) antihydrogen are then described and the concepts related to several mechanisms are introduced. The ATRAP and ATHENA experiments are briefly described, as well as their methods for producing and detecting cold antihydrogen. Finally, the current direction in antihydrogen physics is outlined.

1.1 Why Study Antihydrogen?

Antihydrogen is the antimatter analog of hydrogen. That is, while hydrogen consists of a proton (p) and an electron (e^-), antihydrogen contains an antiproton ($\bar{p}$) and a positron (e^+). It is the simplest atomic system entirely composed of antiparticles. Due to the scarcity of antiparticles, antihydrogen is the first antiatomic system to be produced and studied. As it is breaking new ground, antihydrogen provides exciting research opportunities not previously available.

Matter-antimatter symmetry is one of the most fundamental relations in physics and has been studied since the prediction and discovery of the positron [11, 12]. Positron

properties are predicted to be identical (although opposite in some cases) to those of the electron. Indeed, positron mass [13, 14], charge [15, 16, 17], and gyromagnetic ratio [18, 19] have all been measured to a high precision and these characteristics were all found to be in excellent agreement with those of the electron. The same agreement is found between the proton and the antiproton [20, 21, 22, 23]. It remains to be seen, however, if this symmetry holds for more complex systems. Although antihydrogen is the most elementary antiatomic system, it offers the opportunity to study some of the most fundamental symmetries of particle physics to unprecedented precisions.

1.1.1 The *CPT* Theorem

The *CPT* theorem is one of the most important theorems in particle physics. It applies to a broad class of quantum field theories and its validity impacts high-energy physics in general. The *CPT* theorem states that all fundamental interactions are invariant under the combination of charge conjugation (*C*), parity inversion (*P*), and time reversal (*T*) transformations [24, 25, 26]. In other words, the behaviour of a particle is the same as the behaviour of an identical particle of opposite charge, which is inverted through the origin and moving backwards through time. Any quantum theory that is both local and Lorentz-invariant will obey the *CPT* theorem [27]. Moreover, the *CPT* theorem implies that there exists an antiparticle for every particle, with the same mass and natural lifetime, but equal and opposite charge and magnetic moment.

If one is entirely confident in the accuracy and completeness of the *CPT* theorem, then careful investigation of antimatter is unnecessary as the properties and behaviour of antimatter correspond directly to the properties and behaviour of matter. This position is supported by the fact that *CPT*-invariance has been verified in every experiment done to date [28]. However, these results do not prove that the *CPT*-invariance will continue to hold up to some yet unreachable precision as experimental tests continue to

push these precision limits forward. Indeed, violation of C , P , and CP have all been shown experimentally [29, 30], demonstrating that even the most fundamental, or well accepted, symmetries can break down under careful examination. As such, experimental examination of the CPT symmetry is not only prudent, but necessary.

Antihydrogen provides an ideal system in which to test the CPT theorem. A direct comparison can be made between the spectra of hydrogen and antihydrogen. Since CPT -invariance requires that these spectra be identical, any deviation would be an indication of CPT violation. Using high-precision laser spectroscopy, the antihydrogen spectrum should be measurable, in principle, to an accuracy comparable to what has been achieved in the hydrogen spectrum, namely, a few parts in 10^{14} [31, 32]. Such a comparison would place new limits on CPT -violation. To date, CPT tests based on comparisons of charged matter and antimatter properties have been made using positrons and antiprotons. For example, the mass difference between electrons and positrons has been measured as $|m_{e^+} - m_{e^-}|/m_{avg} < 8 \times 10^{-9}$ [14], while for antiprotons $|m_p - m_{\bar{p}}|/m_p < 1.0 \times 10^{-8}$ [23]. The $\bar{p}/p$ charge-to-mass ratio has also been measured to a precision of 9×10^{-11} [22]. Thus, we can see that a precision spectroscopic measurement on antihydrogen could potentially provide an excellent comparison between atomic and antiatomic systems and place a very strict limit on CPT -violation.

1.1.2 The Gravitational Interaction of Antimatter: Weak Equivalence Principle

The CPT theorem equates the inertial masses of particles and antiparticles, and thus the behaviour of an antiparticle in an antiuniverse. It makes no predictions about the gravitational mass of antiparticles. It is the Equivalence Principle of general relativity that specifies the equivalence of inertial and gravitational masses, although strictly speaking this equivalence has only been established for matter. Neither the CPT theorem nor the Equivalence Principle describes the interaction between antimatter and a gravitational

field generated by some configuration of conventional matter. This situation is instead covered by the Weak Equivalence Principle (WEP). The WEP states that all bodies accelerate in a gravitational field, regardless of their internal structure or mass [33, 34]. This implies that antiparticles should accelerate in a gravitational field the same as particles; i.e. the gravitational behaviour of matter and antimatter should be identical.

Although WEP implies the equivalence between matter and antimatter in gravitational fields, this equivalence has not yet been tested experimentally. Gravitational experiments using charged particles (and antiparticles) have proven to be extremely difficult. These experiments must be well-shielded against even the smallest stray electric and magnetic fields, as even small electromagnetic forces tend to overwhelm the gravitational force on charged particles. For example, if we consider the ratio of gravitational force to Coulomb force between two protons (or antiprotons), we see that $F_{\text{Grav}}/F_{\text{Elec}} = (Gm_p^2/r^2)/(e^2/4\pi\epsilon_0 r^2) \cong 10^{-36}$ where $G = 6.67 \times 10^{-11} \text{ Nm}^2\text{kg}^{-2}$, $m_p = 1.67 \times 10^{-27} \text{ kg}$, and $\epsilon_0 = 8.85 \times 10^{-12} \text{ m}^{-3}\text{kg}^{-1}\text{s}^4\text{A}^2$, which shows the large discrepancy between the magnitudes of the electric and gravitational forces. Even with drift tubes to electrically shield and isolate the charge of particles under the influence of gravity, patch effects, or inconsistencies in the surface of the drift tube create electric field gradients, which affect the transit of the particle [35]. In addition, the relative scarcity of antiparticles makes using antiparticles to measure the gravitational interaction almost inherently unfeasible. As such, to this point no accurate measurement of the gravitational acceleration of antimatter has been made.

Being electrically neutral, antihydrogen would not be significantly influenced by stray electric fields and is thus a perfect candidate for the measurement of gravitational interactions with antimatter. By timing the transit of antihydrogen atoms over a known displacement, the gravitational acceleration of antimatter could be measured directly and compared with the gravitational acceleration of matter. This would be the first

measurement of the symmetry between matter and antimatter with regards to the gravitational interaction. Moreover, this would be a direct test of the WEP, which could have significant consequences for both current and future gravitational theories.

1.1.3 Antihydrogen as an Energy Source

Antimatter annihilation is the most efficient energy conversion known, with twice the energy corresponding to the rest mass of the particle being released. It produces more than ten thousand times more energy per unit mass than any known fission or fusion reaction. Antimatter might therefore be a very attractive source of stored energy. However, compared to conventional fuel sources, it is also extremely expensive. It costs significantly more energy to produce the antiparticles needed than is released during annihilation. This makes the use of antimatter as an everyday fuel source untenable.

However, for applications where the energy per unit mass ratio is critically important, such as deep-range space probes, antimatter as fuel is still an option. The ability to minimize the mass and maximize the efficiency of fuel is a major concern when designing space vehicles to transverse large distances. Once again, charged antiparticles are limiting, as the storage density is limited by the Brillouin density, n_0 , which is given by

$$n_0 = \frac{B^2}{2\mu_0 mc^2}, \quad (1.1)$$

where B is the applied magnetic field, μ_0 is the permeability of free space, m is the particle mass, and c is the speed of light [36]. For a strong applied field of 6T, positrons would be limited to a density of $1.8 \times 10^{14} \text{ cm}^{-3}$, while antiprotons would be limited to about $1 \times 10^{11} \text{ cm}^{-3}$. Nieto, Holzscheiter and Phillips give an estimate that 5 g of stored antimatter fuel would be required for a 500 g space probe to travel about 200 AU in one year [37]. For a 6T applied storage field, the storage volume for the charged

antimatter would then be about $3 \times 10^{13} \text{ cm}^3$ (i.e. a $300 \text{ m} \times 300 \text{ m} \times 300 \text{ m}$ cube). The size constraint is a serious restraint in the use of charged antiparticles as an energy source. Again, antihydrogen provides an advantage, as it is electrically neutral and thus is not subject to the electrostatic repulsion that affects charged particles. Much greater storage densities could be then be reached, to the point where some speculate that a Bose-Einstein Condensate of antihydrogen atoms might be used [37, 38].

These schemes are optimistic, and highly speculative, in terms of the numbers and densities of antihydrogen to be used. New technologies and methods, such as a much improved method of antihydrogen production and new handling procedures, would be needed before antihydrogen fuel can seriously be considered for space probe implementation. Moreover, the large amount of energy necessary to produce antihydrogen atoms would make the accumulation of significant amounts prohibitively expensive.

1.2 Production of Antihydrogen

Antihydrogen has been produced and detected experimentally, both at high kinetic energies and nearly at rest. Experiments conducted at CERN's Low Energy Antiproton Ring (LEAR) and Antiproton Decelerator (AD), as well as Fermilab's Antiproton Accumulator have contributed to more than a decade of antihydrogen research. Two clear stages of research can be seen: high-energy antihydrogen produced in flight through an antiproton interaction with a heavy nucleus (hot antihydrogen), and low-energy antihydrogen produced nearly at rest by combining low-energy positrons and antiprotons (cold antihydrogen).

1.2.1 Hot Antihydrogen Production

The first observation of antihydrogen was made in 1996 at the Low Energy Antiproton Ring (LEAR) at CERN [2]. In this experiment, an antiproton beam from LEAR was

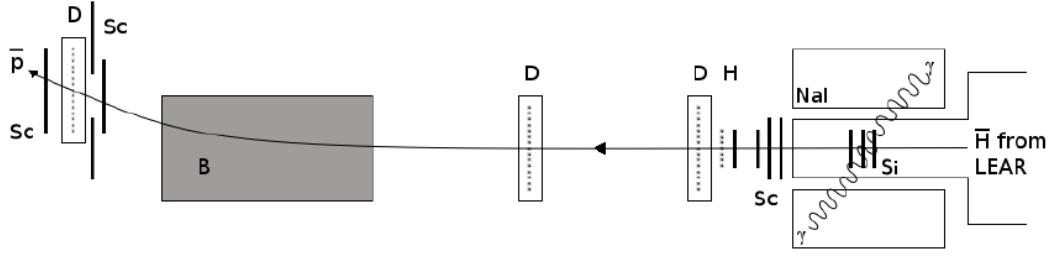


Figure 1.1: Schematic of the PS210 antihydrogen detection apparatus at LEAR (figure created based on the content of [2]). Sc are the trigger and time of flight scintillators, Si are the silicon counters, D are the delay wire chambers, NaI the segmented NaI detector, H is the scintillating fiber hodoscope and B is the magnetic dipole field.

passed through a Xe gas jet. An antiproton passing near an atomic matter nucleus can create an electron-positron pair, and in a small fraction of the interactions, a positron will be captured by the antiproton and an antihydrogen atom will be formed in flight through the process [39, 40],

$$\bar{p} Z \rightarrow \bar{p} e^+ e^- Z \rightarrow \bar{H} e^- Z, \quad (1.2)$$

where Z is the number of protons in the nucleus. The resulting antihydrogen atoms were then observed in an apparatus specially designed to record the antihydrogen signatures (Fig. 1.1). Neutral antihydrogen formed in the Xe gas jet will no longer be confined and will leave the accelerator storage ring into the detection apparatus.

Within the detection apparatus, the positron is stripped from the antiproton at the first of three silicon counters. The second silicon counter measures the energy loss of the antiproton and the kinetic energy of the positron, while the third silicon counter measures the energy loss of the antiproton only. Photons released from the annihilation of the positron on the silicon counter are detected in a segmented NaI detector situated around the silicon counters. The continuing antiprotons pass through two scintillators before

being deflected in a magnetic field. The deflection of the antiprotons is measured with a spectrometer and used to isolate the events generated by antiprotons from those produced by other particles of differing charge or mass. With this setup, eleven antihydrogen atoms were observed [2].

A similar experiment was performed in 1998 at the Fermilab Antiproton Accumulator [3]. In this case an electron-positron pair is created when an antiproton interacts with the Coulomb field of a proton ($Z = 1p$ in Eqn. 1.2),

$$\bar{p} p \rightarrow \bar{p} e^+ e^- p \rightarrow \bar{H} e^- p. \quad (1.3)$$

Again, the resulting antihydrogen atoms were observed through the ionization and detection of the constituent particles (Fig. 1.2). The neutral antihydrogen atoms travel in a straight line and separate from the curved path of the antiproton beam, which is deflected by the dipole magnets that make up the storage ring. After exiting the storage ring, the antihydrogen atoms ionize on a thin carbon foil. The positrons and antiprotons retain the velocity of the pre-ionized atom, although the positrons change direction due to scattering within the foil. The positrons were then deflected into a scintillator surrounded by a NaI detector, which is designed to detect the photons released in positron annihilation. The antiproton momentum and position was measured in a series of scintillator counters and proportional wire chambers interspersed between magnetic dipoles, which deflect the charged particles. A three-way coincidence between the between the scintillators and any one of the wire chambers was used as the indication of antihydrogen. In this way, 57 antihydrogen atoms were observed [3].

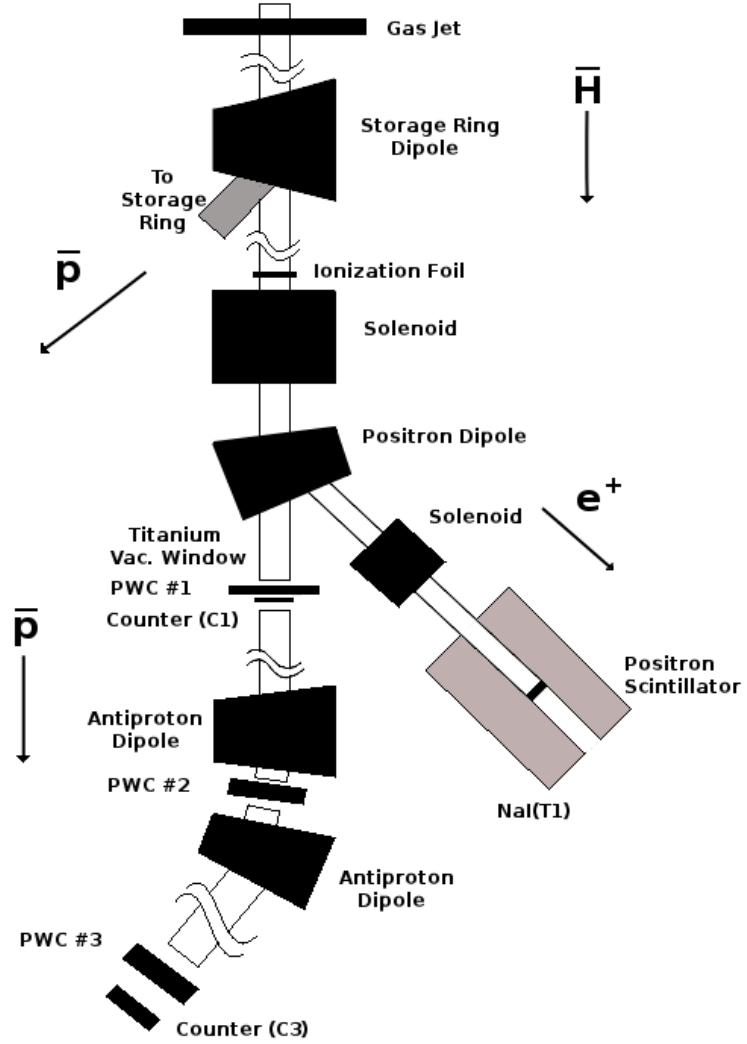


Figure 1.2: Schematic of the Fermilab E862 antihydrogen detection apparatus (figure created based on the content of [3]). PWC 1-3 are proportional wire chambers, C1, C2 and CE are scintillation counters, Na(Tl) is two half-cylindrical NaI crystals.

1.2.2 Cold Antihydrogen

While the production of hot antihydrogen demonstrated the existence of a bound-state of positrons and antiprotons, antihydrogen produced in-flight is not well-suited for careful study of its characteristics. For high-precision studies, the atoms need to be isolated, at rest, and at or near their ground state energy. Isolation is required to minimize the perturbation from the environment. In the case of antimatter, isolation is also needed to provide a sufficient particle lifetime to make the measurements, as contact with our environment will result in the loss of the antiparticle through matter-antimatter annihilation. Atoms are required at rest (or as low an energy as possible), especially for laser spectroscopy, not only so that they remain in the laser beam, but also to reduce the doppler spread of the spectral lines.

Producing cold antihydrogen requires an entirely different approach than producing hot antihydrogen. Instead of observing high-energy collisions and looking for a small cross-section result, low-energy positrons and antiprotons are brought together and directly combined to form low-energy antihydrogen. There are several low-energy mechanisms which result in antihydrogen formation, all involving the direct combination of positrons and antiprotons. Often, the matter equivalent mechanisms involving electrons and protons are considered. The antimatter processes are then examined by extension; taking the charge conjugate process with the same rate and properties to describe the antimatter reaction. Three such processes are described in detail below:

Spontaneous Radiative Recombination

Schematically, the simplest mechanism of antihydrogen production is spontaneous radiative recombination (SRR). In this case, positrons and antiprotons are brought together and form antihydrogen, with the excess energy carried away through the emission of a

photon, or

$$\bar{p} + e^+ \rightarrow \bar{H} + h\nu. \quad (1.4)$$

Time-reversed and charge conjugated, this is the well-studied photoionization of hydrogen [41]. The cross section $\sigma_{SRR}(n, E_{cm})$ for a state with quantum number n and center of mass energy, E_{cm} , is given as [42]:

$$\sigma_{SRR}(n, E_{cm}) = (2.10 \times 10^{-22} \text{cm}^2) \frac{E_0^2}{nE_{cm}(E_0 + n^2E_{cm})}, \quad (1.5)$$

where $E_0 = 13.6$ eV, the ground state binding energy of hydrogen. Summing over the quantum states gives an approximation for the total cross section over all attainable states,

$$\sigma_{SRR}(E_{cm}) = \sum_{n=1}^{n_{cut}} \sigma_{SRR}(n, E_{cm}). \quad (1.6)$$

The cutoff value, n_{cut} , is determined by the experimental conditions. For example, for recombined atoms in large n states, ionization can easily occur due to small electric fields or collisions with stray particles [43].

By integrating the product of the cross section and the velocity distribution for the positrons and antiprotons, we can obtain the recombination coefficient for the radiative recombination process, α_{SRR} ,

$$\alpha_{SRR}(v_r) = \int \sigma_{SRR}(v) v f(v) dv, \quad (1.7)$$

where v_r is the average relative speed, with $E_{cm} = mv_r^2/2$. With this, an upper bound on the formation rate of antihydrogen per antiproton is given as

$$R_{SRR} = N_{\bar{p}} n_{e^+} \langle \alpha_{SRR}(v_r) \rangle, \quad (1.8)$$

where $N_{\bar{p}}$ is the number of antiprotons, n_{e^+} is the positron density, and the brackets indicate an average over the relative particle velocities. Holzscheiter, Charlton and Nieto [28] use this formula with the realistic values $N_{\bar{p}} = 10^4$ and $n_{e^+} = 10^8 \text{ cm}^{-3}$ along with average rate coefficients given by Müller and Wolf [41] to give an estimated formation rate of about 30 s^{-1} for an initial antiproton energy of 1 meV. This process has a fairly small recombination rate, as the time necessary to emit a photon is often greater than the collision time between the positron and antiproton.

Three-Body Recombination

A second, very important, mechanism is possible when a large density of positrons is available, that is three-body recombination (TBR). In this approach the extra energy and momentum produced in the capture of a positron by an antiproton is transferred to an additional positron:

$$e^+ + e^+ + \bar{p} \rightarrow \bar{H} + e^+. \quad (1.9)$$

The calculated rate of three-body recombination, R_{TBR} , is given by

$$R_{TBR} = 6 \times 10^{-13} \left(\frac{4.2}{T} \right)^{9/2} n_{e^+}^2 [\text{s}^{-1}] \quad (1.10)$$

where T and n_{e^+} are the positron temperature and density, respectively, in units of K and cm^{-3} [44]. With the nominal values $n_{e^+} = 10^8 \text{ cm}^{-3}$ and $T = 4.2 \text{ K}$, the expected recombination rate is 6000 s^{-1} . This mechanism predicts a very high rate of recombination, and although the temperature dependence of $T^{-9/2}$ suggests that this process should only be relevant at low temperatures, experiments have shown three-body recombination to be significant at higher temperatures [6].

Positronium-Antiproton Collision

Electrons and positrons can form a bound state exotic atom called positronium (Ps). Positronium atoms are short lived (with a ground state lifetime of at most 100 ns [45]) as the electron and positron will transit into lower energy states, decreasing the atomic radius until they finally annihilate. The collision between an antiproton and a positronium atom provides another mechanism for antihydrogen formation, where the antiproton exchanges with the electron, which carries away the excess energy [46]:

$$Ps + \bar{p} \rightarrow \bar{H} + e^-. \quad (1.11)$$

This process involving the charge exchange of $\bar{p}$ and e^- within the bound system can occur via a resonant process. Using classical trajectory Monte Carlo simulations Hessel et al. [47] calculated the charge exchange cross section between the antiproton and positronium atom, $\sigma_{Ps-\bar{p}}$, as

$$\sigma_{Ps-\bar{p}} = 58n_{Ps}^4\pi a_0^2, \quad (1.12)$$

where $a_0 = 5 \times 10^{-11}\text{m}$ is the Bohr radius and n_{Ps} is the positronium principle quantum number. Then given a 4π steradian distribution and the distance, d , between the two trapped species, the absolute production of antihydrogen atoms can be calculated as $N_{Ps}N_{\bar{p}}\sigma_{Ps-\bar{p}}/(4\pi d^2) = 100$ antihydrogen atoms, where $N_{Ps} = 10^6$ positronium atoms, $N_{\bar{p}} = 10^4$ antiprotons, a principle quantum number of $n_{Ps} = 34$, and a $d = 0.2$ cm separation [47]. The production of these antihydrogen atoms is expected to occur in the first few milliseconds, corresponding to an instantaneous production rate of about 10^5 s^{-1} . With such a high expected formation rate, positronium-antiproton collision is an appealing method for producing cold antihydrogen.

1.3 Cold Antihydrogen Experiments

In 2002, two experiments at the Antiproton Decelerator (AD) at CERN succeeded in producing cold antihydrogen [4, 5]. The ATHENA and ATRAP experiments both used nested Penning traps to combine positrons and antiprotons, eventually producing and detecting low-energy antihydrogen. However, the experimental approaches differed significantly between the two groups.

1.3.1 ATHENA

The ATHENA apparatus consisted of an external positron accumulator, antiproton catching and antiproton-positron mixing traps, and an antihydrogen vertex detector (Fig. 1.3). Antiprotons were delivered from the AD directly into the ATHENA apparatus. After passing through a silicon beam diagnostic counter, energy degrading foil, and several vacuum windows, the antiprotons would arrive at the catching trap. The antiprotons would be stored in the catching trap while, simultaneously, positrons would be accruing in the positron accumulator. The two species would then be brought together in the mixing trap to form antihydrogen.

The trap system (including the collinear antiproton catching, positron, and mixing traps) consisted of a series of electrodes which would produce the electric potential used to manipulate the charged particles along the trap axis. Radial confinement in all the traps was provided by the strong 3 T external superconducting solenoid that encompassed the traps. Two high-voltage electrodes bordered the catching trap and were used to provide the large electrostatic barrier that would catch and confine the incoming antiprotons. The mixing trap was designed so that the nested harmonic potential [48] (Fig. 1.4) could be applied and positrons and antiprotons combined [8].

The positron accumulator employed a solid neon moderator and a nitrogen buffer gas to cool and store high energy positrons from a radioactive ^{22}Na source [49]. The positrons

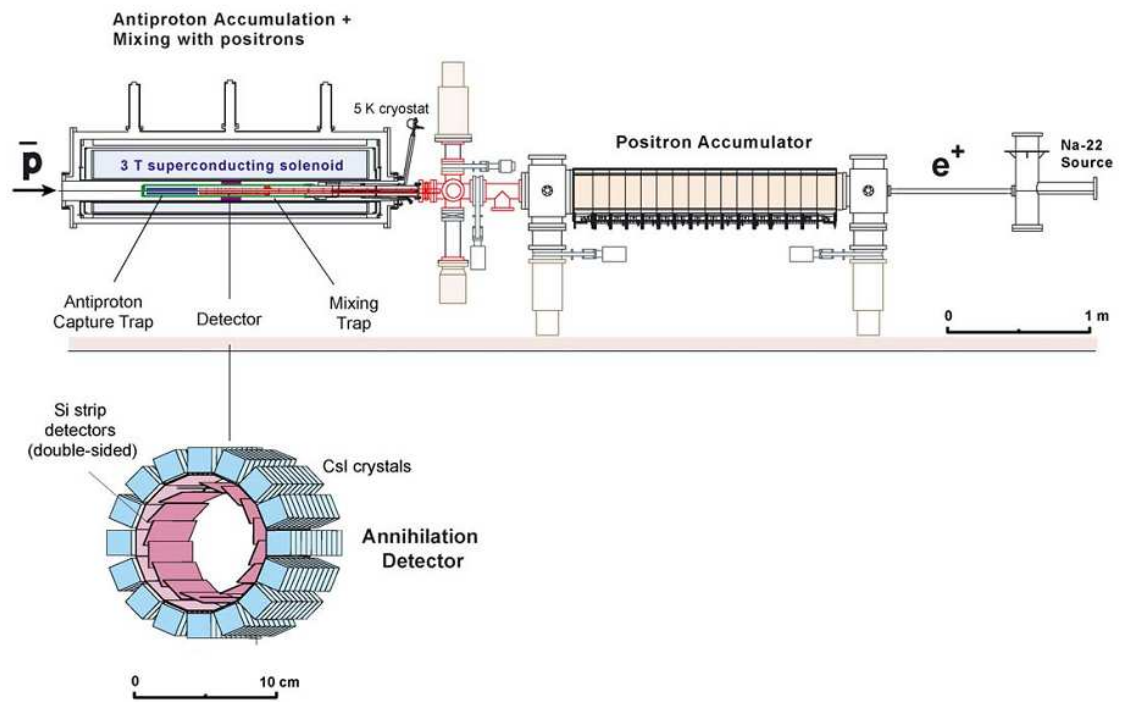


Figure 1.3: ATHENA antihydrogen apparatus, reprinted with permission from ref. [4]. Highlighted are the main components: the antiproton accumulation and mixing trap, the positron accumulator, and the antihydrogen annihilation detector.

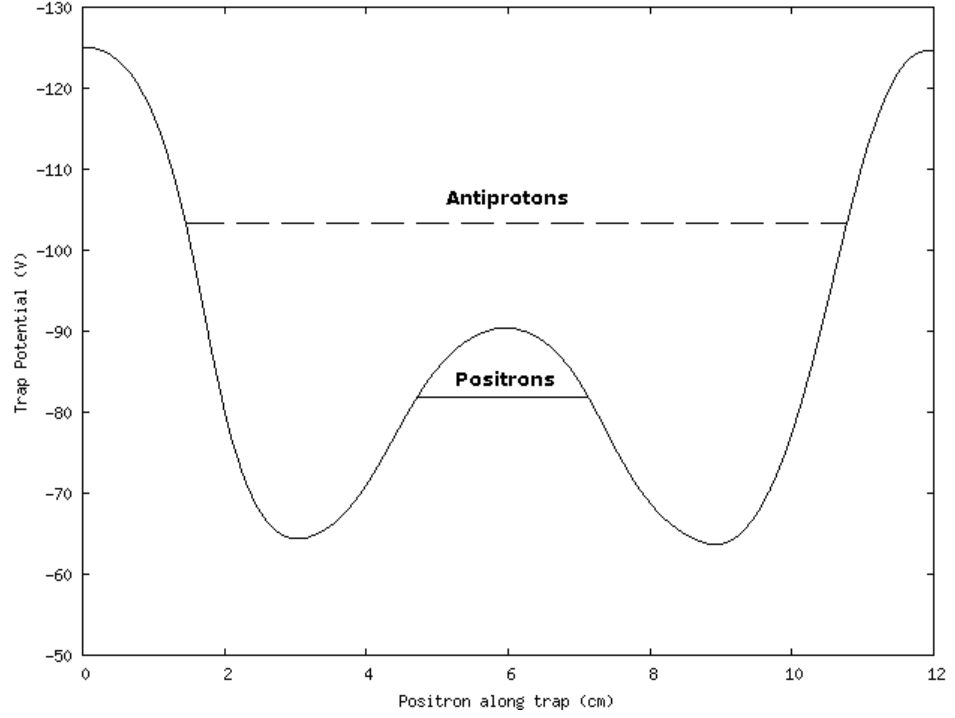


Figure 1.4: Nested harmonic potential used to simultaneously confine both positrons and antiprotons.

were then ballistically transferred to the mixing trap. A segmented Faraday cup was used for diagnostics of the position and number of positrons. A rotating wall potential could be applied to the accumulation trap to compress the trapped positrons [49].

Around the mixing trap was a vertex reconstruction antihydrogen detector (see inset of Fig. 1.3). This detector included a layer of silicon microdetection strips for the detection of the charged pions released during antiproton annihilation. Around the silicon microdetection strips was a layer of CsI scintillation crystals. These crystals detected the back-to-back 511 keV photons produced by electron-positron annihilation. Both layers encompass a roughly 2π steradian solid angle detection window around the mixing trap. When antihydrogen was formed inside the mixing trap it was no longer confined by the electric and magnetic fields and would rapidly annihilate against the electrode walls. The spatial and temporal coincidence of positron and antiproton annihilation (indicating the

presence of antihydrogen) was recorded through the reconstruction of vertices defined by the intersection of particle trajectories originating from triggered detector crystals. The vertex reconstruction method is very powerful in that it could resolve the antihydrogen atom location to within 5 mm (the uncertainty is due to the unmeasured curvature of the charged pion trajectories in a strong magnetic field [4]). This allowed for an accurate measurement of the spatial distribution of antihydrogen formation [50], as well as the dynamics of antiprotons with respect to antihydrogen formation [1].

The flexible ATHENA apparatus was also used to investigate the temperature dependence of antihydrogen formation [6], laser stimulation of radiative recombination [51], and positron control and diagnostics [52]. ATHENA completed experimental work in 2004 after an impressive record of antihydrogen production and study. Much of the ATHENA apparatus, and a significant number of the collaboration members, then evolved into then ALPHA (Antihydrogen Laser Physics Apparatus) collaboration, with the goal of creating, trapping and studying antihydrogen (as outlined in Sec. 1.4).

1.3.2 ATRAP

The ATRAP experiment was also successful in creating cold antihydrogen atoms [5]. While the ATRAP apparatus also operates by trapping and mixing low-energy positrons and antiprotons, the experimental methods differ significantly from the ATHENA experiment [53, 54]. A separate positron accumulator was not used, nor was a vertex detector. However, similar to ATHENA, the nested Penning trap method to collect and mix particles was effectively exploited. The method used to collect positrons in the ATRAP apparatus differs greatly from the ATHENA approach (Fig 1.5). While a ^{22}Na radioactive positron source was used, the outgoing positrons were directed through a metal foil, creating positronium atoms. A weakly ionizing electric field was then used to deposit the positrons into a catching potential. After a suitable number of positrons had been

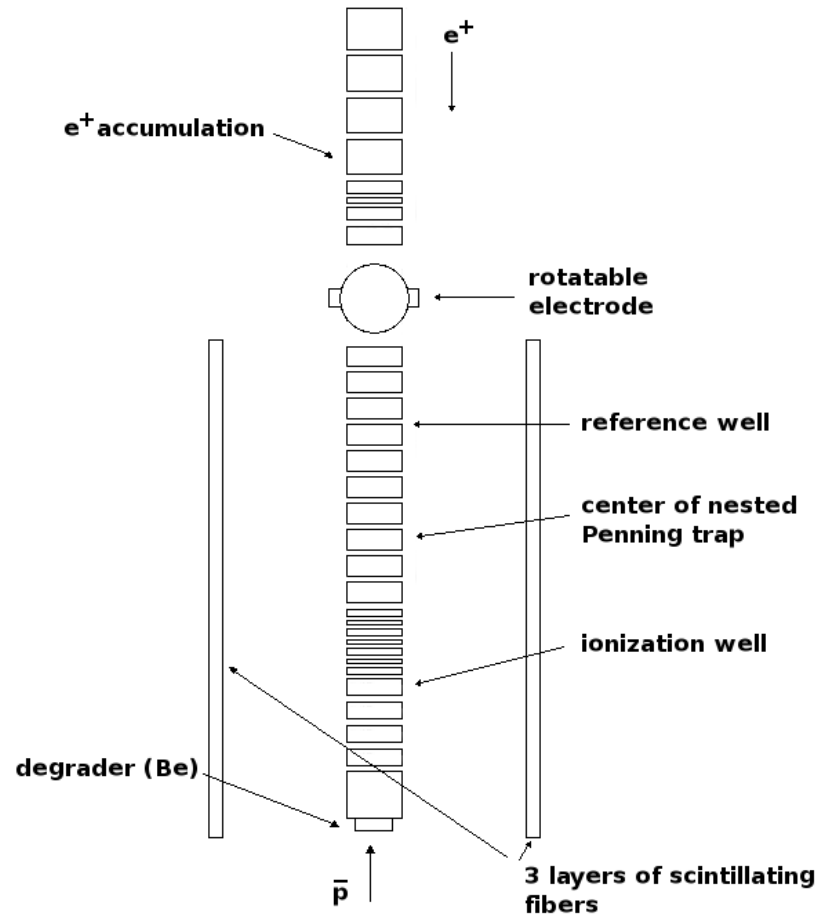


Figure 1.5: Schematic of the ATRAP trap and detector (similar as in [5]).

collected within the trap, they could be combined with antiprotons from the AD in much the same way as the ATHENA apparatus.

To detect the formed antihydrogen, ATRAP used a field ionization method. This method involves creating an electrostatic potential gradient within a region through which only neutral particles can access (Fig. 1.6). By placing this region directly adjacent to the antihydrogen mixing and formation region, a small percentage of the formed antihydrogen would drift into the ionization region. The weakly bound antihydrogen would then be ionized in the strong electric field, with the antiproton deposited in the collection well. The collected antiprotons were then counted by ramping down the confining potential and detecting the resulting annihilations in the surrounding scintillators. The number of antihydrogen atoms produced was then inferred by considering a situation where antihydrogen was produced isotropically, then calculating the total number of atoms produced given the number that were found in the collection well (a fraction of the total number determined by the solid angle the collection well occupies). An advantage of the field ionization method is that the binding energy spectrum of formed antihydrogen can be measured. Antihydrogen will only be ionized if the applied field is greater than the binding energy between the antiproton and positron. By varying the ionization potential, and thus the ionizing field, the binding energy spectrum could be obtained.

In addition to producing cold antihydrogen and measuring its energy spectrum, the ATRAP experiment also measured the velocity distribution of formed antihydrogen atoms [55]. ATRAP also demonstrated the first laser controlled production of antihydrogen through the double charge exchange process [56]:

$$Cs^* + e^+ \rightarrow Ps^* + Cs^+, \quad (1.13)$$

$$Ps^* + \bar{p} \rightarrow \bar{H}^* + e^-. \quad (1.14)$$

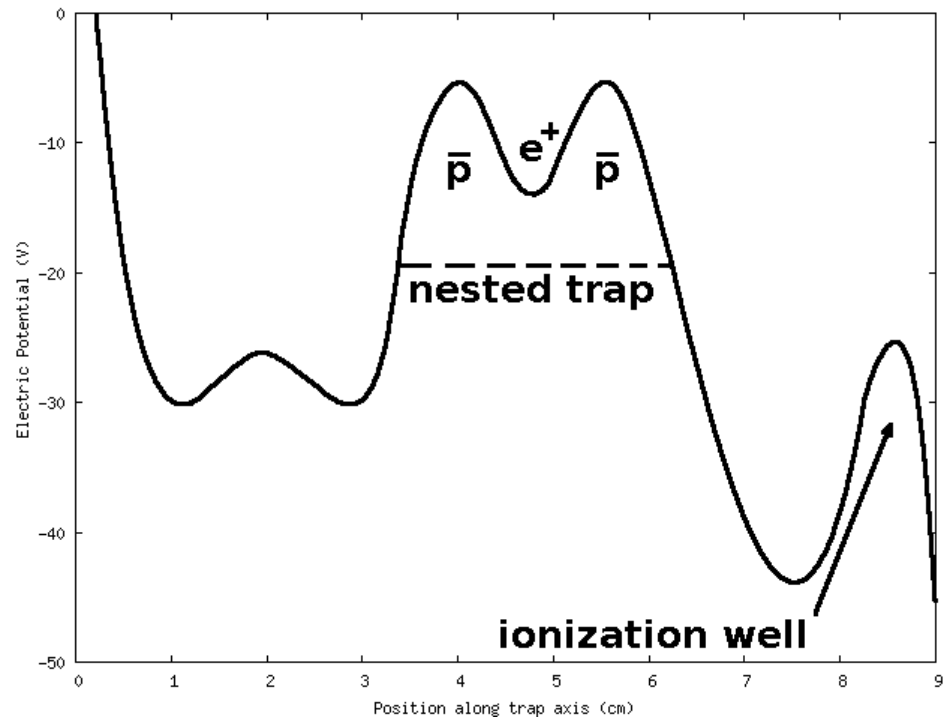


Figure 1.6: The ATRAP field ionization scheme (similar as in [5]). Highlighted are the nested trap region for the mixing of positrons and antiprotons and the ionization well, where the antiprotons from the ionized antihydrogen atoms collect.

By colliding positrons with laser-selected Cesium atoms, labelled Cs^* , excited positronium atoms, Ps^* , are produced. Then through the interaction of antiprotons with the positronium atoms, excited antihydrogen, $\bar{H}^*$, is produced. This method is attractive in that the laser controls the antihydrogen binding energy. Therefore, this technique could, in principle, produce very tightly bound antihydrogen atoms.

The ATRAP collaboration continues to produce and study antihydrogen. ATRAP built upon their existing apparatus with plans to trap and perform precision measurements on antihydrogen (as mentioned in Sec. 1.4).

1.4 Current Efforts

With the production of cold antihydrogen by both the ATHENA and ATRAP experiments, the experimental antihydrogen effort has shifted towards trapping of the produced neutral atoms. Since the antihydrogen atoms are not strongly affected by the electric fields, only a magnetic neutral atom trap will effectively confine the atoms. Neutral magnetic traps are already widely used in the trapping and study of conventional atomic systems. These traps work by superimposing a radially confining magnetic field as well as an axially confining mirror field. These fields interact with the atomic magnetic moment, μ , to produce a three-dimensional minimum potential, based on the magnetic dipole potential ($U = -\vec{\mu} \cdot \vec{B}$), where the neutral atoms can be trapped. These traps have the challenge of a very shallow well depth, given by $\mu \cdot \Delta B$, where ΔB is the difference in magnetic field between the minimum region and edge of the trap. The radially confining magnetic field is provided by a multipolar magnetic field. Although a quadrupolar magnetic field may be used due to its simplicity, higher order fields are also employed so as to reduce the magnetic perturbation near axis [57]. With such a shallow well depth, only very low-energy antihydrogen atoms will remain in the trap. This then requires that ei-

ther the antihydrogen atoms be cooled down to below the trap depth energy once formed or the antihydrogen atoms be formed at low enough energy to remain in the magnetic trap. To this end, significant effort is devoted to slowing and cooling the positrons and antiprotons before and during mixing.

The scarcity and difficulty of handling of antimatter severely limits the number of particles that can be used to form, and possibly trap, antihydrogen. Maximizing the number of antihydrogen atoms produced is important to maximize the number of antihydrogen atoms trapped. Thus, it is very important to understand the antihydrogen formation mechanisms and the environmental influence on antihydrogen production. Computer simulation is an important tool in this effort. Numerical simulations are inexpensive and quick compared to the construction and operation of a sophisticated antihydrogen apparatus. While simulations cannot replace actual experimentation, they can provide useful insight and elucidation into areas and aspects where experiments have difficulty exploring.

Two experiments are currently working towards the magnetic trapping of antihydrogen: ALPHA and ATRAP. Both experiments continue to build upon the work previously done at the AD. While ATRAP has already been discussed, ALPHA is the continuation of the ATHENA experiment, retaining much of the experience and apparatus developed through ATHENA. Both ALPHA and ATRAP are developing neutral atom traps utilizing multipolar and non-uniform magnetic fields. This thesis, however, will be confined to discussing the ATHENA and ALPHA experiments, being the experiments with which the author has worked.

This thesis will examine the production of antihydrogen shortly after the mixing of positrons and antiprotons and provide two models based on simple rate production equations. These models will be compared to experimental data collected by the ATHENA experiment. The ALPHA apparatus will also be described with emphasis on its setup

and commissioning. Details will be given about its operation and performance. Special attention will be placed on the data acquisition system and analysis program.

Chapter 2

Modelling the Short-timescale Formation of Antihydrogen

This chapter deals with the study of antihydrogen formation using numerical models. By simulating the formation behaviour of antihydrogen, it is hoped that some physical insight can be gained into aspects of the process that are either inaccessible or too difficult for experiments. The first section of this chapter outlines the motivation for pursuing numerical methods and outlines the issue to be discussed throughout this chapter. The second and third sections will describe three models, a simple “toy” model to illustrate the general concepts of the physical system and a pair of more detailed physically-motivated models, which attempt to more accurately reflect the system. Finally, a comparison between the models and experimental results will be given, along with a short conclusion.

2.1 Motivation

Antihydrogen is produced by mixing together antiprotons and positrons. The antiprotons are delivered from CERN’s Antiproton Decelerator (discussed in detail in Sec. 3.2), while the positrons are collected from the beta decay of a radioactive source (described in Sec. 3.4). The positrons cool in a strong magnetic field via synchrotron radiation to the ambient temperature of the cryogenic system (~ 15 K in the case of ATHENA). During mixing, the antiprotons will collisionally cool to the positron temperature and antihydrogen will form (through processes described in Sec. 1.2.2) on the time scale of 10’s to 100’s of milliseconds (Fig. 2.1). It can be seen from the inset in Fig. 2.1 that, immediately following the initial mixing of the antiparticles, there is a steep rise in the rate of production of antihydrogen. The antihydrogen signal is generated by the atoms that

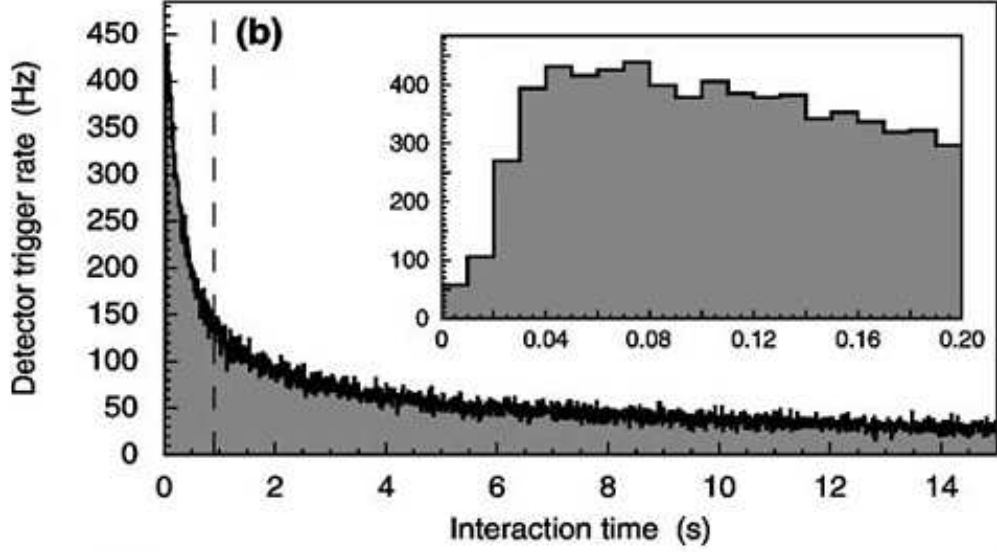


Figure 2.1: Detector trigger rate as a function of time for a typical ATHENA mixing cycle (reproduced with permission from [1]). The inset is an expansion of the graph between 0.0s and 0.2s, showing the start of antihydrogen formation.

survive ionization by the plasma and trap fields and annihilate on the trap walls. This signal peaks at about 50 ms, then quickly drops off. Since most antihydrogen experiments require a large number of atoms to be effective, it is important to understand the short-time behaviour such that the formation rate can be optimized. Also of interest is the antiparticle temperatures during formation, as this is an important parameter in the effort to magnetically trap the antihydrogen atoms. By numerically modelling the interaction between positrons and antiprotons and the formation of antihydrogen, valuable insight can be gained with regards to the physical processes involved in antihydrogen production, as well as ideas that might lead to improvements in antihydrogen production rates and reduced formation temperatures.

Detailed numerical simulations of antihydrogen formation in Penning traps are difficult given the complicated motion of charged particles in the combined electric and magnetic fields. The intricate dynamics of such a system can only be represented faithfully in full three dimensional simulations. Such a simulation would illustrate that the

Motion	Period	
	Antiproton	Positron
Cyclotron	3 ns	2 ps
Axial	$0.4 \mu\text{s}$	10 ns
Magnetron	0.1 ms	0.1 ms

Table 2.1: Periods of motion in a cylindrical Penning trap for a typical magnetic field of 3T, trap depth of 140 V and trap length of 5 cm. Descriptions and derivations given in Section 3.1.

trapped particle motion can be described in terms of a superposition of three motional modes (as well as collective degrees of freedom in the case of plasma dynamics), where the timescales of each mode differ significantly (see Table 2.1, full derivations given in Sec. 3.1). It is important to note the orders of magnitude difference between the independent periods of motion. To fully reflect the motion of a charged particle in a Penning trap using full, three-dimensional Molecular Dynamical (MD) simulations, the program could run over a number microseconds, for example, with divisions in fractions of picoseconds. This would require more than 10^9 timesteps, with each timestep involving numerous calculations depending upon the number of particles included. As the number of simulated particles increases, the computational time necessary to complete the simulations soon becomes an issue. Despite these challenges, much work has been done in regards to antihydrogen simulations. Namely, classical Monte Carlo simulations of three-body recombination and Rydberg charge exchange [58, 59, 60, 61], as well as large-scale molecular dynamical simulations of antihydrogen formation [62, 63, 64].

Given the difficulties involved in performing MD simulations and the complexity of the generated trajectories, it might instead be possible to gain some physical insight through the use of simplified theoretical models which do not involve integrating the full equations of motion. By using a simple rate-equation approach to the modelling of antihydrogen formation, the mechanisms associated with the maximal antihydrogen production over short-times ($t < 100$ ms), as well as over longer times ($t > 1$ s), can be

illuminated.

2.2 Simple Temperature Dependant Model

In order to assist with achieving a conceptual understanding of the physical processes associated with antihydrogen formation, a simple “toy” model was developed to illustrate the qualitative characteristics of the system. The dynamics of the system have been drastically simplified in order to explore the interplay of several key processes. For this reason, numerical comparisons and predictions have been deemphasized, and instead, the general shape and behaviour of the model examined. This “toy” model is presented below with more physically accurate models being outlined in Sec. 2.3 & 2.4. Some of the physically important process being suppressed in this model include the spatial decoupling of the antiproton and positron plasmas and the field ionization of weakly bound antihydrogen atoms.

The temperature dependence of the rate of antihydrogen formation has been investigated experimentally and has been shown to be significant [6]. By controlling the positron plasma temperature through RF interactions with the plasma’s axial dipole mode, it was shown that antihydrogen production decreases with the rise of the positron plasma temperature until no antihydrogen signal is seen at all (Fig 2.2). This is not surprising, as a relative thermal velocity larger than the binding energy of antihydrogen would prevent the recombination of positrons with antiprotons. Likewise, any weakly bound pairs would be quickly ionized through collisions with energetic neighboring particles.

When the positrons are free from RF interactions, they will quickly cool in the constant magnetic field through synchrotron radiation until the positron plasma reaches thermal equilibrium with the surrounding trap electrodes. When antiprotons are added to the nested trap, and the two species are allowed to mix, the antiprotons interact with

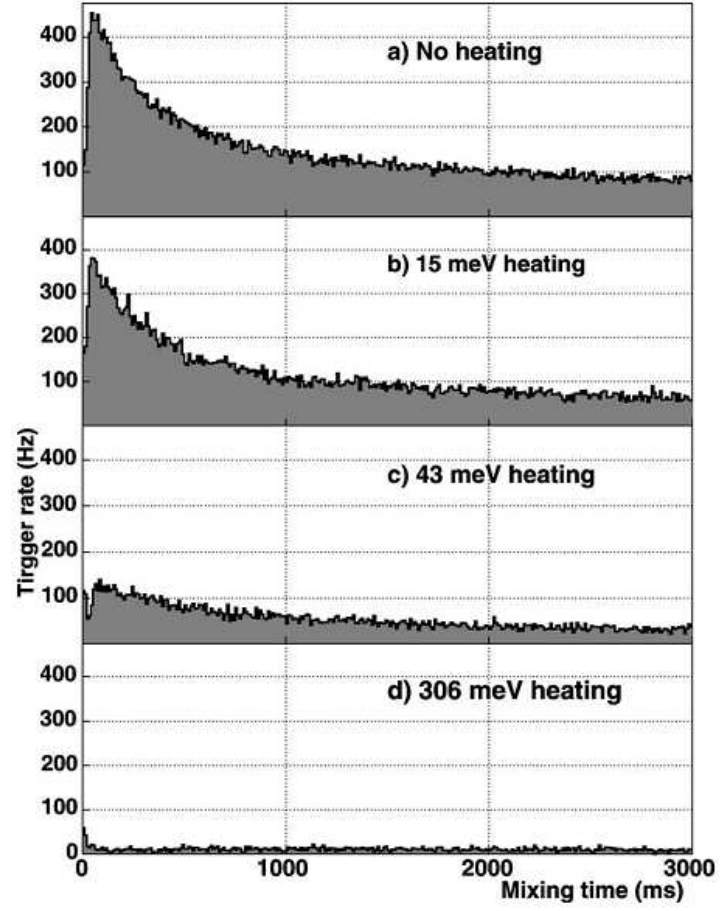


Figure 2.2: ATHENA detector rates with respect to positron heating potentials (reproduced with permission from [6]). Shown are a) with no positron heating, then b) – d) with various positron heating potentials. Clearly, the antihydrogen signal depends significantly upon positron plasma temperature.

the cold positrons and lose energy through Coulombic collisions. The change in antiproton plasma temperature will be proportional to the difference in temperatures between the positrons and antiprotons (according to Newton's Law of Cooling):

$$\frac{dT_{\bar{p}}}{dt} = -\frac{(T_{\bar{p}} - T_{e^+})}{\tau_c}, \quad (2.1)$$

where $T_{\bar{p}}$ and T_{e^+} are the antiproton and positron temperatures, respectively, and τ_c is the cooling constant. For the purposes of this model, the exchange of longitudinal and perpendicular temperatures is ignored, along with heating of the positron plasma by the higher energy antiprotons.

In the current experimental setups (including both ATHENA and ALPHA) the available positrons greatly outnumber the available antiprotons and thus the positron number can be approximated as a constant during the antihydrogen formation process and integrated into an atomic formation rate constant. The rate equation governing antihydrogen formation can then take the form:

$$\frac{dN_{\bar{H}}}{dt} = R_{\bar{H}}(N_{e^+}; T_{\bar{p}}, T_{e^+})N_{\bar{p}}, \quad (2.2)$$

where $N_{\bar{H}}$ is number of antihydrogen atoms, $N_{\bar{p}}$, the number of antiprotons, the antihydrogen production rate constant, $R_{\bar{H}}(N_{e^+}; T_{\bar{p}}, T_{e^+})$, and N_{e^+} is the (constant) number of positrons.

Antiprotons are removed from the system as they capture positrons, form antihydrogen and leave the trap. The antiproton conversion rate in this model is equal to the antihydrogen production rate, so we can write,

$$\frac{dN_{\bar{p}}}{dt} = -R_{\bar{H}}N_{\bar{p}}, \quad (2.3)$$

which has the solution, for constant $R_{\bar{H}}$,

$$N_{\bar{p}}(t) = N_{\bar{p}}^0 e^{-R_{\bar{H}}t}, \quad (2.4)$$

where $N_{\bar{p}}^0$ is the initial number of antiprotons in the system. Then Eqn. 2.4 can be substituted into Eqn. 2.2, which gives

$$\frac{dN_{\bar{H}}}{dt} = R_{\bar{H}} N_{\bar{p}}^0 e^{-R_{\bar{H}}t}. \quad (2.5)$$

This equation describes an exponentially decaying observed number of antihydrogen atoms. Such an exponential decay qualitatively follows the long-term production seen in Fig. 2.1, although experimentally, a simple exponential decay is not enough to describe the long-term production [1]. Many different mechanisms, such as the separation of the antiproton and positron plasmas, contribute to the shape of the decay of Fig. 2.1.

Given the explicit temperature dependence of the positrons and antiprotons, as well as the shape of the formation time spectrum (inset of Fig. 2.1), we might posit that the production rate varies according the plasma temperatures. Moreover, in this toy model we will make the production rate peak for the simple case of thermal equilibrium between the positron and antiproton plasmas ($T_{e^+} = T_{\bar{p}}$). To satisfy this condition, the production rate can be split into an absolute rate, and a temperature dependent factor, $P_{\bar{H}}(T_{\bar{p}}, T_{e^+})$. The production rate can then be written as:

$$R_{\bar{H}}(T_{\bar{p}}, T_{e^+}) = R'_{\bar{H}} P_{\bar{H}}(T_{\bar{p}}, T_{e^+}), \quad (2.6)$$

$$= R'_{\bar{H}} \left(1 - \frac{|T_{\bar{p}} - T_{e^+}|}{T_{\bar{p}} + T_{e^+}} \right), \quad (2.7)$$

where $R'_{\bar{H}}$ is the absolute production rate and the absolute values are to insure a positive production rate, as well as producing a maximum rate when $T_{e^+} = T_{\bar{p}}$.

Then by inserting Eqn. 2.7 into Eqn. 2.2, the production of antihydrogen atoms can be modelled as:

$$\frac{dN_{\bar{H}}}{dt} = R'_{\bar{H}} \left(1 - \frac{|T_{\bar{p}} - T_{e^+}|}{T_{\bar{p}} + T_{e^+}} \right) N_{\bar{p}}. \quad (2.8)$$

Together with Eqn. 2.1, the system can be solved numerically by discretizing the two equations and evolving the system iteratively. Labeling the timestep n and partitioning the temperatures and numbers of particles, the system can be written as:

$$N_{\bar{H}}^{n+1} = N_{\bar{H}}^n + R'_{\bar{H}} \left(1 - \frac{|T_{\bar{p}}^n - T_{e^+}^n|}{T_{\bar{p}}^n + T_{e^+}^n} \right) N_{\bar{p}}^n, \quad (2.9)$$

$$T_{\bar{p}}^{n+1} = T_{\bar{p}}^n - \frac{(T_{\bar{p}}^n - T_{e^+}^n)}{\tau_c}. \quad (2.10)$$

As we have now developed a simple model system, we can now use it to improve our understanding of how each input parameter influences the antihydrogen production curve. Figures 2.3 through 2.6 show the results of the Simple Model where the model parameters are being varied. First, the antihydrogen production temporal spectrum is shown for τ_c varied between 2-5 ms (Fig. 2.3). This shows clearly that the production onset (and the time for the production to peak) is related to τ_c (the antiproton cooling constant). This is what might be expected given the assumption of a peaked rate for the thermal equilibrium between positrons and antiprotons. For large cooling constants, the antiprotons will take longer to reach an equilibrium with the positrons and it will therefore take longer for the antihydrogen production to peak. Next, the antihydrogen formation is shown with varying numbers of antiprotons, $N_{\bar{p}}$ (Fig. 2.4). The antihydrogen production temporal spectrum is shown for antiproton numbers between 1500 and 15000, and what can be seen is a relationship between the number of antiprotons and the amplitude of the antihydrogen production. Since, for this model, the antihydrogen production rate is directly related the number of antiprotons, an increase in the number of antiprotons

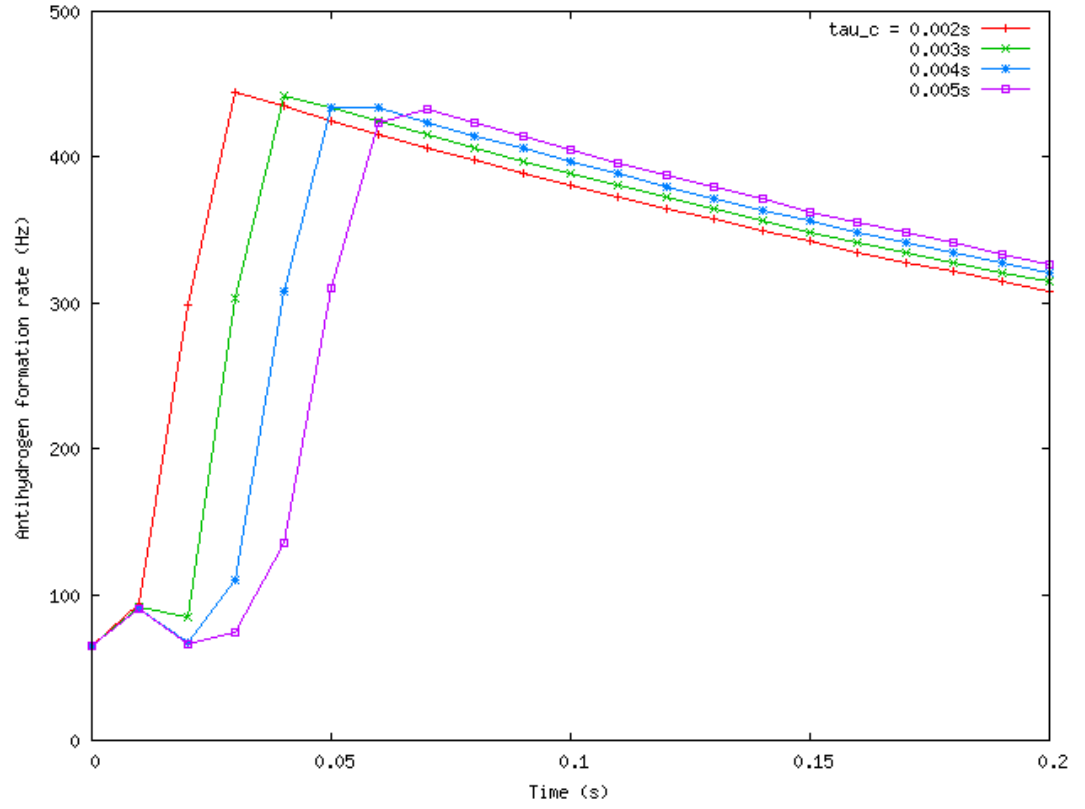


Figure 2.3: Results of the Simple Model with varying antiproton cooling constants, τ_c (in colour). The lines are to guide the eye.

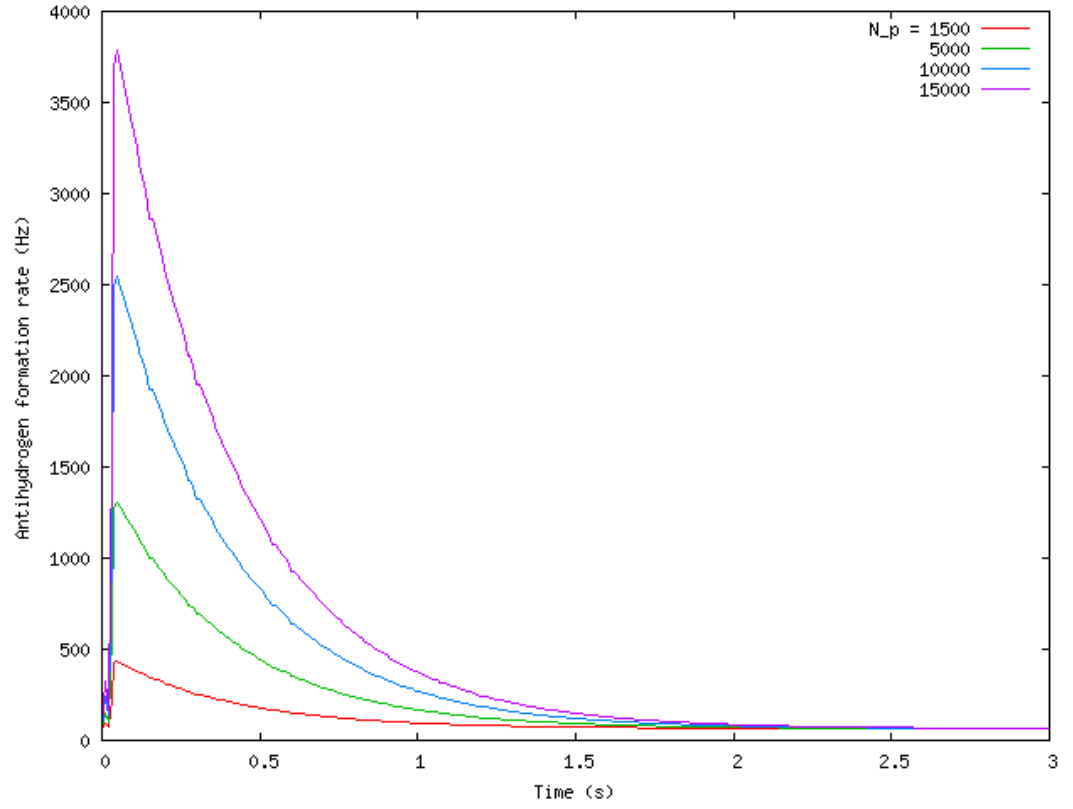


Figure 2.4: Results of the Simple Model with varying numbers of antiprotons, N_p (in colour). The lines are to guide the eye.

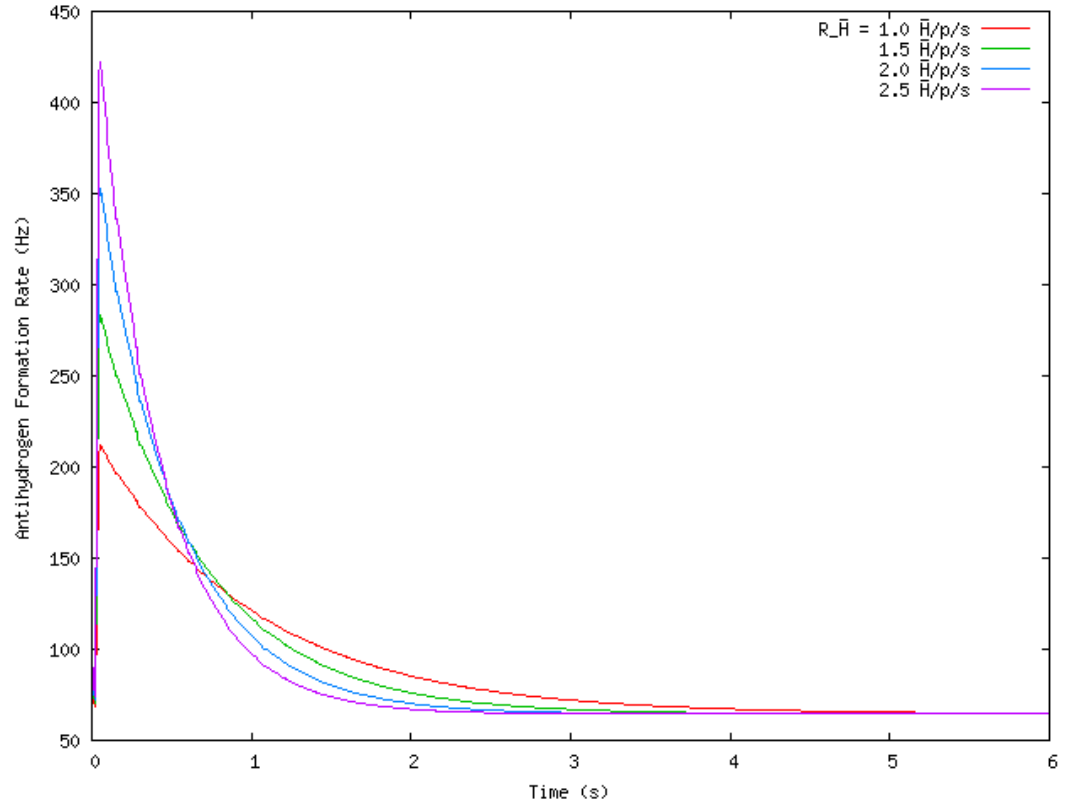


Figure 2.5: Results of the Simple Model with varying antihydrogen rate constants, $R_{\bar{H}}$ (in colour). The lines are to guide the eye.

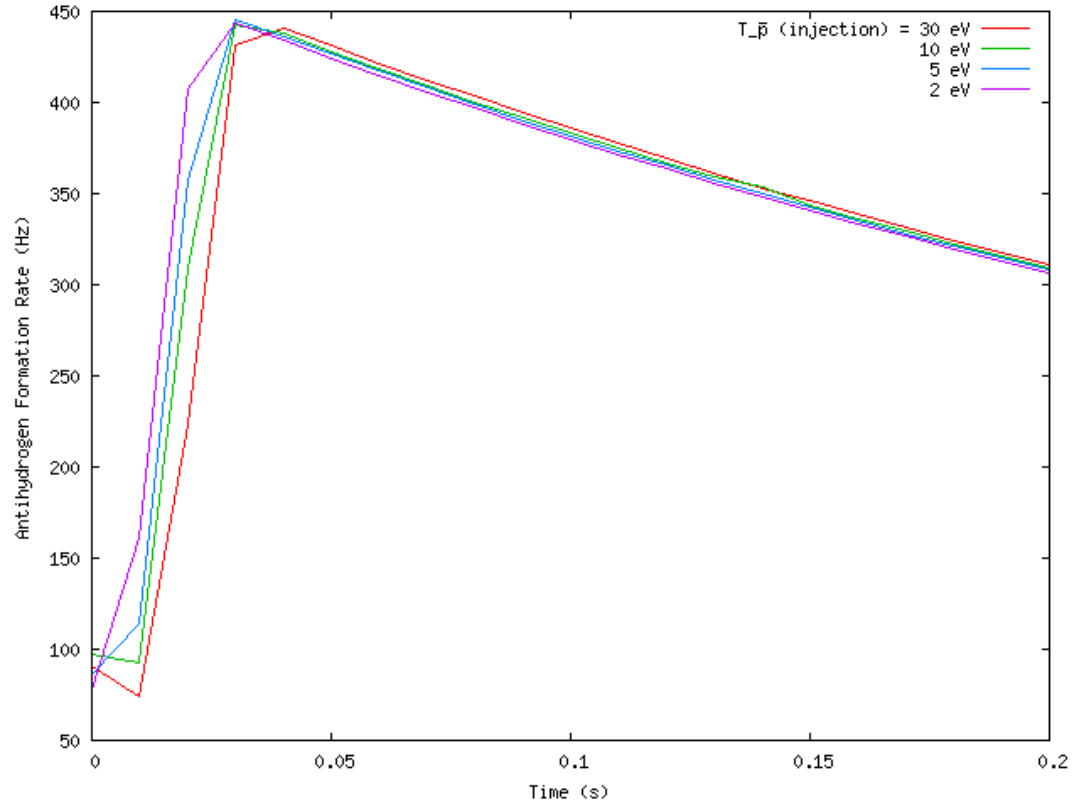


Figure 2.6: Results of the Simple Model with varying antiproton injection energies, $T_{\bar{p}}$ (in colour). The lines are to guide the eye.

should consequently increase the number of antihydrogen atoms formed.

Figure 2.5 gives the results of the Simple Model where the antihydrogen production rate constant ($R_{\bar{H}}$) is varied from 1.0 $\bar{H}/p/s$ to 2.5 $\bar{H}/p/s$ with the other model parameters held constant. As expected, for larger production rates the initial antihydrogen production is more pronounced, but falls off more quickly as the antiprotons are swiftly depleted. Likewise, lower production rates have a shorter rise accompanied by a longer tail, with more antiprotons available for antihydrogen formation. Finally, Fig. 2.6 shows the short-time antihydrogen spectrum as the initial antiproton energy is varied between 2-30 eV. As the antiproton injection energy is lowered, the peak of antihydrogen production comes increasingly earlier. This is due to the smaller relative energy between the positron and antiproton which results in the antiprotons taking less time to reach an equilibrium with the positrons. This effect is strongly coupled to the antiproton cooling constant set by τ_c , as this parameter also determines how quickly the antiprotons will cool to the positrons.

So we have illustrated that the four parameters of the Simple Model can be used to manipulate the antihydrogen production curve, with the number of antiprotons controlling the magnitude, the cooling constant and production rate together controlling the shape of the curve in terms of maximum production and rate of production increase and decay, and initial antiproton injection energy influencing the initial production rate. With this knowledge, we can now move on to attempt to match the model curve with the experimentally-observed results from ATHENA. Figure 2.7 shows the short-time antihydrogen formation (0.0–0.2 s) compared with the ATHENA values, while Fig. 2.8 shows the long-time simulation results. Table 2.2 summarizes the initial and fitted values for Figures 2.7 and 2.8.

In this model, the background rate is an added constant value that is applied to each time bin and which vertically offsets the graph as a whole. The fitted background

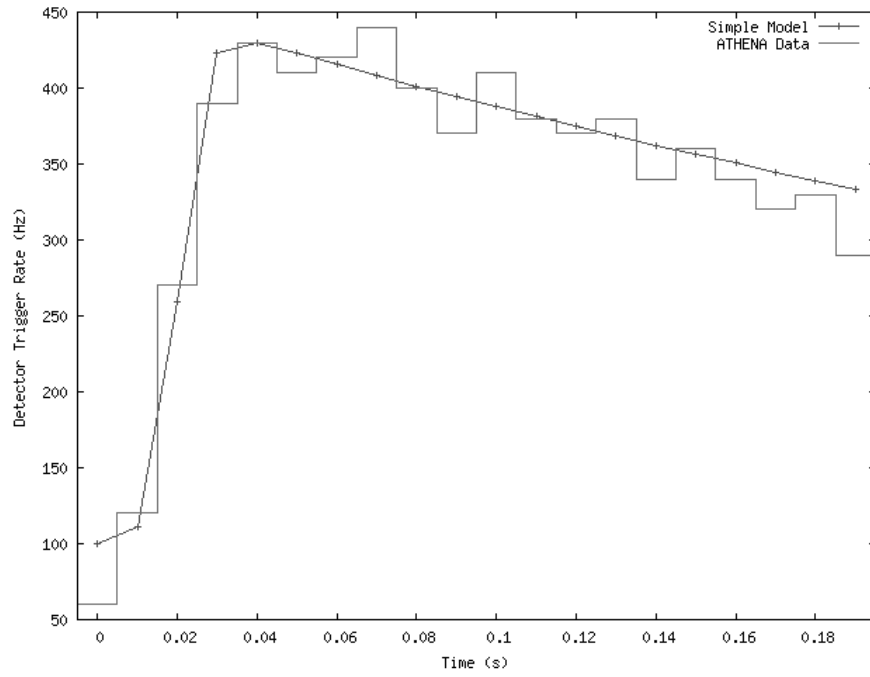


Figure 2.7: Comparison of the Simple Model (Eqn. 2.9) to ATHENA results (Fig. 2.1) over 0.0–0.2 s. The simulation results are shown as the solid lines, while the ATHENA values are given as histogram bars.

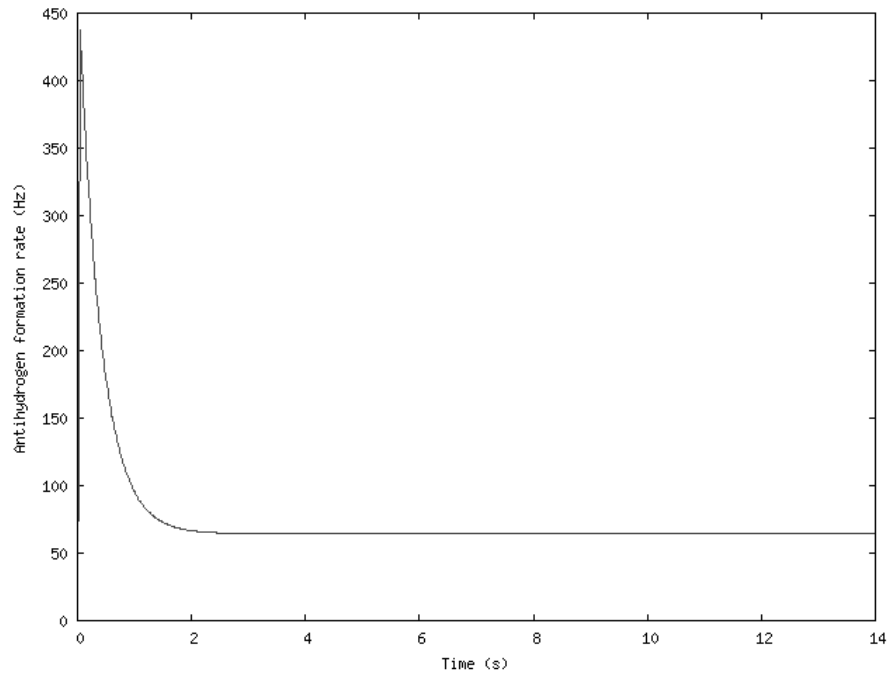


Figure 2.8: Results of the Simple Model over 0.0–14.0s.

Initial Values		Fit Parameters	
$T_{\bar{p}}$	30 eV	$N_{\bar{p}}$	$(1.5 \pm 0.7) \times 10^3$
T_{e^+}	15 K	τ_c	$(3.20 \pm 0.01) \times 10^{-3}$ s
N_{e^+}	10^8	Background	(67 ± 4) Hz
		$R'_{\bar{H}}$	$(2.61 \pm 0.02) \bar{H}/\bar{p}/s$
		$\tilde{\chi}^2$	11.9

Table 2.2: Initial values (ATHENA values [1]) and fitted parameters for the Simple Model. Descriptions of parameters given in the text. Errors in the values are due to the systematics of the fitting routine, reflecting the constraints on the $\tilde{\chi}^2$ minimization.

rate for the simple model was found to be (67 ± 4) Hz, and would be interpreted as a constant antihydrogen production rate of 67 Hz regardless of the number of antiprotons present in the system or the plasma temperatures. It can be seen from Fig. 2.8 that after ~ 2 s, it is only the background rate contributing to antihydrogen production. This is unsatisfying, as this background value is completely physically unmotivated within this toy model, and is treated largely as a fitting parameter. This is the most obvious drawback of the Simple Model, along with the difficulty in physically interpreting the temperature dependent production rate, $P_{\bar{H}}(T_{\bar{p}}, T_{e^+})$. While this factor was motivated by the temperature dependence of antihydrogen production, which requires a peaking formation rate, the mathematical form is largely arbitrary and provides little physical insight into the process involved during antihydrogen production. Given the simplified and unphysical nature of the model, it is difficult to draw any conclusions from the parameters extracted from this model. However, it should be noted that the model reproduces the general qualitative behaviour seen in the antihydrogen signal.

2.3 Inverse Velocity Model

The previous section provides a simple, almost naïve, toy model of antihydrogen formation based on the assumption of a maximum production rate when $T_{e^+} = T_{\bar{p}}$. While retaining the simplicity of the rate equation approach, this section will improve upon the

model and provide a more physical rate equation.

The ATHENA apparatus operated at an ambient temperature of 15 K (provided experimentally by a liquid helium cryostat). Positrons will spontaneously radiate down to the ambient temperature in the large applied magnetic field and the antiprotons will lose energy through Coulombic collisions with the positrons. Emulating a typical ATHENA experimental procedure, the positrons in the model are initially at the ambient temperature before being interacted with the antiprotons. In the previous model, the positron temperature was assumed to remain at the ambient temperature throughout the mixing process. In reality, the energy transfer between antiprotons to positron during the cooling of antiprotons will contribute to an increase of thermal energy of the antiprotons. This can be included through the change in positron temperature as follows:

$$\frac{dT_{e^+}}{dt} = \frac{N_{\bar{p}}}{N_{e^+}} \frac{1}{\tau_c} (T_{\bar{p}} - T_{e^+}) - \frac{(T_{e^+} - T_t)}{\tau_e}, \quad (2.11)$$

where T_t is the ambient temperature ($T_t = 15$ K) and τ_e is the time constant for synchrotron cooling of the positrons. Figure 2.9a) shows the antiproton temperature over the 0.0–0.2s time range from an initial temperature of 30 eV (3.5×10^5 K), and Fig. 2.9b) shows the positron temperature over the same range with an initial positron temperature of 15 K.

We might then consider antihydrogen formation due to spontaneous radiative recombination, as discussed in Section 1.2.2. Recalling the radiative recombination cross-section (Eqn. 1.5), we see that the cross-section is inversely proportional to the center of mass energy, which in turn is proportional to the square of the mean velocity ($\sigma_{SRR} \propto 1/v^2$). The recombination rate per antiproton can be written as $R_{\bar{H}} = \sigma v n_{e^+}$, where n_{e^+} is the positron density [65]. Thus, the recombination rate is inversely propor-

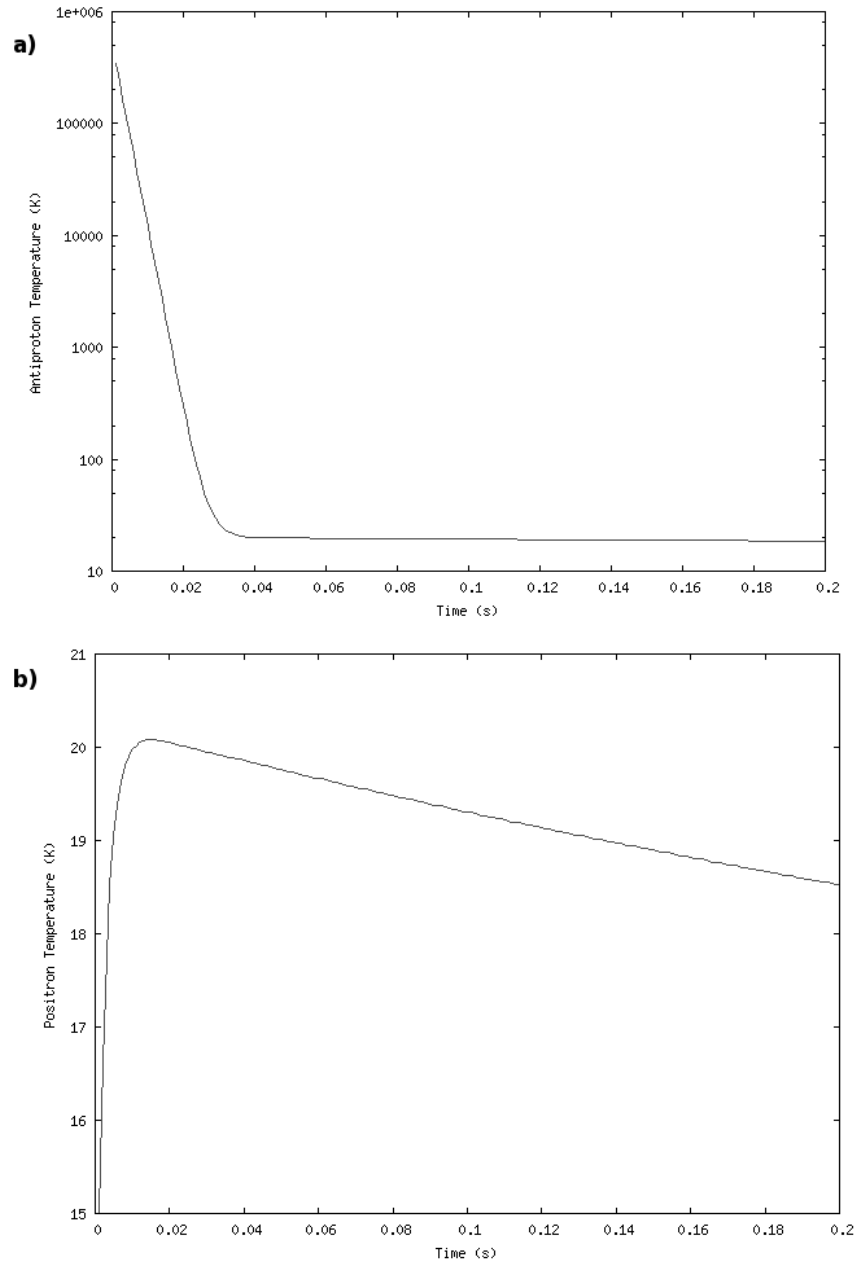


Figure 2.9: Modelled antiparticle temperatures over 0.0–0.2s, a) is the antiproton temperature, and b) is the positron temperature. The initial antiproton temperature is 30 eV (3.5×10^5 K) and the initial positron temperature is 15 K.

tional to the velocity:

$$R_{\bar{H}}(T_{\bar{p}}, T_{e^+}) \propto v(T_{\bar{p}}, T_{e^+})^{-1}, \quad (2.12)$$

where we consider the thermal velocities of the particles,

$$v(T) = \sqrt{\frac{k_B T}{m}}, \quad (2.13)$$

where k_B is Boltzmann's constant, T is the absolute temperature and m is the mass of the particle.

Again, we consider the production of antihydrogen atoms per antiproton (Eqn. 2.2). Although the antiproton velocity is a dynamic quantity, the positron velocity is also considered to keep the production rate finite in the asymptotic limit as $T_{\bar{p}} \rightarrow 0$. The antihydrogen production equation for this model can then be written as:

$$\frac{dN_{\bar{H}}}{dt} = R'_{\bar{H}} \frac{v_0}{\sqrt{\frac{k_B T_{\bar{p}}}{m_{\bar{p}}} + \frac{k_B T_{e^+}}{m_{e^+}}}} N_{\bar{p}}, \quad (2.14)$$

where v_0 is the velocity normalization factor,

$$v_0 = \sqrt{\frac{k_B T_t}{m_{\bar{p}}} + \frac{k_B T_t}{m_{e^+}}}, \quad (2.15)$$

$$= \sqrt{k_B T_t \left(\frac{1}{m_{\bar{p}}} + \frac{1}{m_{e^+}} \right)}, \quad (2.16)$$

with $T_t = 15$ K, the ambient temperature of the apparatus. This equation can be discretized in the same way as Eqn. 2.8:

$$N_{\bar{H}}^{n+1} = N_{\bar{H}}^n + R'_{\bar{H}} \frac{v_0}{\sqrt{\frac{k_B T_{\bar{p}}^n}{m_{\bar{p}}} + \frac{k_B T_{e^+}^n}{m_{e^+}}}} N_{\bar{p}}^n, \quad (2.17)$$

Initial Values		Fit Parameters		
$T_{\bar{p}}$	30 eV	$N_{\bar{p}}$	2.0	$\pm 0.1 \times 10^3$
T_{e^+}	15 K	τ_c	3.20	$\pm 0.01 \times 10^{-3}$ s
T_t	15 K	Background	53	± 4 Hz
N_{e^+}	10^8	$R'_{\bar{H}}$	2.25	± 0.01 $\bar{H}/\bar{p}/s$
τ_e	0.5 s	$\tilde{\chi}^2$	7.5	
v_0	352 m/s			

Table 2.3: Initial values (ATHENA values [1]) and fitted parameters for the Inverse Velocity Model. Descriptions of parameters given in text. Errors in the values are due to the systematics of the fitting routine, reflecting the constraints on the $\tilde{\chi}^2$ minimization.

and the change in antiproton and positron temperatures:

$$T_{e^+}^{n+1} = T_{e^+}^n + \frac{N_{\bar{p}}^n}{N_{e^+}^n} \frac{1}{\tau_c} (T_{\bar{p}}^n - T_{e^+}^n) - \frac{(T_{e^+}^n - T_t)}{\tau_e}, \quad (2.18)$$

$$T_{\bar{p}}^{n+1} = T_{\bar{p}}^n - \frac{(T_{\bar{p}}^n - T_{e^+}^n)}{\tau_c}, \quad (2.19)$$

where τ_e is the positron synchrotron cooling constant, and τ_c is the characteristic cooling constant between the positrons and antiprotons. Then using the initial values given in Table 2.3 and minimizing the $\tilde{\chi}^2$ between the simulation and ATHENA values over the 0.0–0.2s range, the fitted values in Table 2.3 were found.

Fitting results for the Inverse Velocity Model are give in Table 2.3. The number of antiprotons, $N_{\bar{p}} = 2.0 \pm 0.1 \times 10^3$, is an order of magnitude smaller than the typical number of antiprotons in an ATHENA production cycle ($\sim 10^4$ antiprotons). This discrepancy might possibly be the result of the model not taking into consideration processes that affect the interaction between positrons and antiprotons. For example, weakly bound antihydrogen can be field ionized and the antiprotons ‘recycled’ back into the system. In terms of this model, this effect would cause the number of antiprotons needed to increase as fewer antihydrogen atoms would be produced per antiproton. The exclusion of such processes consequently lowers the number of antiprotons required by the model.

The antiproton cooling constant, $\tau_c = (3.20 \pm 0.01) \times 10^{-3}$ s is reasonable considering

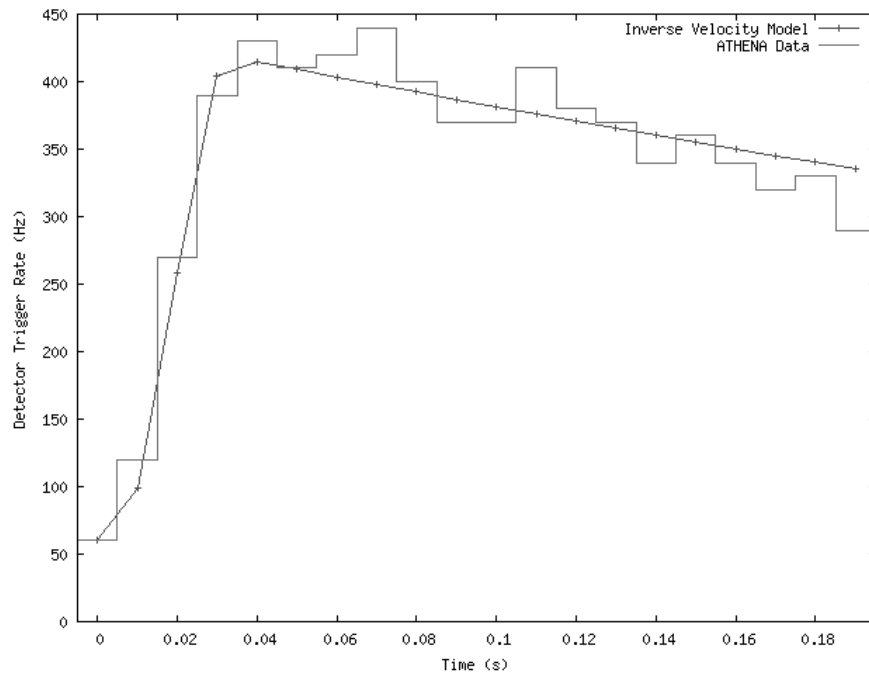


Figure 2.10: Comparison of the Inverse Velocity Model to ATHENA results [1]. The solid line shows the values produced with the Inverse Velocity Model (Table 2.3), while the bar graph shows the corresponding ATHENA values (Fig. 2.1).

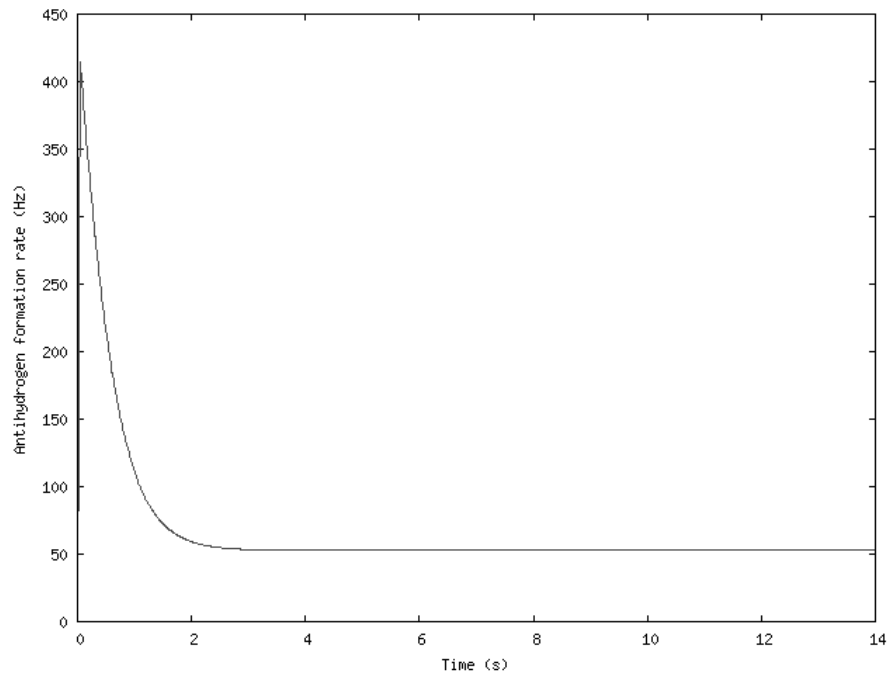


Figure 2.11: Results of the Inverse Velocity Model over 0.0–14.0 s.

the millisecond timescale of onset of antihydrogen production. However, the background rate (53 ± 4 Hz) does not reflect the ATHENA situation, where the background rate was measured to be ~ 1 Hz. This indicates that there is some physical process absent from the model that would account for this discrepancy in the background rate. One possibility is the radial decoupling of antiprotons and positrons, wherein the two plasmas radially separate and weakly interact to form antihydrogen over a longer timescale. A process which forms antihydrogen at a slower, but constant, rate over a long time interval (such as radial decoupling) would make the addition of a background rate into the model unnecessary.

2.4 Scaled Inverse Velocity Model

Experimentally, antihydrogen does not seem to follow a simple temperature scaling [6]. We might then look at how our model is affected by changing the scaling. Starting with the Inverse Velocity Model, we might add a velocity scaling factor, η onto Eqn. 2.12:

$$R_{\bar{H}}(T_{\bar{p}}, T_{e+}) \propto v(T_{\bar{p}}, T_{e+})^{-\eta}. \quad (2.20)$$

The production of antihydrogen is then written as (similar to Eqn. 2.14),

$$\frac{dN_{\bar{H}}}{dt} = R'_{\bar{H}} \left(\frac{v_0}{v(T_{\bar{p}}, T_{e+})} \right)^\eta N_{\bar{p}}, \quad (2.21)$$

where

$$v(T_{\bar{p}}, T_{e+}) = \sqrt{\frac{k_B T_{\bar{p}}}{m_{\bar{p}}} + \frac{k_B T_{e+}}{m_{e+}}}, \quad (2.22)$$

and $v_0 = v(T_t, T_t)$.

By including η as a parameter and minimizing $\bar{\chi}^2$, we can find fitted values of $\eta = 0.63$, with $\bar{\chi}^2 = 4.11$ (Table 2.4). The comparison of the model to the ATHENA values is shown

Initial Values		Fit Parameters		
$T_{\bar{p}}$	30 eV	$N_{\bar{p}}$	$1.6 \pm 0.1 \times 10^3$	
T_{e^+}	15 K	τ_c	$9.4 \pm 0.3 \times 10^{-3}$ s	
T_t	15 K	Background	0 ± 4 Hz	
N_{e^+}	10^8	η	0.63 ± 0.01	
τ_e	0.5 s	$R'_{\bar{H}}$	4.30 ± 0.05 $\bar{H}/\bar{p}/s$	
v_0	352 m/s	$\tilde{\chi}^2$	4.11	

Table 2.4: Initial values (ATHENA values [1]) and fitted parameters for the scaled inverse velocity model (Fig. 2.12). Descriptions of parameters given in text. Errors in the values are due to the systematics of the fitting routine, reflecting the constraints on the $\tilde{\chi}^2$ minimization.

as Fig. 2.12, and the long-time results given as Fig 2.13.

The Scaled Inverse Velocity Model results in a $\tilde{\chi}^2$ of 4.11 (over the 0.0–0.2s range), which is an improvement over both the Inverse Velocity Models. This improvement is due to a closer agreement between the simulation and experimental results just after the rate peaks (between 0.05–0.20s). This model predicts roughly the same number of antiprotons, $N_{\bar{p}} = (1.6 \pm 0.1) \times 10^3$, as the previous models. However, the antiproton cooling constant, $\tau_c = (9.4 \pm 0.3 \times 10^{-3})$ s, and production rate, $R'_{\bar{H}} = (4.30 \pm 0.05)$ $\bar{H}/\bar{p}/s$, are different, although of the same order of magnitude. These differences are due to the inclusion of η as a scaling factor on the temperature dependent production factor. The fitted scaling factor was found to be $\eta = 0.63 \pm 0.01$, which in the model represents a temperature scaling of $T^{-0.63 \pm 0.01}$, and is close to the experimentally determined temperature scaling of $T^{-0.7 \pm 0.2}$ [6].

Over 0.0–0.2 s, the Background rate was found to be 0 ± 4 Hz. While the lack of background rate is convenient over the short timescale where it is tempting to try to describe antihydrogen production without the addition of a constant background rate. However, as shown in Fig. 2.13, without the constant background rate the antihydrogen production rate falls off to zero after about 2 s. This deviation implies that these models are inadequate in their description of the long-term antihydrogen formation seen

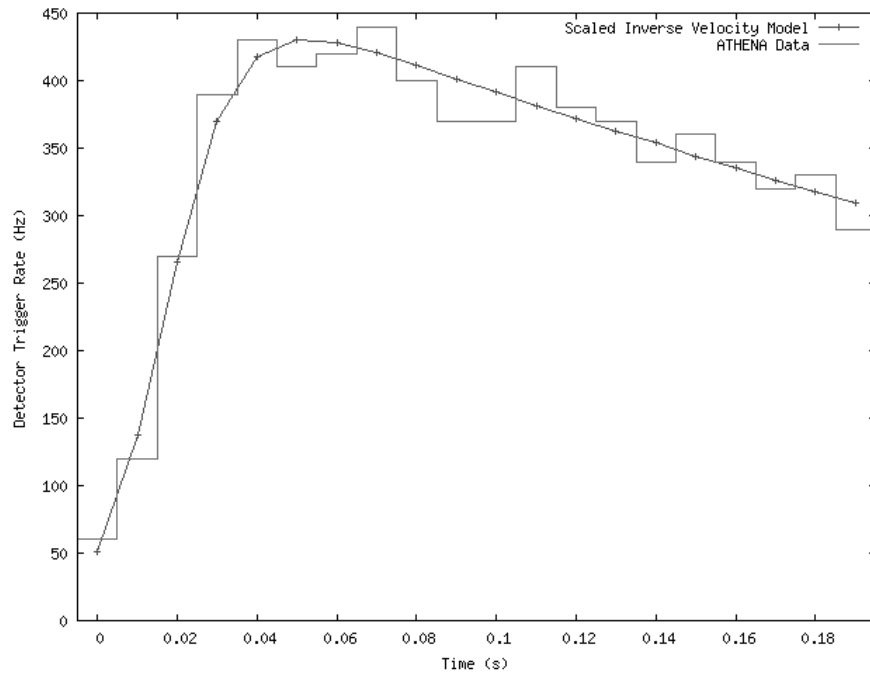


Figure 2.12: Comparison of Scaled Inverse Velocity Model (Eqn. 2.21) to ATHENA results [1]. Initial values and fitted parameters given in Table 2.4.

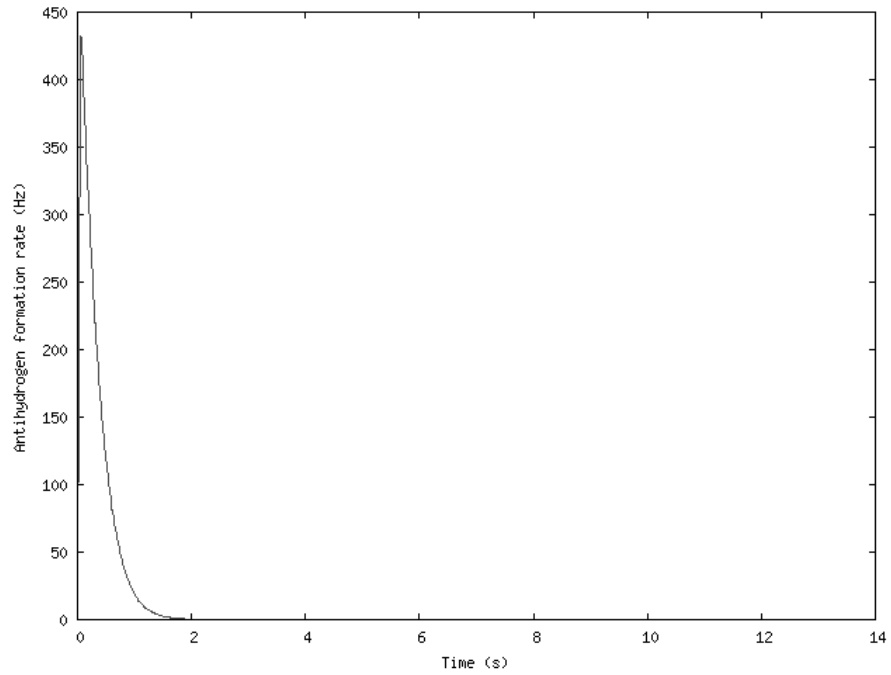


Figure 2.13: Results of the Scaled Inverse Velocity Model over 0.0–14.0 s.

experimentally (Fig. 2.1). Without a more sophisticated representation of the particle dynamics in the mixing region, it is difficult to model both the short and long timescale antihydrogen production. However, given the goal of producing a simple system to model the short-time antihydrogen production behaviour, and the exclusion of many long-time effects, the poor agreement over longer times is neither surprising nor concerning.

2.5 Chapter Summary & Model Comparison

Fig. 2.14 shows the results of all three models along with the ATHENA values. All three models follow the same general behaviour as seen in ATHENA, that is, a sharp rise in formation until about 0.05 s after mixing, when the rate starts to decrease. The commonality between the models that would account for this behaviour is the thermal equilibration between the positron and antiproton plasmas. As the higher-energy antiprotons cool to the positrons, antihydrogen production is more likely as the positron and antiproton energies become comparable.

The Simple Temperature Dependant Model (Sec. 2.2) is used to motivate the more physical models and illustrate the interplay of antihydrogen formation processes. While this model is less useful for qualitative analysis, it is interesting in that the antihydrogen annihilation can be reproduced with very few assumptions.

The Inverse Velocity Model (Sec. 2.3) is a better description in terms of physical processes, with the efficiency of positron capture scaling as the inverse positron velocity. Just as with the Simple Model, to match the ATHENA data, a constant background rate is required, and similar to all three models, the calculated initial number of antiprotons is well below that present in the ATHENA experiment.

The Scaled Inverse Velocity Model (Sec. 2.4) provides a better quantitative fit to the ATHENA values ($\bar{\chi}^2 = 4.11$), but again, is difficult to interpret. The scaling term, $\eta =$

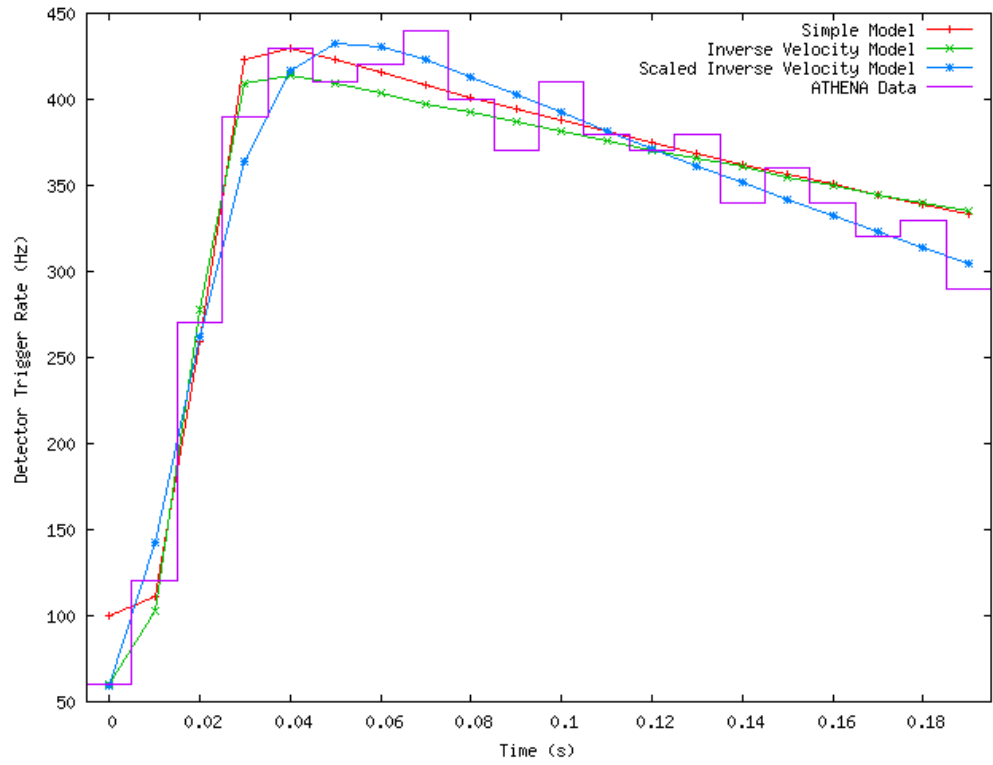


Figure 2.14: Three antihydrogen formation models: the Simple Temperature Dependant Model (Sec. 2.2), the Inverse Velocity Model (Sec. 2.3), and the Scaled Inverse Velocity Model (Sec. 2.4). Also shown are the ATHENA values [1]. Solid lines are to guide the eye.

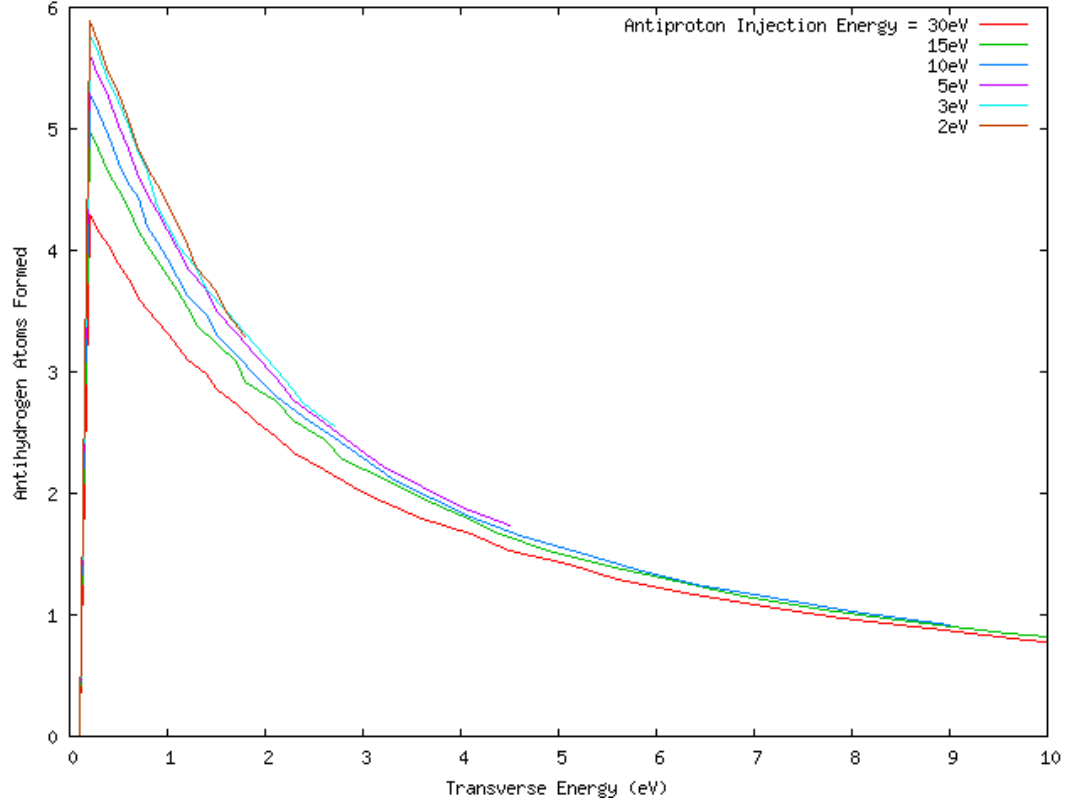


Figure 2.15: Antihydrogen formed as a function of final transverse energy. Values calculated using the Scaled Inverse Velocity Model and the various curves (in colour) show varying antiproton injection energies. The axial antihydrogen energy is taken to be that of the antiproton during positron capture.

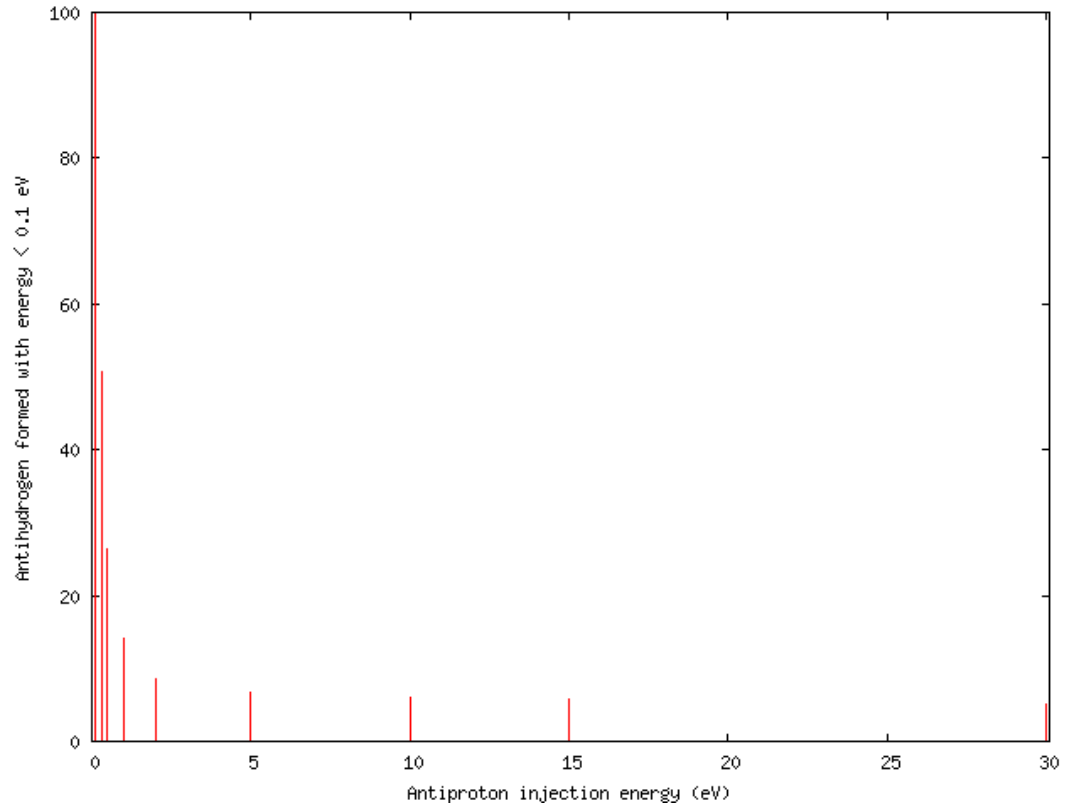


Figure 2.16: Percent of antihydrogen atoms formed with transverse energy less than 0.1 eV for varying antiproton injection energies.

0.63, added to the temperature dependent production factor provides a result for which a physical interpretation is difficult. Moreover, the long-time antihydrogen production rate does not follow the ATHENA result and calls into question the validity of using rate equations to model both short and long time antihydrogen formation.

These simulations can also be used to give an estimate of other parameters important to the study of antihydrogen. Fig. 2.15 shows the amount of antihydrogen formation as a function of the resulting transverse antihydrogen energy. This calculation assumes that the antihydrogen atoms are formed at the velocity of the capturing antiprotons and uses the Scaled Inverse Velocity Model to produce values for the number of antihydrogen atoms formed. The transverse energy (which is related to the velocity) is then compared to the number of antihydrogen atoms. Figure 2.16 then shows the percentage of antihydrogen atoms that form with transverse energies less than 0.1 eV as a function of antiproton injection energy. What can be seen is that a small fraction (about 5.2% < 0.1 eV with an antiproton injection energy of 30 eV) of the produced antihydrogen atoms are formed with small transverse energies, although reduction of the injection energy can significantly increase this fraction. This is important, given that for neutral atom trapping, the atoms must be of very low-energy to remain in the shallow magnetic trap. Therefore, a large component of current ALPHA efforts are focused on minimizing the positron and antiproton temperatures before mixing is initiated.

Simulations do not, and cannot, replace experiments. They can, however, provide some insight as to the physical processes involved as well as guidance as to what to expect, or what to look for when conducting experiments. The ALPHA project is one such experiment with the goal of producing and studying antihydrogen. As the methods employed by ALPHA are very similar to those of ATHENA, these simulations may help to elucidate some of the process and results encountered.

Chapter 3

The ALPHA Apparatus

The ALPHA experiment employs an unique and versatile apparatus that combines many state-of-the-art technologies to produce and study antihydrogen (Fig. 3.1). This chapter will outline some of the technologies and techniques and describe the function of some of the major components in this novel apparatus. First, the dynamics of a charged particle in a Penning trap will be examined with emphasis on the harmonic nested trap configuration. Then the Antiproton Decelerator and its method of slowing and cooling antiprotons will be described. The technique used to catch and cool antiprotons in the experimental apparatus will be outlined, along with the method of removing the intermediary electrons used for cooling. Finally, the positron accumulation system is briefly described.

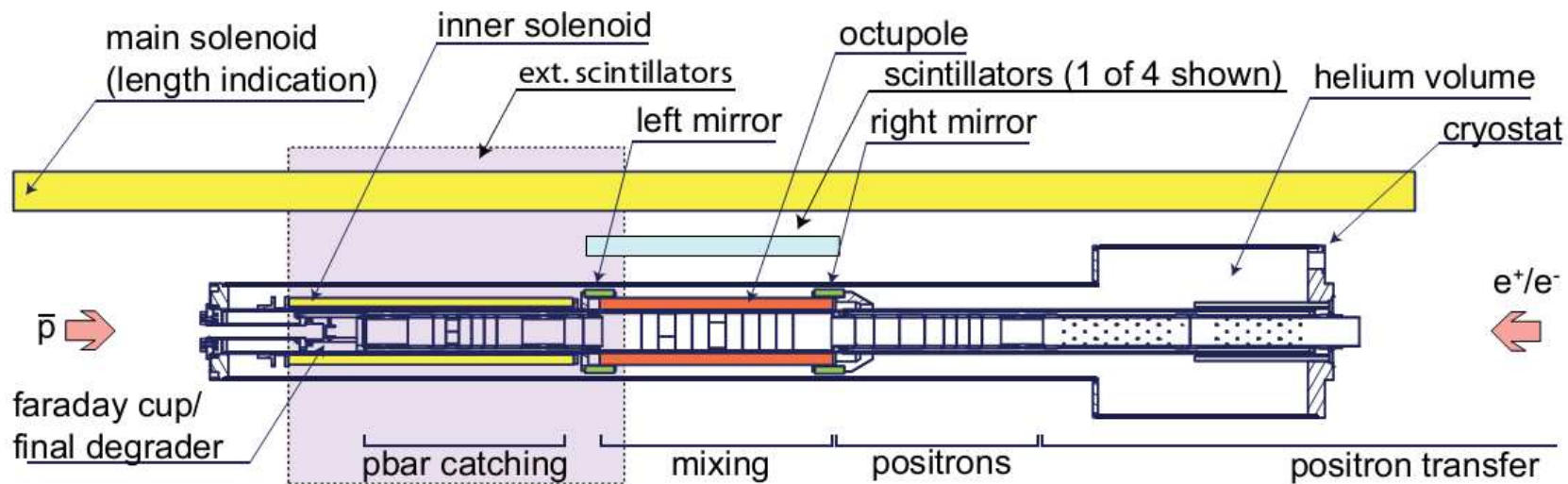


Figure 3.1: Schematic of the ALPHA apparatus (reproduced with permission from [7]). Shown is the trapping region containing the antiproton catching, mixing and positron traps. Also shown is the large external solenoid and internal inhomogeneous superconducting magnets.

3.1 Penning Traps

Integral to the the study of antiparticles is the ability to confine and manipulate the antiparticles without destructive interactions with normal matter. The use of static electric and magnetic fields then becomes critical, since electric and magnetic fields can be used similarly on matter and antimatter without risking annihilation. Moreover both positrons and antiprotons can be trapped by using appropriate electromagnetic potentials.

Charged particles in electric and magnetic fields experience the Lorentz force,

$$\vec{F} = q(\vec{E} + \vec{v} \times \vec{B}), \quad (3.1)$$

where q is the charge of the particle (or antiparticle), $\vec{E}$ is the applied electric field, $\vec{v}$ is the velocity of the particle and $\vec{B}$ is the magnetic field. A typical Penning trap features a homogeneous magnetic field along the trap axis, which we define to be the $\hat{z}$ direction, and thus $\vec{B} = B\hat{z}$. A moving charged particle (or antiparticle) will orbit around the magnetic field lines, trapping the particle in the $x - y$ plane. However, this magnetic field has no effect on the z -component of motion, so we need to apply an additional electric field to trap the particle in the z -direction. This electric trapping field can be written in terms of a time independent scalar potential Φ as $\vec{E} = -\vec{\nabla}\Phi$. To provide the necessary z -directional trapping in the case of a harmonic trap, we use the potential

$$\Phi(x, y, z) = \frac{V_0}{2d^2}(2z^2 - x^2 - y^2), \quad (3.2)$$

where V_0 is the applied trap voltage and d is the characteristic trap length. The equation of motion for a particle with mass m in the trap can then be written with as

$$m \frac{d^2 \vec{r}}{dt^2} = q(-\vec{\nabla}\Phi(\vec{r}) + B \frac{d\vec{r}}{dt} \times \hat{z}), \quad (3.3)$$

with Φ and B as given in Eqns. 3.1 and 3.2, respectively. By defining the cyclotron frequency, $\omega_c = \frac{qB}{m}$, and the axial frequency, $\omega_z = \sqrt{\frac{qV_0}{md^2}}$, the particle motion can now be expressed in terms of the three spatial directions as

$$\frac{d^2x}{dt^2} - \omega_c \frac{dy}{dt} - \frac{1}{2}\omega_z^2 x = 0, \quad (3.4)$$

$$\frac{d^2y}{dt^2} + \omega_c \frac{dx}{dt} - \frac{1}{2}\omega_z^2 y = 0, \quad (3.5)$$

$$\frac{d^2z}{dt^2} + \omega_z^2 z = 0. \quad (3.6)$$

From Eqns. 3.4 and 3.5, it can be seen that the particle motion in the x and y directions is coupled. The $x - y$ motion can be simplified by considering the complex substitution $u = x + iy$, which allows Eqns. 3.4 and 3.5 to be now written as [66]:

$$\frac{d^2u}{dt^2} + i\omega_c \frac{du}{dt} - \frac{1}{2}\omega_z^2 u = 0. \quad (3.7)$$

This complex, ordinary differential equation can be solved using the ansatz $u = e^{-i\omega t}$, which reduces the problem to the quadratic equation

$$\omega^2 - \omega_c \omega + \frac{1}{2}\omega_z^2 = 0, \quad (3.8)$$

which has roots at frequencies

$$\omega_{\pm} = \frac{1}{2} \left(\omega_c \pm \sqrt{\omega_c^2 - 2\omega_z^2} \right). \quad (3.9)$$

Then defining the magnetron frequency as $\omega_m \equiv \omega_-$, and noting that $\omega_+ + \omega_- = \omega_c$, we can write $\omega'_c \equiv \omega_+ = \omega_c - \omega_m$, where ω'_c is called the modified cyclotron frequency. However, since $\omega_c \gg \omega_m$, we can make the approximation $\omega_+ \cong \omega_c$.

It is then useful to multiply the two root frequencies together, yielding

$$\omega_+\omega_- = \frac{1}{4} \left(\omega_c + \sqrt{\omega_c^2 - 2\omega_z^2} \right) \left(\omega_c - \sqrt{\omega_c^2 - 2\omega_z^2} \right) \quad (3.10)$$

$$= \frac{1}{4} \left(\omega_c^2 - (\omega_c^2 - 2\omega_z^2) \right) \quad (3.11)$$

$$= \frac{\omega_z^2}{2}, \quad (3.12)$$

and since $\omega_- = \omega_m$ and $\omega_+ \cong \omega_c$,

$$\omega_m \cong \frac{\omega_z^2}{2\omega_c}. \quad (3.13)$$

We have now derived the three fundamental frequencies of motion (Fig 3.2) of a charged particle in a Penning trap:

$$\begin{aligned} \omega_c &= \frac{qB}{m} && \text{(Cyclotron),} \\ \omega_z &= \sqrt{\frac{qV_0}{md^2}} && \text{(Axial),} \\ \omega_m &= \frac{\omega_z^2}{2\omega_c} && \text{(Magnetron).} \end{aligned}$$

The motion of the particle is now simply made up of superpositions of oscillations at these fundamental frequencies, as illustrated in Fig. 3.2.

A necessary condition for stability of the charged particle in the trap is found from an examination of Eqn. 3.9. Given that we require real fundamental frequencies for oscillatory (trapped motion), we must have

$$\omega_c^2 > 2\omega_z^2, \quad (3.14)$$

otherwise, exponential solutions to the particle motion are found, corresponding to particles leaving the trap. It should be noted that the above derivation was done for the case of single particles in a Penning trap. For the case of many particles or plasmas in a trap (such as with antihydrogen experiments), collective motion and space charge effects can become important.

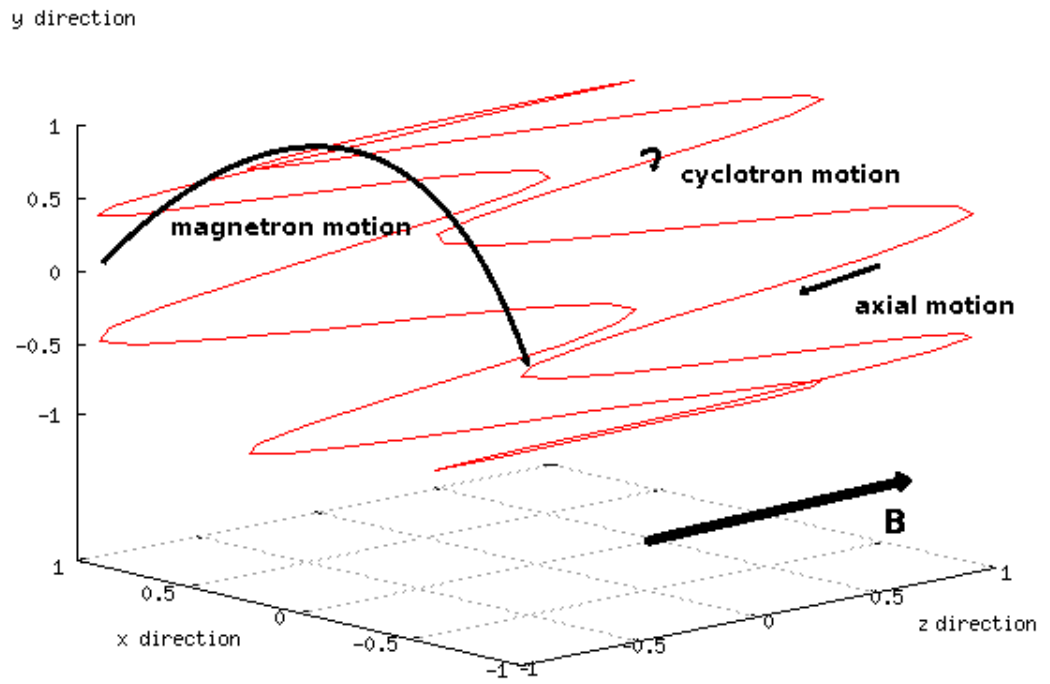


Figure 3.2: Confined particle motion in a Penning trap. The magnetic field orientation is shown, and the electric potential is given as Eqn. 3.2. The resulting motion is a superposition of three oscillatory modes: the cyclotron, axial, and magnetron modes.

Nested Penning Traps

Penning traps rely on electrostatic potentials to constrain the motion in the z -direction, with the charged particles seeking their electric potential energy minimum. For one species of charge a global minimum in the z -direction can be established at the center of the trap. However, this potential cannot be used to simultaneously confine two species with opposite charge (such as positrons and antiprotons), as a potential that confines one charge species will repel the other. To produce antihydrogen, charged positron and antiproton plasmas must be spatially overlapped while still being confined in a trap. This can be accomplished with a superposition of harmonic potentials, called a nested Penning trap potential [48] (Fig. 1.4). In this configuration, the positron plasma is held in a local minimum within a larger, opposite curvature, potential to confine the antiproton plasma. The antiproton and positron plasmas are then overlapping for a short section of the trap while remaining confined by the overall electrostatic potential.

3.2 The Antiproton Decelerator

While the previous section describes a technique in which charged (anti)particles can be confined, it does not detail how these (anti)particles are obtained. Both positrons and antiprotons are needed for the formation of antihydrogen, and although positrons are produced through the beta decay of some radioactive isotopes, antiprotons are not so easily acquired. Fortunately, antiprotons can be produced during high-energy collisions between protons through the process,

$$p + p \rightarrow 3p + \bar{p}. \quad (3.15)$$

This process requires that the proton beam overcomes a threshold energy of 6 GeV in the Lab frame before an antiproton can be released [67]. Conventionally, high-energy protons

are accelerated and directed into a stationary target, where antiprotons are released and collected. This technique is used at CERN's Antiproton Decelerator (AD) to produce high-energy antiprotons. First, a high-energy pulse of 10^{13} protons is supplied by the Proton Synchrotron (PS). These protons have a momentum of 26 GeV/c and collide with a thin iridium rod embedded in graphite where 10^7 antiprotons are released, collected in a magnetic-horn, and injected into the AD storage ring [67].

The AD is a specialized device designed to decelerate and cool antiprotons to an energy of 5.3 MeV. This is accomplished through a series of RF-deceleration and beam-cooling stages. RF-deceleration involves an oscillating electric field opposing the motion of the circulating antiproton beam as it passes through a special RF-cavity. The antiproton beam starts with a momentum of 3.57 GeV/c as the antiprotons are injected into the AD storage ring where they undergo alternating decelerating and cooling stages (Fig. 3.3). Beam cooling is necessary to compensate for the adiabatic blow-up of the beam during deceleration. Due to the conservation of phase-space density, the decrease in momentum during deceleration expands the conjugate position spread of the particles. With beam cooling, the antiproton beam can be reduced in size and energy spread. By reducing the beam size, stability is added to the circulating beam, as well as an increase in the phase-space density, allowing for more precise manipulation and control of the beam. Both stochastic and electron cooling are employed by the AD. Stochastic cooling involves a correction of the mean position deviation of the circulation beam (outlined in Section 3.2.1), whereas electron cooling uses co-propagating electrons to transfer energy away from the antiprotons through Coulombic collisions (described in Section 3.2.2).

3.2.1 Stochastic Cooling

Stochastic cooling involves a series of beam diagnostic and correction devices to adjust the mean position and momentum of the circulating particle beam. By correcting for the

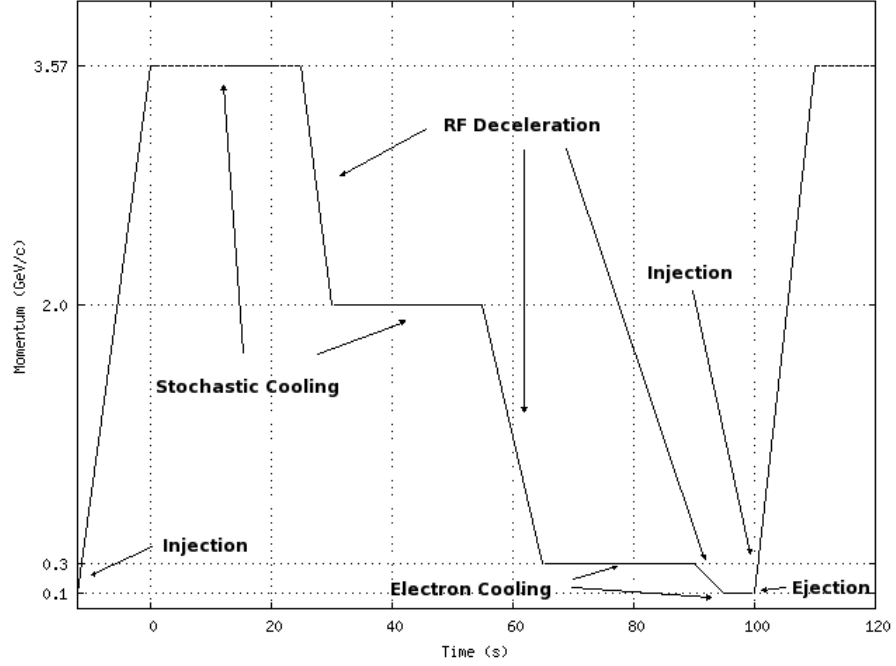


Figure 3.3: Antiproton momentum for a typical AD cycle. Highlighted are the RF-deceleration along with stochastic and electron cooling stages. Injection from the PS and ejection to the experiments are also shown.

divergence of the beam from its ideal path, a high-energy beam can be effectively cooled and the beam stability improved. In the case of a single particle, the absolute deviation could be measured by the difference in the current induced between parallel plates across the beamline (pick-ups) and a correction applied using an electrical field further down the beamline (kicker).

However, when dealing with a large number of particles N , the resolution of the circulating particles is limited by the bandwidth, W , of the pickups. Therefore, corrections are made to the mean of the sampled particles and the stochastic nature of this sampling is where the method gets its name. For these corrections to be made, the pick-ups must be placed some distance before the kickers with a geometry such that signal from the pick-ups is able to reach the kickers before the circulating particles, allowing the correction to be applied as the beam is passing through the kicker region. In the case of most storage

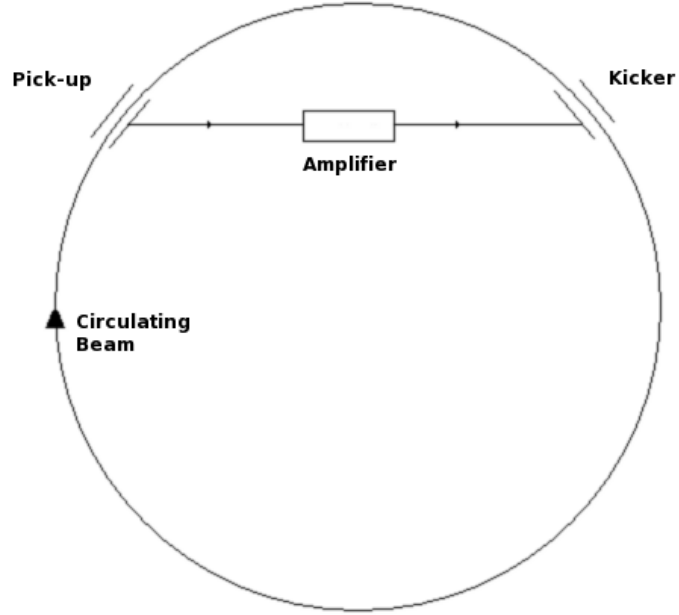


Figure 3.4: Overview of stochastic cooling in a storage ring. The circulating beam passes through the pick-up and a correction is later applied by the kicker. The connection between the pick-up and kicker passes across the storage ring and through an amplifier.

rings, which are circular or nearly circular, the signal from the pick-ups is simply sent transversely across the inside of the storage ring in a straight line as the beam rounds a curved section (Fig. 3.4). Ideally, stochastic cooling measures and makes corrections to a random sample of particles. In this way the mean of the sample is shifted and the overall variance diminished. However, due to the momentum spread of the circulating beam, faster particles will overtake slower ones. Thus, any sample that was initially random will quickly be separated according to the momentum distribution of the particles. Statistical errors vanish for non-random samples and stochastic cooling becomes ineffective. Fortunately, the same momentum spread will cause the particles to remix as the faster ones continue to overtake the slower particles. Incomplete mixing will result in slower cooling; if a particle takes M turns around the storage ring to shift by one sample length relative to a nominal reference particle, it will take M times longer to cool [68]. This introduces the mixing parameter, M , defined as the number of revolutions necessary to

shift a badly mixed particle by one sample length ($M > 1$). There is also some mixing between the pickup and kicker, which will affect the corrections made to the beam much in the same way as the mixing from the kicker to pickup. This mixing is reflected in the parameter $\tilde{M}$ ($\tilde{M} > 1$), which is proportional to M by $M = \alpha\tilde{M}$, where α is the ratio of the distance from the pickup to kicker to the distance from the kicker around the storage ring and back to the pickup.

The pick-ups used to measure the beam are also subject to noise due to the electronics or surrounding environment. Any noise incurred at the pick-ups will be multiplied in the amplifier electronics and applied as a correction to the beam at the kicker. Moreover, as the particles are decelerated and circulate with lower momentum, the induced signal in the pick-ups will diminish, causing the noise to signal power ratio U ($U > 0$) to increase.

Taking into account these mixing and noise parameters, along with the number of particles and sampling bandwidth, the characteristic cooling time, τ , can be written as

$$\frac{1}{\tau} = \frac{W}{2N} \left[2g(1 - \tilde{M}^{-2}) - g^2(M + U) \right] \quad (3.16)$$

where g is the gain parameter of the pickups ($g < 1$) [69].

Stochastic cooling is most effective for high-energy beams with a small number of particles. Since $\tau \propto N$, a larger particle density will take longer to cool with this method. In addition, as the beam cools the ratio of signal to noise power will increase as the momentum spread decreases. This makes it harder for the stochastic method to cool lower energy beams. In the AD, two stages of stochastic cooling are applied. The first occurs after the antiproton beam is injected into the storage ring at 3.57 GeV/c, with the process being repeated after the beam has been decelerated to 2.0 GeV/c (Fig. 3.3). For lower energies where stochastic cooling is not as effective, electron beam cooling is applied.

3.2.2 Electron Beam Cooling

Electron beam cooling uses the Coulomb interaction between the antiproton beam and a cold electron beam to reduce the energy spread of the beam. Cold electrons are first injected into the path of the antiproton beam with the same relative velocity of the antiprotons. In a reference frame moving with the particles the higher energy antiprotons interact with and heat the electrons through Coulombic collisions. The electrons are then removed from the antiproton beam along with the excess energy transferred from the antiprotons. Viewed in the electron-rest frame, the antiprotons lose energy and are finally stopped by Coulomb interactions [70].

Higher energy antiproton beams require higher energy electrons such that the velocities of the co-propagating beams are matched. Thus, electron cooling is less effective for high-energy antiprotons, as the power needed by the electron current becomes unreasonable and difficult to maintain. Likewise, electron cooling is highly dependent upon the relative velocity spread, such that the cooling is more effective for colder antiproton beams [70]. In this way, stochastic and electron cooling are complementary. Stochastic cooling is most efficient on higher energy beams where electron cooling is difficult, and for lower energy beams, electron cooling succeeds where stochastic cooling is less effective. This is reflected in the design of the AD, where the first two cooling stages involve stochastic cooling, while the final two cooling stages apply electron cooling when the antiproton beam has a momentum 0.3 GeV/c and again at 0.1 GeV/c [71].

Once the antiproton beam has been decelerated to 0.1 GeV/c (5.3 MeV), the cold antiprotons can be delivered to the experiments. The AD supplies an experiment with $\sim 2 \times 10^7$ antiprotons every cycle of 100 s in bunches of about 200 ns in length. The extraction beamline, which leads the antiprotons from the storage ring into the experiments, is designed with optics to focus the antiproton bunches inside the experiments. This is to minimize the volume and ease the process of trapping and manipulating the

antiprotons.

3.3 Antiproton Catching

In order to carry out cold antihydrogen experiments it is necessary to control and manipulate cold antiprotons. Once the antiprotons have been delivered from the AD, they have to be trapped and cooled further before they are suitable to use for antihydrogen production. This involves degrading and catching the slow antiprotons in a Penning trap.

While the AD significantly reduces the energy of the antiprotons, further deceleration is needed before they can be caught and confined. As such, when entering the apparatus the antiprotons interact with one or more thin degrader foils, which, while causing annihilation for many antiprotons, also slows some of the antiprotons to an energy where they can be trapped. By changing the thickness of the foil, the number of antiprotons slowed can be optimized by examining the number of antiprotons caught versus the degrader thickness (known as a degrader range curve; the ALPHA range curve is given in Section 4.3.2).

Once the antiprotons have been sufficiently reduced in energy they enter the strong magnetic field (3 T) provided by the external superconducting solenoid, which helps focus and direct the antiprotons along the field lines into the antiproton catching trap (shown in Fig. 3.5). Inside the catching trap the antiprotons can be confined between two high-voltage electrodes which act as a large potential well where antiprotons with energy below the applied voltage (~ 5 kV corresponding to antiprotons with longitudinal energies of < 5 keV) will remain. The trapping sequence is outlined in Fig. 3.6: the antiprotons enter the catching trap and, with the downstream high-voltage electrode engaged, the antiprotons with kinetic energy below ~ 5 keV will not be able to overcome the electrode potential and will rebound, travelling back upstream towards the AD entrance. An

upstream electrode with the same high-voltage is engaged before the antiprotons can leave the trap. The antiprotons will then be confined between the two electrodes where they will remain until needed. The lifetime of the antiprotons in the trap is actually largely determined by the quality of the trap vacuum, as any residual gas in the trap will tend to interact with the antiproton plasma and annihilate. Therefore, a very good vacuum is needed if the antiprotons are going to be stored for longer time periods, which can be the case if antiprotons from multiple AD cycles are to be contained in the catching trap, a process known as stacking, which is discussed further in Section 4.4.4.

The bunch length of the antiprotons has to be such that all the antiprotons that pass through the degrader are able to enter the trapping region before the second barrier is engaged. By adjusting the high-voltage timing, the sequence can be optimized such that the maximum number of antiprotons are within the two high-voltage barriers when the trap is closed (the graph of the number of caught antiprotons versus closing time is called a closing curve; the ALPHA closing curve is give in Section 4.2.3).

3.3.1 Electron Cooling of Trapped Antiprotons

By adding electrons into the antiproton catching sequence, the antiproton catching trap can be used to both confine and cool antiprotons. The method of using two high-voltage electrodes as potential barriers to confine the antiprotons is still employed, but cold electrons are pre-stored in a shallow well inside the antiproton catching trap (Fig. 3.7). As described earlier, the incoming antiprotons bounce off the upstream high-voltage barrier and are confined between the two high-voltage barriers before the antiprotons can leave the trap. The antiprotons will then transfer their excess energy to the cold electrons through the Coulombic collisions, and the electrons will then disperse that energy through spontaneous synchrotron radiation, which results from their orbital motion in the strong 3 T magnetic field. This is a process referred to as synchrotron cooling (see ref [72]),



Figure 3.5: Photograph of the antiproton catching trap. The segmented electrodes can be seen with their signal wires. The two high-voltage electrodes are shown bordered by white electrical insulation.

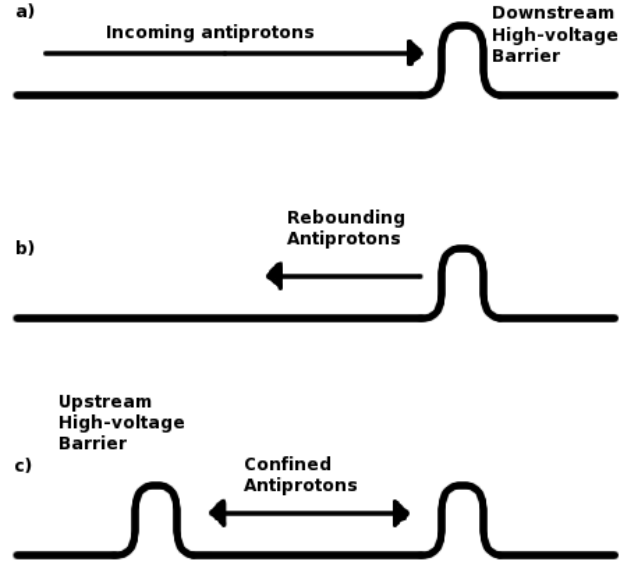


Figure 3.6: Antiproton catching sequence, where a) shows incoming antiprotons from the AD with the downstream high-voltage electrode engaged, b) shows the antiprotons rebounding on the high-voltage potential and travelling back upstream and c) shows both high-voltage potentials engaged, with the antiprotons confined between.

which efficiently keeps the light electrons at, or near, the temperature of the vacuum apparatus. Therefore, in principle, by cooling the system with liquid Helium, a 4 K electron bath can be maintained.

The cooling of the antiprotons, and concurrent heating of electrons, can be modelled [8] as:

$$\frac{dT_{\bar{p}}}{dt} = -\frac{T_{\bar{p}} - T_e}{\tau_c}, \quad (3.17)$$

$$\frac{dT_e}{dt} = \frac{n_{\bar{p}}}{n_e} \frac{1}{\tau_c} (T_{\bar{p}} - T_e) - \frac{(T_e - T_t)}{\tau_e}, \quad (3.18)$$

where $T_{\bar{p}}$ and T_e are the temperatures of the antiprotons and electrons, respectively. T_t is the ambient temperature of the trap environment, $n_{\bar{p}}$ and n_e are the antiproton and electron densities, τ_e is the synchrotron cooling constant and τ_c is the plasma cooling

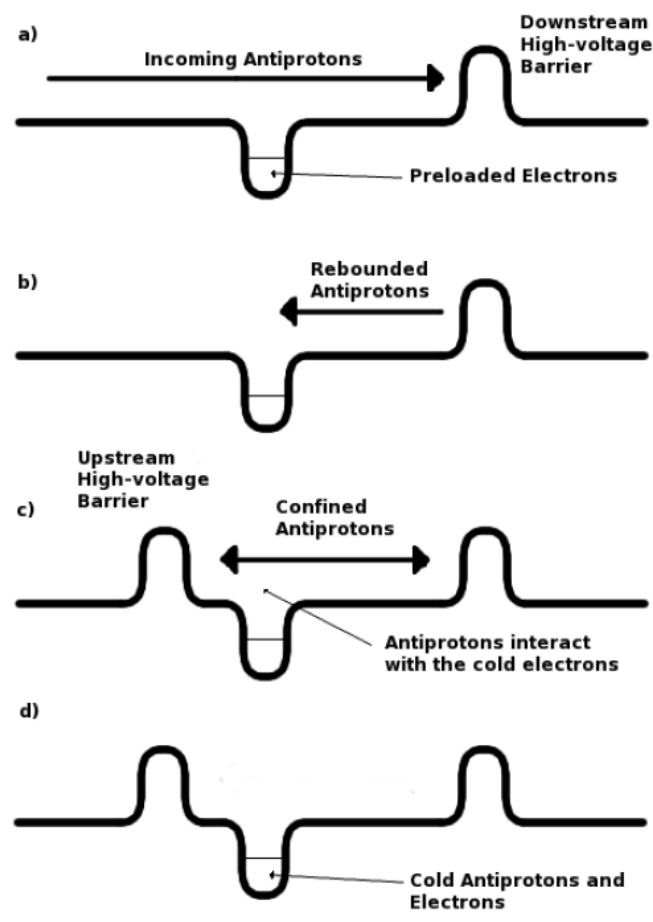


Figure 3.7: Antiprotons catching and cooling sequence, where a) preloaded electrons in a shallow well within the catching trap with the incoming antiprotons from the AD, b) shows the rebounding antiprotons from the high-voltage barrier, c) shows the antiprotons being confined between two high-voltage barriers where the antiprotons cool through interactions with the electrons and finally d) cool into the shallow well and remain there with the electrons.

rate, given by:

$$\tau_c = \frac{3m_e m_{\bar{p}} c^3}{8\sqrt{2}\pi n_e e^4 \ln(\Lambda)} \left(\frac{kT_{\bar{p}}}{m_{\bar{p}} c^2} + \frac{kT_e}{m_e c^2} \right)^{3/2}, \quad (3.19)$$

where k is Boltzmann's constant, $m_{\bar{p}}$ and m_e are the antiproton and electron masses, e is the fundamental electric charge, and $\ln(\Lambda)$ is the Coulomb logarithm, representing the sum effect of all Coulombic collisions for the area of interest with

$$\Lambda = \frac{4\pi}{\sqrt{n_e}} \left(\frac{\epsilon_0 kT}{e^2} \right)^{3/2}. \quad (3.20)$$

The solution of this system of differential equations shows that 10^4 antiprotons, initially with keV energy, will cool into the eV range in a few hundred milliseconds, assuming a complete overlap of the plasmas at electron densities of $10^7 - 10^8 \text{ cm}^{-3}$ [8]. This should leave the antiprotons at the temperature of the surrounding environment, which, as the traps are contained in a liquid helium cryostat would be 4.2 K in the absence of heating processes.

3.3.2 Electron Kick-Out

The use of cold electrons provides a very effective means of cooling the antiprotons down to cryogenic temperatures, but what remains is a mixture of electrons and antiprotons. Although this state is ideal for the manipulation of antiprotons within the traps, as the electrons will keep the antiprotons cold, a plasma containing electrons is non-ideal when it comes to mixing with positrons. The electrons will quickly cool into the side-wells of the nested potential and cool the antiprotons down into the side-wells also. This axially separates the antiproton plasma into regions of the trap where it cannot interact with the positron plasma, prohibiting the formation of antihydrogen. Also, the presence of electrons in the plasma could result in the depletion of positrons due to the electron-positron annihilations. Therefore, it is necessary to remove the electrons before the

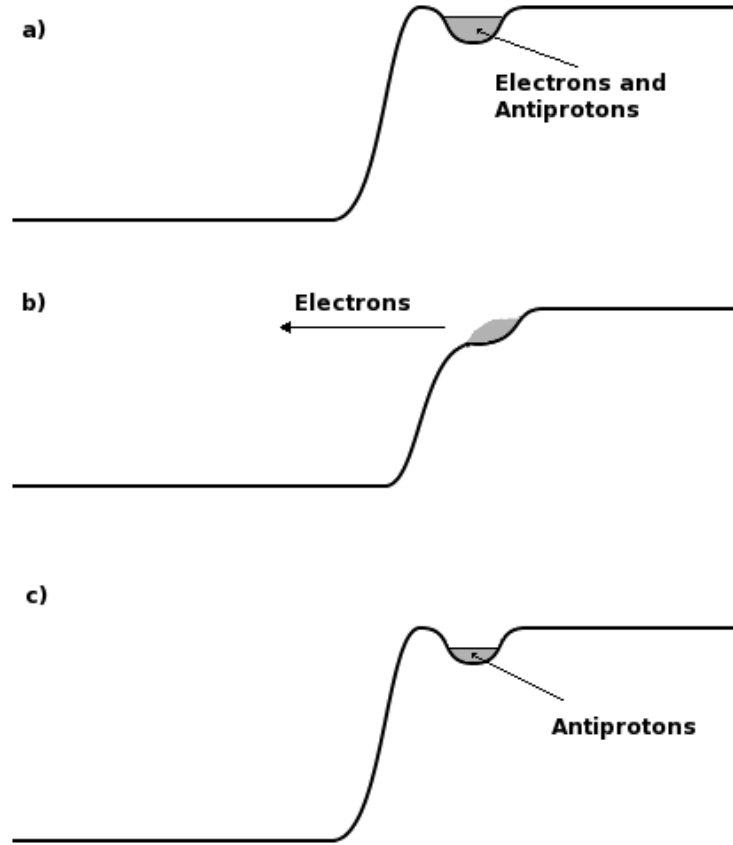


Figure 3.8: Overview of the electron kick-out procedure. Caption a) shows the initial well containing both electrons and antiprotons which is then opened on one side in caption b) to release the lighter electrons. The well is then reestablished in caption c), containing only antiprotons.

antiprotons can be mixed with the positrons.

The large mass difference between the electrons and antiprotons can be exploited to effectively remove the electrons. The thermal velocity, v , of a massive particle is given by

$$v(T) = \sqrt{\frac{kT}{m}}, \quad (3.21)$$

where T is the temperature, k is Boltzmann's constant, and m is the mass. Since antiprotons are almost 2000 times heavier than electrons, their velocities at 4.2K are ~ 200 m/s

and ~ 8000 m/s, respectively. With such discrepant velocities the antiprotons and electrons will separate almost immediately when not confined by a trapping field. For example, it would take the electrons $6.25 \mu\text{s}$ to cross a typical electrode length of 5 cm, while the antiprotons would take 250 ms to cross the same distance. Thus, to remove the electrons, a simple procedure can be employed where the well containing both antiprotons and electrons is changed to a potential where one side of the well is separated from the ground potential by a single electrode providing the confining potential to the side of the well. The potential applied to this end electrode is quickly lowered to ground, where it remains for enough time for the electrons to escape the region before the confining potential is reestablished. When the mixed plasma is axially unconfined only for a time long enough for the electrons to leave, the majority of the antiprotons remain in the same region. This results in an all but pure antiproton plasma when the confining potential is reinstated. In practice, not all of the electrons will be expelled in a single attempt, as some very slow electrons may remain mixed with the antiprotons. Several iterations may be necessary to separate all the electrons from the antiprotons before the pure antiproton sample is ready to be mixed with the positrons.

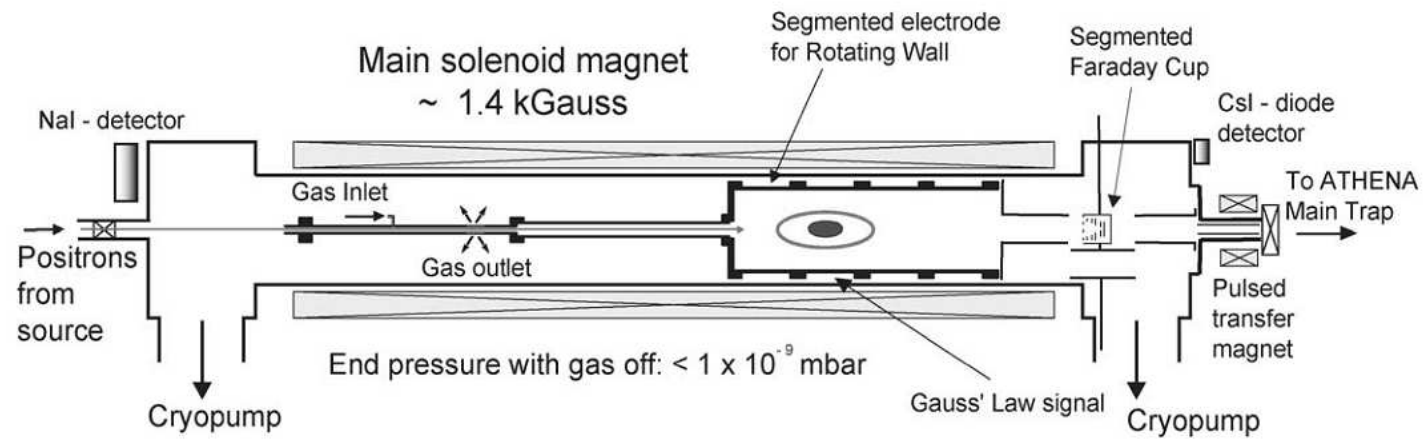


Figure 3.9: Schematic of the ATHENA positron accumulator (reproduced with permission from [8]). The ALPHA positron accumulator is identical to the ATHENA accumulator.

3.4 Positron Accumulator

Aside from cold antiprotons, the other ingredient necessary for the production of anti-hydrogen is cold positrons. These are provided by a dedicated positron accumulation apparatus developed for the ATHENA experiment [49, 8]. ALPHA has retained the ATHENA positron accumulator with only minor changes.

The positron accumulator works by interacting positrons emitted from a radioactive source with a solid moderator, followed by a neutral buffer gas, before finally trapping and manipulating the cold positrons. Positrons can be obtained from from a ^{22}Na radioisotope through the spontaneous beta decay process,

$$^{22}\text{Na} \rightarrow ^{22}\text{Ne} + \beta^+ + \nu + \gamma, \quad (3.22)$$

where ^{22}Na is the radioactive sodium source, ^{22}Ne is the resulting element after a proton in the sodium nucleus decays via the weak interaction into a β^+ particle (positron) and neutrino (ν). A gamma ray (γ) of energy 1.274 MeV follows shortly after (3.7 ps). The ^{22}Na radioisotope is commonly used, as the β^+ branching ratio is $\sim 90\%$ and the half-life of the radioisotope is about 2.6 years [9]. This makes it a convenient choice, with its large positron emission branching ratio and usable radioactive lifetime.

Positrons emitted from a radioactive source have a wide range of initial kinetic energies, with some reaching into the MeV range. Similar to the antiproton case, the positrons must have low kinetic energy to be trappable. Also, to facilitate the three-body recombination process (Sec. 1.2.2), a high density positron plasma is desired. To accomplish all these tasks, the emitted positrons are first interacted with a solid moderator, then a neutral buffer gas, before finally being trapped in a Malmberg-Penning type trap. This technique was pioneered by the University of San Diego positron group [73, 74].

Moderation is achieved by passing the emitted positron through a layer of solid

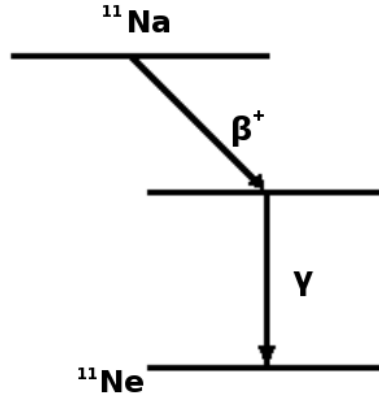


Figure 3.10: Level diagram of positron emission from beta decay of ^{22}Na . Figure created based on content from [9].

neon deposited directly on the radioactive source. While passing through the neon, the positrons quickly thermalize and diffuse through the material. A fraction ($\sim 0.4\%$) of the incoming positrons will reach the surface and be released into the vacuum, providing about 5×10^6 positrons per second [28]. The positrons that emerge from the moderator will do so in the eV range and will follow external magnetic field lines towards the trap region.

The trapping region contains a series of electrodes to provide the electrostatic potential along with a 0.15 T axial magnetic field which acts to radially confine the positrons as they follow the field lines. In such a magnetic field, the positrons will have a long synchrotron cooling constant, necessitating a different mechanism for cooling the positrons into the trap, and without cooling, positrons with enough energy to enter the electrostatic trap will have enough energy to leave. This cooling is provided by a nitrogen buffer gas, where the positrons lose kinetic energy through electronic excitation of the nitrogen gas. About 20% of the incoming positrons will cool into the trap and continue to cool through further collisions with the buffer gas.

The trap electrodes are of varying diameter to establish a buffer gas pressure gradient between the different regions. As the positrons traverse and cool in the trap, they

will eventually come to reside in the low-pressure region, corresponding to a special six-way segmented electrode. This electrode is used to provide a varying electric field, which applies a torque to the positron plasma and compresses it radially [49, 75, 76]. This “rotating wall” technique increases the positron density, but also heats the plasma. Fortunately, the nitrogen buffer gas continues to provide cooling as the rotating wall compression is being applied.

The reason for using this system of moderator, buffer gas and stationary potential, as opposed to the high-voltage switching used to catch antiprotons is that since the ^{22}Na source continuously emits positrons, they can be continuously accumulated in the trap until a large number of positrons are collected. When a sufficient number of positrons have accumulated, they can be ballistically transferred into the mixing trap to be mixed with the antiprotons. The positron transfer involves pumping out the nitrogen gas before opening the separation between the positron accumulator and mixing region, and then using a pulsed magnet to force the positrons across the low radial magnetic field region between the accumulator and mixing region. This transfer has an efficiency of about 50%, with up to about 10^8 positrons entering the mixing trap and being used for antihydrogen production.

As mentioned earlier, this positron accumulator was developed and optimized during the ATHENA experiment and it was simply incorporated into the ALPHA apparatus. By using established technology there is less emphasis on proving the functionality, and all the appropriate diagnostics and optimization routines are already in place. However, this is not the case with the antiproton region of the ALPHA apparatus, which was constructed for the 2006 AD run with new elements, such as a magnetic neutral atom trap, added to a new support structure and trapping system. All of the new equipment then had to be commissioned to test and confirm its operation. The commissioning of the ALPHA apparatus is described in Chapter 4.

Chapter 4

Commissioning of the ALPHA Apparatus

After the construction of the ALPHA apparatus came the activity of confirming that its operation and results were understood. This is a necessary step before proceeding on to attempt new experiments. By checking in sequence that all of the equipment was in working order and performing as expected, later measurements using the apparatus could be relied upon to be accurate and precise.

This chapter describes the commissioning of the ALPHA apparatus, as carried out in the summer and fall of 2006, starting with a description of the ALPHA antiproton extraction beamline and the silicon beam counter used to detect incoming antiprotons. A description is then made of the beam steering measurement made to center the antiproton beam in the catching trap. The antiproton catching sequence is then outlined, including the timing electronics and detection method. Measurements to optimize timing and catching are given along with typical operational values. The technique of electron cooling of antiprotons in the apparatus is described along with the optimization of the cooling in terms of the electron-antiproton interaction time. Additional measurements including the lifetime of cold antiprotons in the catching trap and the stacking of multiple antiproton injections are given.

Many people were involved in the measurements described in this chapter, namely, Gorm Andresen (University of Aarhus), Will Bertsche (University of California Berkeley), Dr. Paul Bowe (University of Aarhus), Prof. Claudio Lenz Cesar (Federal University of Rio de Janeiro), Steve Chapman (University of California Berkeley), Prof. Joel Fajans (University of California Berkeley), Dr. Makoto Fujiwara (TRIUMF), Dr. Ryo Funakoshi (University of Tokyo), Dr. Dave Gill (TRIUMF), Prof. Jeffrey Hangst (Univer-

sity of Aarhus), Matthew Jenkins (University of Wales Swansea), Dr. Lars V. Jørgensen (University of Wales Swansea), Dr. Niels Madsen (University of Wales Swansea), Alex Povilus (University of California Berkeley), Dr. Art Olin (TRIUMF), Konstantin Ochanski (TRIUMF), Dr. Eli Sarid (Nuclear Research Center Negev), Dr. Daniel de Miranda Silveira (Federal University of Rio de Janeiro), James Storey (TRIUMF), Dr. Dirk Peter van der Werf (University of Wales Swansea) and Prof. Jonathan Wurtele (University of California Berkeley).

The author was involved for all measurements described below. This involvement includes the setup and maintenance of the experimental apparatus, as well as a physical presence, either making the measurement or assisting. The author was personally responsible for the upkeep of the data acquisition system (described in the Appendix) and wrote a significant portion of the data analysis and display software (called ALPHA-ROOT, and described in Sec. A.3). Using this software, the data collected from the experiment was analyzed, wherein the author took a large role.

4.1 Beam Counter and Beamline Steering

The first step towards being able to use antiprotons from the AD within the ALPHA apparatus was the interfacing between the AD extraction beamline and the antiproton catching trap in the ALPHA apparatus. While much of the deceleration and cooling of the antiprotons is done in the AD storage ring, each experiment in the AD has a dedicated beamline to carry the low-energy antiprotons into the respective experiments. It is very important for the trapping of the incoming antiprotons that the extraction beamline be setup such that the maximum number of antiprotons arrive in the center of the traps. This is to minimize the outlying particles that are more susceptible to annihilation with the vacuum walls. Indeed, an improperly set up beamline could steer the antiproton

beam directly into the beam pipe, removing any possibility of using those antiprotons for antihydrogen physics.

4.1.1 ALPHA Antiproton Extraction Beamline

The ALPHA extraction beamline is shown in Figure 4.1. It consists of an array of beam steering and diagnostic elements. Starting furthest upstream with the initial bending magnet (DE2.DHZ10), which directs the antiprotons into the ALPHA experimental zone from the extraction beamline common to all experiments, the beam then passes through a multiwire proportional chamber (MWPC) (labelled DE2.MWPC12). These chambers contain a retractable screen of vertical and horizontal wires that work analogously to Geiger-Muller counters (although in a different operational range) [77, 78], registering the passage of charged particles near the wires. The screens can be lowered into the path of the antiproton beam and be used as a beam profile diagnostic. However, in normal operation, the MWPC are left out of the beam path, as employing the MWPC also stops and destroys the beam. Directly after the first MWPC is a set of dipole trim magnets, which independently act to direct the beam in the horizontal (DE2.DHZ15) and vertical (DE2.DVT15) directions. Next downstream are two quadrupole magnets (DE2.QN20 and DE2.QN30) that together can focus the antiproton beam both vertically and horizontally. Finally, the beam passes through another set of dipole magnets (DE2.DHZ35 and DE2.DVT35) and another MWPC (DE2.MWPC40) before entering into the ALPHA apparatus.

The extraction beamline also contains a sensitive transformer (DE.TFA7049), and as the antiproton beam passes through it, a current is induced in the transformer proportional to the number of antiprotons. This provides a measure of the number of antiproton delivered from the AD to the ALPHA experimental zone for each antiproton bunch cycle.

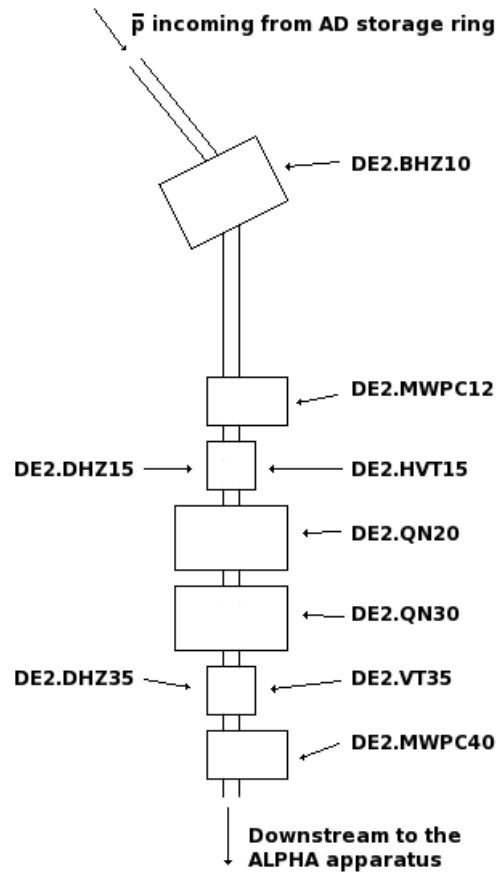


Figure 4.1: The extraction beamline into the ALPHA apparatus. Description of the elements included in the text.

4.1.2 Silicon Beam Counter Diagnostic

Although most of the beamline magnets are carefully set up to steer and focus the beam into the ALPHA apparatus, adjustment is often necessary to correct for the natural drift of the magnets and changes in the antiproton beam path. With the AD equipment, the beam can be steered and centered using the MWPC located immediately before the coupling region for the ALPHA apparatus (DE2.MWPC40). This leaves the region between the AD extraction point and the antiproton catching trap undiagnosed, a concern, since this is the region where accurate delivery to the experiment is most important. Therefore, there is a need to ensure that the antiprotons make the transition into the trapping region by providing some method of measuring the position of the incoming beam so that, if necessary, it can be corrected and aligned with the center of the traps using the final beamline dipole magnets.

For this diagnostic, a silicon beam counter is used (Fig. 4.2), which is mounted just before the antiproton catching trap, downstream from the AD. This is a 60 μm silicon wafer segmented into five sections that can be used to record the beam passage into the trapping region. The antiproton beam intensities incident on each of the five sections are measured independently so that the position of the antiproton beam can be determined from the corresponding section in the beam counter. The semiconducting silicon sections act as a reversely biased diode and as the charged antiprotons pass through the silicon some of their kinetic energy is deposited into the silicon and creates electron-hole pairs. By applying a bias voltage across the silicon, these mobile electrons can be collected before they recombine within the silicon. With a sufficient bias voltage, such that the majority of the freed electrons are collected, the signal induced in the silicon beam counter will be proportional to the number of antiprotons passing through it. Thus, not only can the silicon beam counter determine the position of the antiproton beam as it enters the traps, but it can also be used to determine the number of incoming antiprotons.

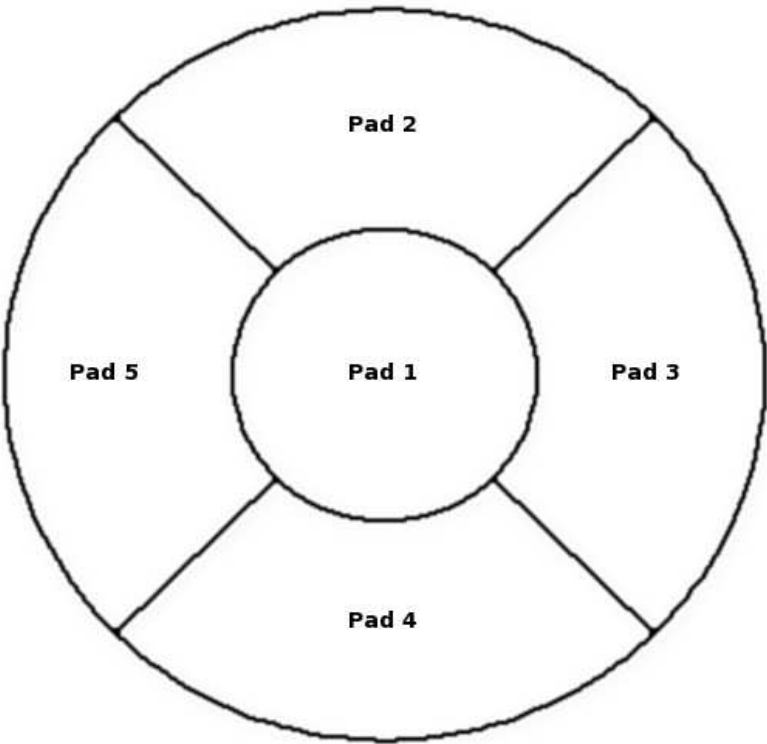


Figure 4.2: Diagram of the silicon beam counter. The five segmented pads are shown and labeled.

4.1.3 Beam Steering and Focusing Measurement

Using the segmented beam counter and controlling the applied current for the final dipole magnets, the trajectory of the antiproton beam can be directed into the catching trap. Once the beam position is known and is centered in the beam counter, the quadrupole magnets can be adjusted to focus the size of the antiproton bunch. Both the beam position and vertical and horizontal profiles are reflected in the relative counts found in the beam counter as the beam trajectory is changed.

For example, the beam profile can be scanned by altering the final horizontal dipole (DE2.DHZ35) and plotting the central beam counter pad value versus the magnet current (Fig 4.3). The values from the beam counter are normalized against the transformer current (DE.TFA7049) to minimize the shot-to-shot variation in the AD by reflecting the absolute number of antiprotons delivered by the AD as given by the transformer current. A vertical scan can be made in the same way by adjusting the final vertical dipole (DE2.DVT35) and examining normalized beam counter values in the central pad versus the vertical dipole magnet current. When the majority of the beam is contained within the central pad, the beam is said to be centered in the beam counter.

The two quadrupole beamline magnets can then be used to focus the centered beam. In terms of the beam profile, the quadrupoles work by compressing the beam in one direction (while elongating the beam along the perpendicular direction). In this way, two quadrupoles can be used to simultaneously compress the beam in both transverse directions. This has the effect of focusing the beam, so as to keep the antiprotons away from the beam pipe walls and delivering as many antiprotons into the trap as possible.

Despite some small day-to-day drifting within the AD steering magnets, the beam position was found to be fairly stable over the course of several days when undisturbed. A major concern for the steering of the antiproton beam into the ALPHA apparatus was the shifting of the beam path upstream due to changing magnetic fields generated by other

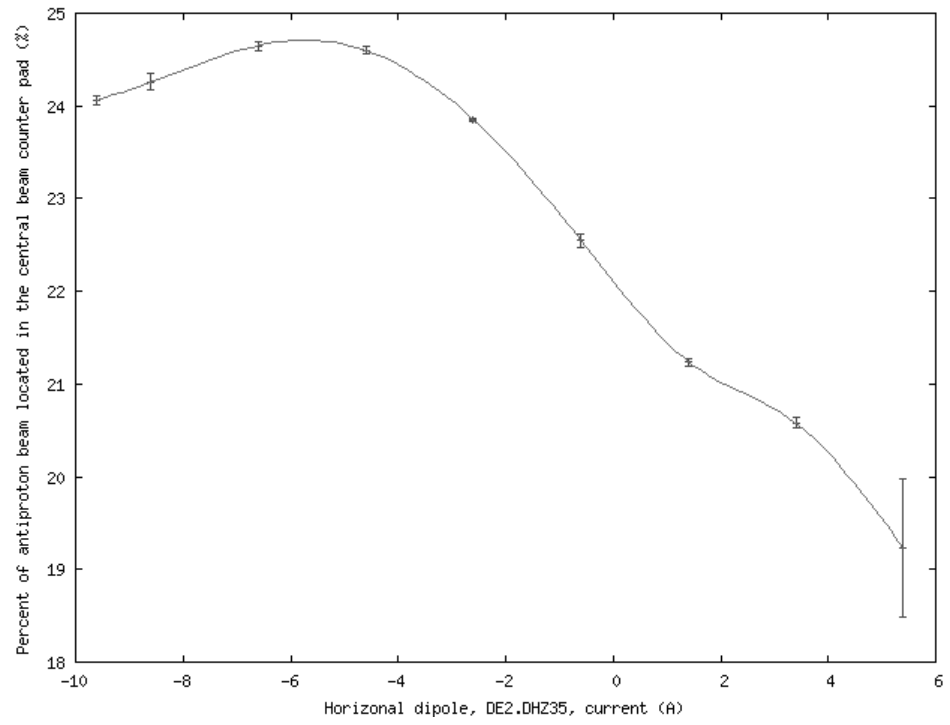


Figure 4.3: Horizontal beam steering scan (values taken from run 1260). Error bars reflect the shot-to-shot variation in the number of antiprotons delivered. Lines are to guide the eye.

experiments in the AD. Due to the close proximity to the ALPHA extraction beamline of a high strength magnet, the entire extraction line had to be resteeered whenever a change was made to the field of this solenoid. Being that this solenoid was part of another active experiment, its magnetic field was often changing to suit the parameters of that experiment. Apart from this external influence, during normal operation (with the offending solenoid at full-field), nominal values for the steering and focusing magnets fell into a predictable range and are given in Table 4.1. These values are also dependent upon the position of the beam counter relative to the AD. While the the AD steering magnets and coupling with the ALPHA apparatus are in a fixed position, the large solenoid containing the traps and beam counter rest upon a movable frame to facilitate access. Thus, any deviation in the solenoid position may result in different magnet current values corresponding to a centered beam. A movable platform which locks into position, as well as the exact coordinates of the traps relative to the beam axis (provided by a CERN metrological survey) help to minimize any positioning error of the apparatus with respect to the antiproton beam.

The ALPHA silicon beam counter was operated in current mode, where a large number of particles passed through the detector in a short bunch and the induced current was proportional to the number of particles. One problem encountered when using the beam counter for steering measurements was saturation due to an insufficient bias voltage. When the bias voltage was too small, the electron-hole pairs created by the passage of an antiproton could recombine before being swept away and counted. This was even more evident as the number of antiprotons increased; there came a point where, for a large number of electron-hole pairs, the bias voltage could not sweep away all the particles before the electrons and holes recombined. In this case, the number of antiprotons passing through the beam counter could increase without being reflected in the beam counter signal. This saturation could be counteracted by increasing the bias voltage, and

Element	Description	Value
DE2.DHZ35	Downstream horizontal dipole magnet	-6.00 A
DE2.DVT35	Downstream vertical dipole magnet	-1.00 A
DE2.QN20	Quadrupole magnet (horizontally focusing)	-143.50 A
DE2.QN30	Quadrupole magnet (vertically focusing)	143.00 A
DEX.WATHENA	AD pretrigger setting	15712
DE.TFA7049	Beamline transformer (typical value given)	$2.10 (\times 10^7)$
DR.SME5307S	Beamline septum	Open
DE2.BHZ10	Horizontal bending magnet	164.02 A
DE2.DHZ15	Upstream horizontal dipole magnet	6.57 A
DE2.DVT15	Upstream vertical dipole magnet	-0.44 A
DE2.MWPC12	MWPC before DE2 magnets (vertical/horizontal)	4375/4317
DE2.MWPC40	MWPC after DE2 magnets (vertical/horizontal)	4834/3906
DE2.VGP45	Beamline vacuum gauge	1.2×10^{-6}
DE2.VGP12	Beamline vacuum gauge	9.7×10^{-9}
DE3.VGP17	Beamline vacuum gauge	9×10^{-9}
DE2.VVS42	Vacuum valve between AD and ALPHA	3 (open)

Table 4.1: Typical operational values for the beamline elements.

thereby increasing the number of electron-hole pairs that could be handled. However, operating the beam counter with too high a bias voltage could damage the silicon diode (reflected by an increased leakage current). The operational bias voltage range could be extended by decreasing the ambient temperature, and indeed, when cooled to cryogenic temperatures, the ALPHA beam counter operated in a linear regime. Care was taken when using low temperatures, as thermal shock could affect the thin silicon wafers. During normal cryogenic operation, the ALPHA beam counter was kept at a bias voltage of -75 V, with a typical leakage current of $1 - 10$ nA.

Since the passage of antiprotons through the silicon created about 3200 electron-hole pairs per μm [79, 80], the rapid transit of $\sim 10^7$ antiprotons through the $60 \mu\text{m}$ silicon beam counter could create a large instantaneous current and sizable signal to be recorded (assuming all 10^7 antiprotons extracted from the beamline arrive in a 100 ns bunch, the instantaneous current would be ~ 6 A). In practice, this signal was large enough that substantial attenuation was needed to place the beam counter signal in the operational

range of the Analog-to-Digital readout Card (ADC). Typically, the beam counter signal was attenuated by 42.5 dB in signal attenuation boxes before reaching the ADC.

4.2 Catching Antiprotons and Closing Curve

Once it was confirmed using the silicon beam counter that antiprotons had entered the catching trap, the antiprotons were then caught and held (as per the description in Sec. 3.3). To reiterate, the incoming antiprotons enter a region of the trap system between two high-voltage electrodes. As the antiprotons enter the trapping region, the downstream high-voltage electrode is already engaged, providing a large potential barrier on which the antiprotons rebound and travel back towards the AD. The upstream high-voltage electrode is then engaged before the antiprotons have left the trapping region, confining the antiprotons between the two electrodes.

4.2.1 Timing Sequence

In order to catch as many antiprotons in the catching trap as possible, the timing of the catching sequence had to be such that the antiproton bunch (typically 100 – 200 ns in length) is contained between the two high-voltage electrodes when engaged. This required precise triggering to apply the high-voltage barriers properly. Fig. 4.4 outlines the triggering sequence used to catch antiprotons (sequence described in Sec. 3.3).

4.2.2 Hot Dumps

The number of antiprotons caught in the trapping region can be examined by releasing (dumping) the confined antiprotons onto the upstream metal foil used to slow the incoming antiprotons, and then counting the resulting annihilations with the external scintillators. The number of antiprotons will be proportional to the counts found in the scintillators during the time it takes the trap to dump all the antiprotons. This procedure

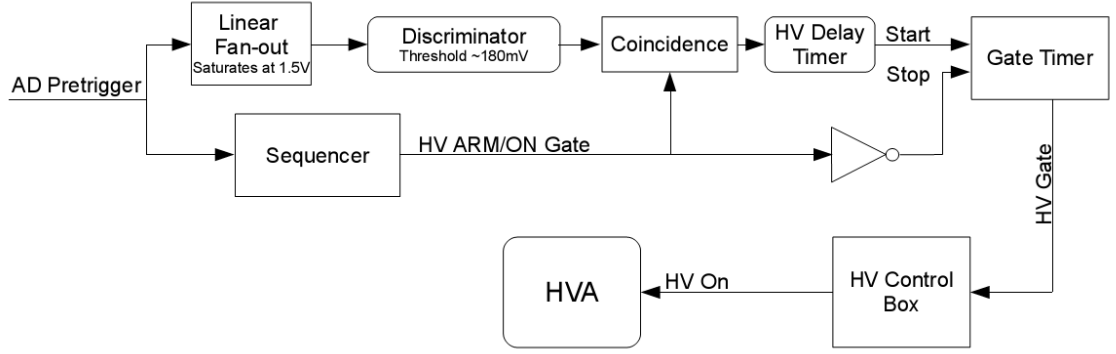


Figure 4.4: High-voltage timing schematic. Description of elements given in text.

is known as a hot dump (as opposed to a cold dump, described in Sec. 4.4.1), and is an important measure of the number of antiprotons in the system. When considering the trapping efficiency and number of antiprotons received from the AD, it is the hot dump number that is observed and optimized (the larger the hot dump, the more antiprotons).

The steering measurements can then be redone using the hot dumps as the indicator of antiprotons in the catching trap. The hot dumps are direct measures of the trapped particles, whereas the beam counter only gives an measure of how many antiprotons arrive at the trap entrance. Also, the beam counter often saturates (i.e. became non-linear), which diminishes its effectiveness as a measure of the number of antiprotons in the system. As a result, the hot dumps, being a direct indicator of the number of trapped particles, are more useful for comparison and optimization purposes.

Figure 4.5 shows a temporal spectrum of the external scintillators as an antiproton bunch enters the traps, is caught, and is then released and detected. What is clearly evident is the peak corresponding to the release of the antiprotons against the degrading foil, a feature not present without antiprotons and a proper catching sequence. This constitutes a hot dump, where the antiprotons confined between the high-voltage electrodes are released and detected as the upstream high-voltage electrode is disengaged. The gray region shown in Fig. 4.5 represents the integration area, generating the antiproton count

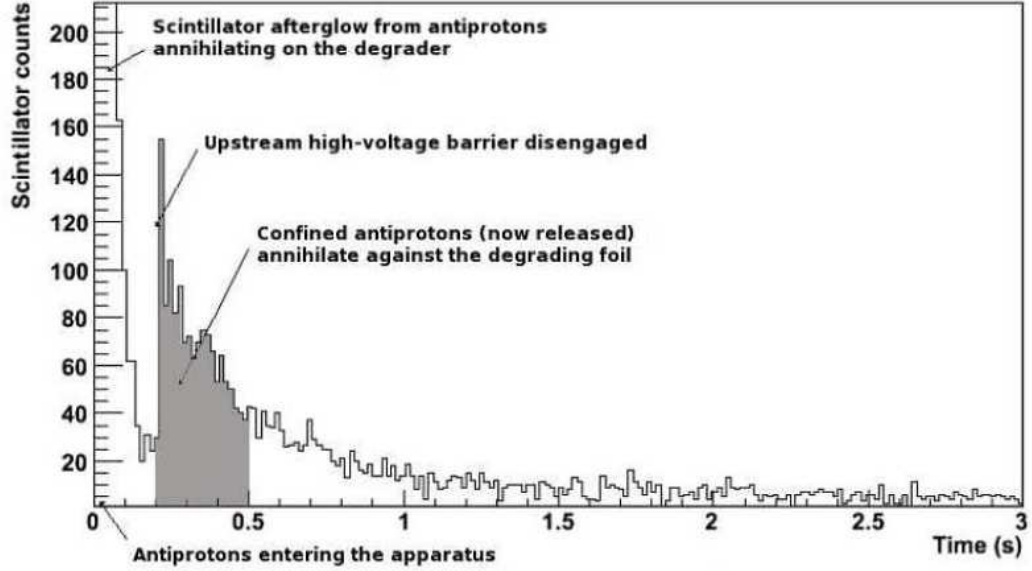


Figure 4.5: Example of scintillator activity during antiproton catching sequence (data compiled from several spills during run 915). The gray area represents the hot dump integration region.

for the hot dump.

4.2.3 Closing Curve

By adjusting the delay between the AD pretrigger and the activation of the upstream barrier (HVA), the timing can be optimized to confine the maximum number of antiprotons. If the HVA electrode is engaged too soon, most of the antiprotons will be barred from the trap before entering, but if HVA is engaged too late, the antiprotons will have already left the trap.

For the ALPHA antiproton catching trap, 5 keV antiprotons see a temporal trap length (the total time it takes to enter the trap, rebound against the far barrier and leave the trap) of 380 ns. It would then be expected that the maximum number of antiprotons will be trapped when the delay between the antiprotons entering the trap and the closing of the high-voltage barrier is about the same as the trap length. Shown in Fig. 4.6 is the

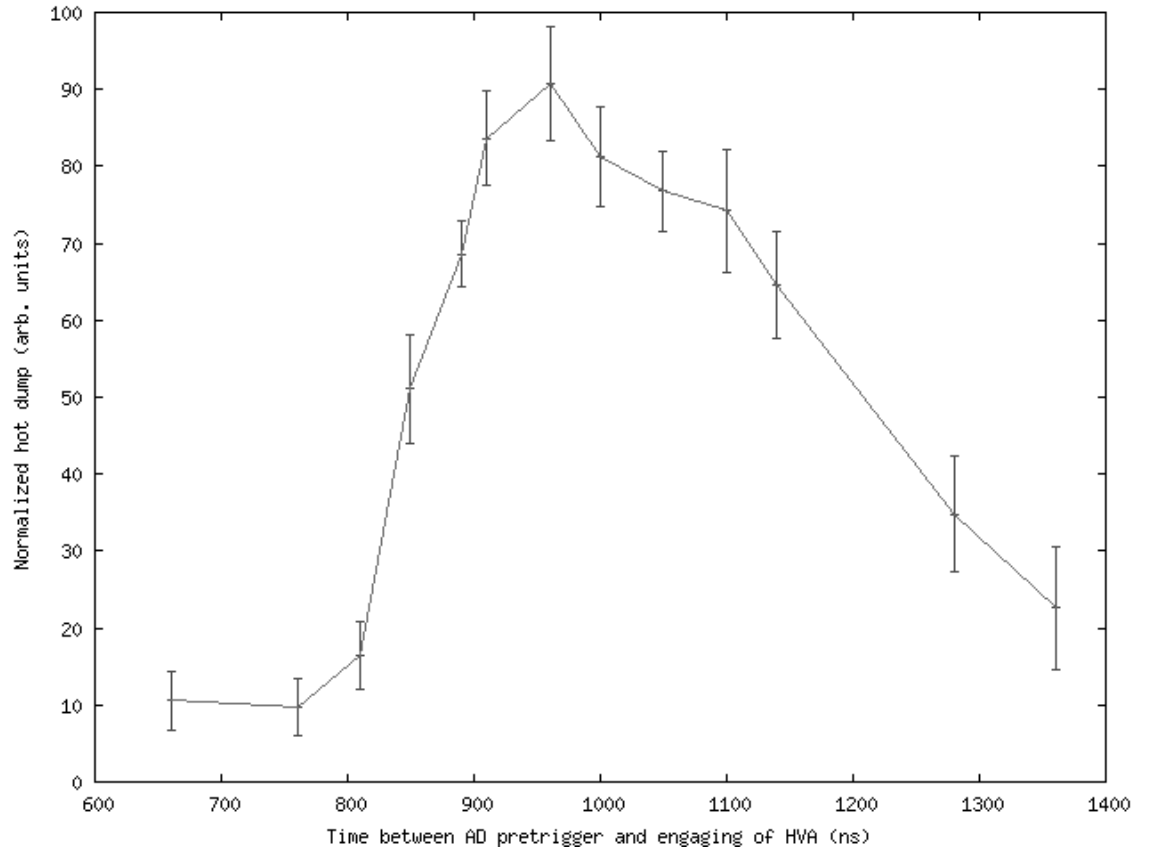


Figure 4.6: Closing curve (values taken from run 929). Error bars represent the shot-to-shot variation of antiprotons delivered. Lines are to guide the eye.

variation of hot dump counts as the high-voltage delay is adjusted. There is a well defined peak at 960 ns, where the maximum number of antiprotons were found to be trapped. Note that delay of 960 ns is relative to an arbitrary zero, but since this setting maximizes the number of caught antiprotons (from this parameter), the identity of the zero point in the sequence is unimportant, as long as it is invariant. Then by varying the time-delay over the full catching range, an estimate can be made of the catching trap length. If HVA is engaged too soon no antiprotons will enter the trap, so none can be trapped. Similarly, if HVA is engaged too late, all the antiprotons will have already rebounded and left the trap. From Fig. 4.6, both the onset and termination of antiproton trapping can be seen and define the effective trap length for the ALPHA antiproton catching trap. The full-width half maximum (FWHM) of about 400 ± 50 ns compares very well with the expected trap length of 380 ns (assuming a small low-energy antiproton tail). The sharp rise time in Fig. 4.6 is due mainly to the short AD beam bunch length (~ 100 ns).

4.3 Degraded Range Curve

With a delivery energy of 5.3 MeV, the antiprotons delivered from the AD are much too energetic to be confined in the catching trap without first being slowed down into the trappable regime (< 5 keV). The method used in ALPHA to slow the incoming antiprotons involves passing the antiprotons through one or more thin metal foils. While many of the antiprotons will annihilate in the foil, some will pass through after having deposited some amount of kinetic energy within the foil in the form of atomic excitations. Some fraction of the antiprotons that emerge from the foil will have slowed enough to be trapped. Since the energy loss depends upon the distance the antiprotons travel within the foil, one would expect an optimal degrading thickness. This optimal thickness represents the point of diminishing returns for the antiproton energy degrading. That is,

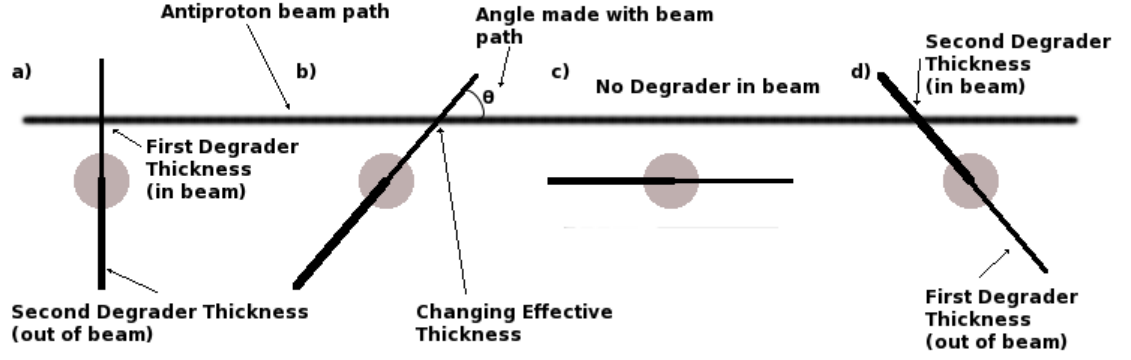


Figure 4.7: Diagram of the rotatable degrader in the beam path (side view). Section a) shows the first foil fully in the beam path (smallest thickness), section b) shows the foil rotated into the beam foil, making an angle of θ with the beam path (larger effective foil thickness). Section c) shows the degrading foil rotated entirely out of the beam path; section d) shows the second foil thickness rotated into the beam path.

with a larger thickness, the antiproton's range within the foil becomes large as compared to the effective degrading thickness and an increasing number of antiprotons are lost to annihilation. With more antiprotons lost to annihilation, fewer reach the catching trap, and therefore, fewer are caught.

4.3.1 Rotatable Degrader

To find this optimal thickness, it is necessary to be able to easily change the effective thickness of the degrading material. All of the degrading material is contained within the vacuum system, so the apparatus should be able to accommodate the change in degrader thickness without the need to open the apparatus and destroy the vacuum. This is accomplished by first separating the degrading material, placing most of the material near the interface between the cryostat and trap system (including the beam counter and Faraday cup for measuring electron and positron charges). The remaining degrading material is placed within a rotatable frame such that the thin foil can be rotated so that the effective thickness changes depending upon the angle the foil makes with the beam

path (Fig. 4.7). The effective thickness, L_{eff} can be expressed as:

$$L_{eff} = \frac{L_{Al}}{\cos(\theta)}, \quad (4.1)$$

where L_{Al} is thickness of the thin aluminum foil, and θ is angle between the foil and beam path. The rotatable frame is coupled, using a mechanical vacuum feedthrough, to a graduated knob on the outside of the apparatus that can be easily accessed and turned to change the total degrader thickness. The frame is made such that there is room for two different foil thicknesses allowing for a larger range of thicknesses which can be achieved. It is also positioned such that the foil can be completely removed from the beam path such that there is no degrading influence from the rotatable degrader.

4.3.2 Range Curve

To determine the optimal degrading thickness, the number of trapped antiprotons was measured as a function of the thickness of the degrading foil. For the ALPHA apparatus this was done by recording the number of hot dump counts as the rotatable degrader was scanned over its full range of thicknesses. Figure 4.8 shows a typical range curve for the ALPHA apparatus. For a small degrader thickness, few antiprotons are caught. However, a peak was found at $25.2 \mu\text{m}$ with a FWHM of $10.1 \mu\text{m}$. This corresponds to the optimum degrading thickness for the 5.3 MeV incoming antiprotons to be caught in the apparatus. As expected, the number of antiprotons trapped is low for the very thin degrader, as there is not enough stopping power to slow the antiprotons. Likewise, for a much thicker degrader there are also fewer trapped antiprotons, since the total degrading material is enough to annihilate most of the antiprotons. A roughly Gaussian relationship was found around the optimum rotatable degrader thickness (Fig. 4.8).

While there are various experimental uncertainties associated with this measurement

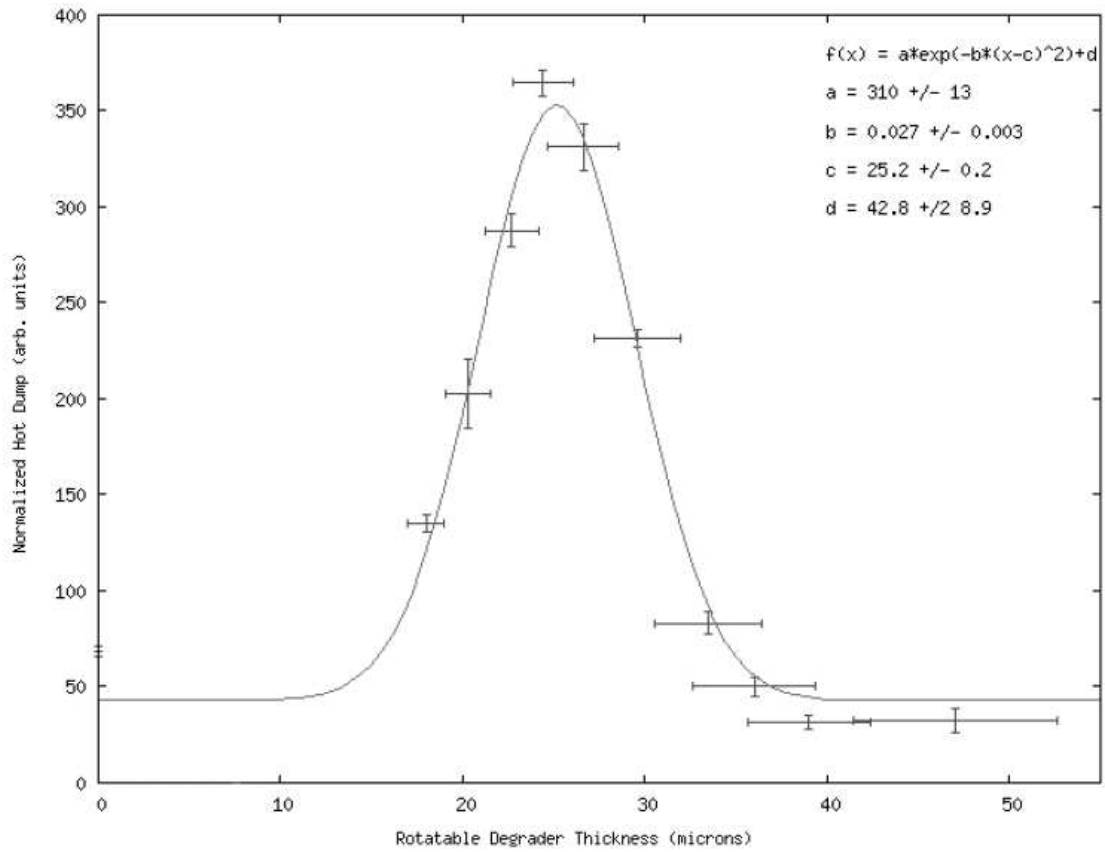


Figure 4.8: Degradation range curve (values taken from runs 1477-1488). Foil thickness used was 18 μm . Error bars represent shot-to-shot variation of delivered antiprotons.

(i.e. uncertainty in the foil thickness and angle made with the beam path), the main problem when using this type of rotatable degrader is beam blow-up due to multiple scattering within the degrading material. Since the rotatable degrader is located ~ 800 mm upstream of the catching trap (outside of the radially confining influence of the strong axial magnetic field), the scattering due to the interaction with the degrading foil will cause the beam to diverge and perhaps some of the more strongly scattered antiprotons will annihilate on the apparatus wall. The small-angle deflection, θ_0 , due to multiple scattering is given by the formula [81],

$$\frac{13.6 \text{ MeV}}{\beta c p} z \sqrt{x/X_0} [1 + 0.038 \ln(x/X_0)], \quad (4.2)$$

where p , βc , and z are the momentum, velocity and charge number of the particle, and x/X_0 is the thickness of the scattering material in radiation lengths (the characteristic amount of matter traversed by the particle wherein energy is lost due to radiative processes). This deflection might explain why, in Fig. 4.8, more antiprotons are caught with the degrading foil removed ($0 \mu\text{m}$ thickness, ~ 65 counts) than for larger degrader thicknesses ($35\text{-}50 \mu\text{m}$, <50 counts). With the foil removed, the antiprotons are not slowed as much, but the beam is much more well focused, and more antiprotons arrive at the trapping region. Whereas for large degrading thicknesses, in addition to some of the beam being annihilated at the foil, some of the continuing antiprotons are also scattered and do not arrive at the catching trap. This problem can be minimized by moving the degrading material further into the magnetic field, which will act to limit the divergence of the beam as the charged particles follow the magnetic field lines into the trapping region, or eliminating the rotatable degrader altogether once the optimum thickness is known.

4.4 Cooling Curve and Antiproton Lifetime in the Catching Trap

With antiprotons contained in the catching trap, the next step is to include electrons to further cool the trapped antiprotons. The procedure for added electrons into the catching trap is outlined in Section 3.3.1 and involves loading electrons into a shallow potential well within the antiproton trapping region before the antiprotons are delivered from the AD. The antiprotons then interact with the cold electrons and cool into the well.

4.4.1 Cold Dumps

The distinction can then be made between the dumping of cold and hot antiprotons. The dumping of hot antiprotons is inevitable; whenever the high-voltage barrier is disengaged, antiprotons that have not fully cooled into the electron well will be released and annihilate on the degrading material. Since it is necessary to lower one of the high-voltage barriers to trap the next injection of antiprotons, there will be a hot dump every cycle before new antiprotons arrive. Cold dumps then refer to the release of antiprotons that have been cooled with the electrons. This is a more controlled process, as the cold antiprotons often reside in shallow potential wells and can be easily manipulated or held for longer periods of time. The cooling of antiprotons with electrons in the apparatus can then be carefully studied.

4.4.2 Cooling Curve

It takes a number of seconds for the antiprotons to come into equilibrium with the cold electrons. This cooling rate can be examined by varying the interaction time between electrons and antiprotons and measuring the number of cold antiprotons. This is accomplished by running the catching and cooling sequence with a range of electron-antiproton interaction times and measuring the number of antiprotons that have cooled into the electron well. Both hot and cold dumps can be recorded and it is expected that the the

total counts (hot and cold) should remain constant unless some antiprotons are leaving the trap or being annihilated.

A typical cooling curve is shown in Fig. 4.9. Both hot and cold dumps are plotted as a function of the interaction time between the electrons and antiprotons. The average of the total dumps (hot + cold) is also shown, although it is clear that for longer interaction times the cold dumps begin to diminish. This is possibly due to interactions between the antiprotons and electrons as they reach equilibrium and the plasma effects become important. This also indicates an optimum interaction time where the antiprotons have cooled to the electron temperature, but before the antiprotons can leave the well. This interaction time was identified as 40 s and this timing sequence employed for the entire run.

Figure 4.9 can also be used for a simplified analysis of the cooling rate of antiprotons into the electron well. Examining the decrease in the hot dump values and recalling Eqn. 3.17, the antiprotons should cool to the electron temperature (4.2 K). Fitting an exponential curve to the hot dump data (shown in Fig. 4.9), we find a characteristic time of $\tau = 15 \pm 1$ s. The nominal interaction time of 40 s, stated above, then corresponds to around 3τ , or $\sim 95\%$ of the antiprotons being cooled into the electron well. This is a reasonable majority of antiprotons cooled and usable for further measurements, with only $\sim 5\%$ discarded during the hot dump. Note the initial cooling is non-exponential, presumably due to the high energy of the initial antiprotons.

In addition, a major consideration when determining a suitable electron-antiproton interaction time is the time constraints placed by the other elements of the apparatus. While cooling the antiprotons is a necessity, not all the antiprotons can be cooled quickly enough to be useful. Since the majority of the caught antiprotons very quickly cool to the electron temperature, for expediency the remaining antiprotons are discarded.

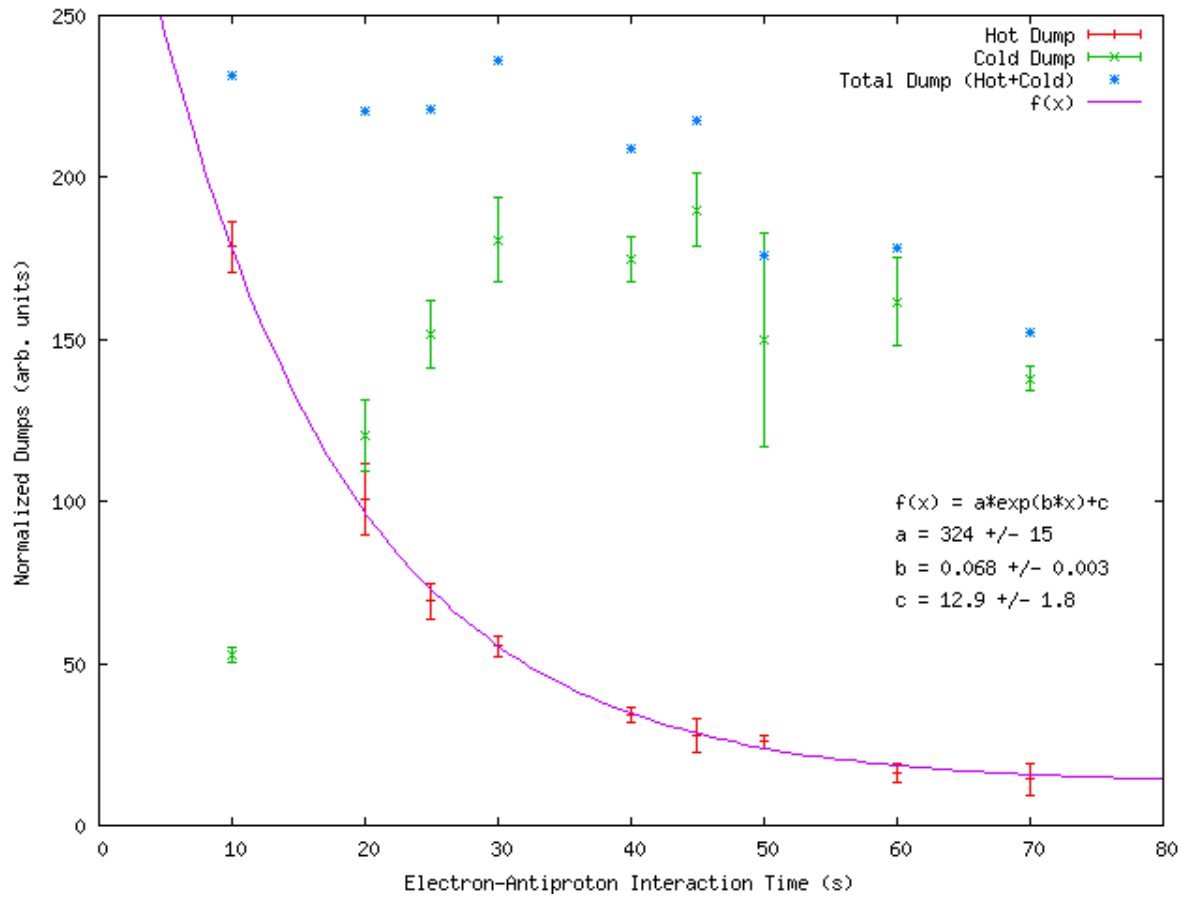


Figure 4.9: Cooling curve (values taken from runs 1111-1119). Hot and Cold dumps are shown along with the their total (Hot+Cold). Error bars represent the shot-to-shot variation of delivered antiprotons.

4.4.3 Cold Antiproton Lifetime

Any antiparticle is extremely sensitive to its environment. Antiprotons can only be kept for significant periods of time in a good vacuum; any residual gas particles will cause the trapped antiprotons to annihilate. To complete any measurement, the antiprotons need to remain in the trap long enough to be utilized. Therefore, it is more than prudent to check that the conditions of the ALPHA apparatus allow sufficient storage time to allow for the manipulations necessary to produce and study antihydrogen.

In the field of high-energy physics, the lifetime of a particle is usually the characteristic time before the particle decays into lighter constituent particles. However, in the context of antihydrogen research, the lifetime of cold antiprotons refers to how long the antiparticles remain in the trap. Losses from the trap will be from antiprotons either leaving the trapping potential or being annihilated by residual gas particles. Since it is difficult for the antiprotons to leave the trap once confined without some mechanism to provide the additional energy to escape, most losses will be due to annihilation. This can be thought of as the mean free time between collisions between protons and antiprotons. Thus, the lifetime of the antiprotons is a direct measure of the trap's vacuum quality.

Figure 4.10 shows cold antiproton dumps as a function of time spent trapped after electron kickout. All values are normalized to the measurement of the cold dump value 1 s after kickout where the majority of antiprotons should still be contained in the trap. With these trap conditions (temperature in the cryostat ~ 8 K with a correspondingly good vacuum) there was very little noticeable decrease in the number of trapped antiprotons over the time range measured. No significant losses seen as far as the 460 s range (where the measurement was concluded). This places a lower bound on the lifetime of antiprotons in the trap, and since no foreseeable measurements requires longer lifetimes, it is sufficient to state that the antiproton lifetime in the trap is greater than 460 s. Using this to estimate a lower limit for the mean free path of the antiprotons in the trap, an upper

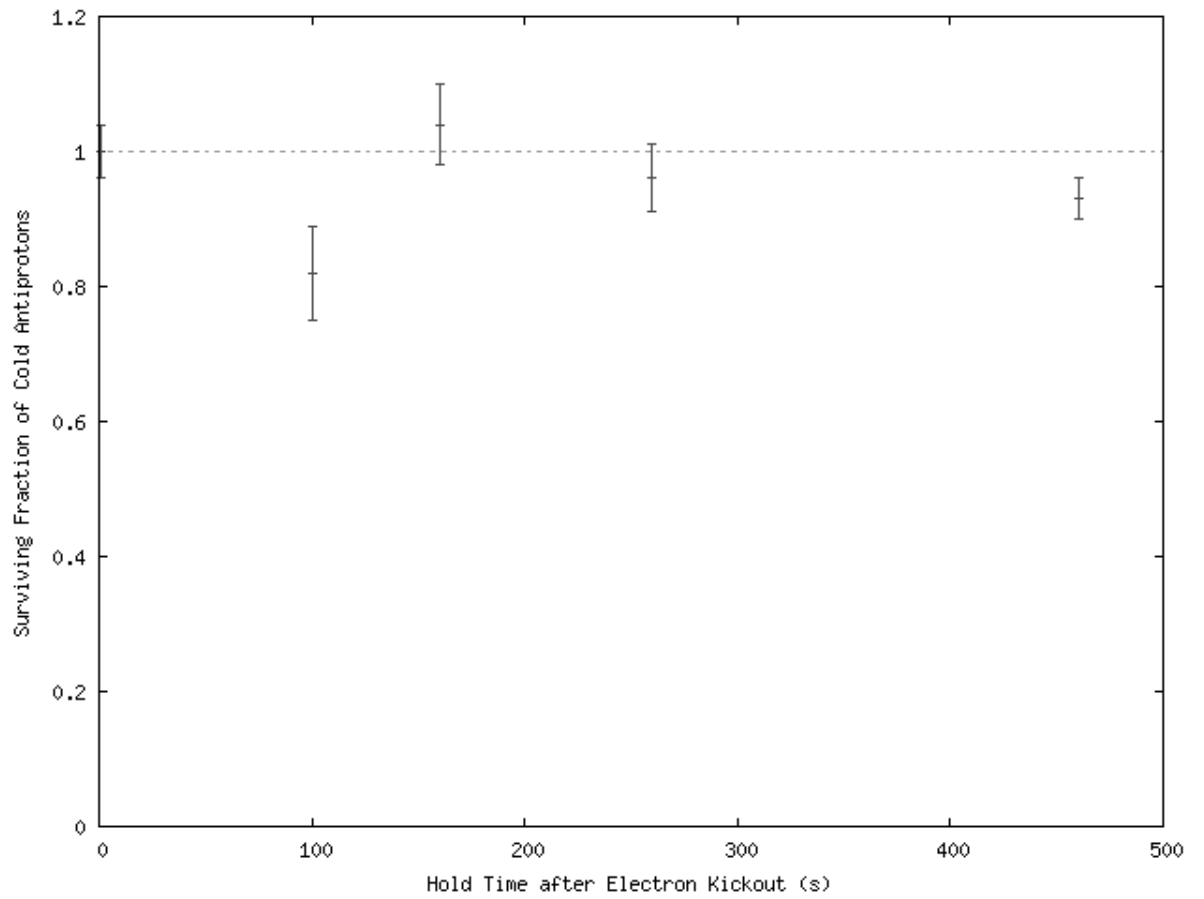


Figure 4.10: Cold antiproton lifetime (values taken from runs 1120-1124,1131). Values are normalized to the 1 s dump. Dotted line shows the surviving fraction of unity.

limit on the vacuum pressure can be placed at $\sim 10^{-10}$ mbar.

4.4.4 Stacking

Some experiments are likely to require a large number of antiprotons, more than can be provided by a single AD injection. In this case, several AD injections will need to be combined to increase the number of usable antiprotons. This method is called ‘stacking’ and requires adequate antiproton lifetimes to accommodate the extra time that the first few injections will remain in the trap as the additional antiprotons are injected. Electrons remain in the collection well throughout the measurement to cool the incoming antiprotons.

The relationship between the number of cold antiprotons in the trap versus the number of AD injections is shown in Fig. 4.11. With these trap conditions (again, a trap temperature of ~ 8 K), there is a clearly linear relationship between the number of trapped antiprotons and the number of AD injections. This is to be expected given the long antiproton lifetime shown in Fig. 4.10 and the rapid cooling of antiprotons into the electron well discussed in Section 4.4.2 (necessary to avoid antiproton escape during subsequent antiproton injections). The antiprotons are able to survive in the trap for the time periods needed to add all the remaining antiprotons. Note that, given the amount of time needed to complete a measurement of the larger number of AD injections, only one measurement was taken for each data point in Fig. 4.11.

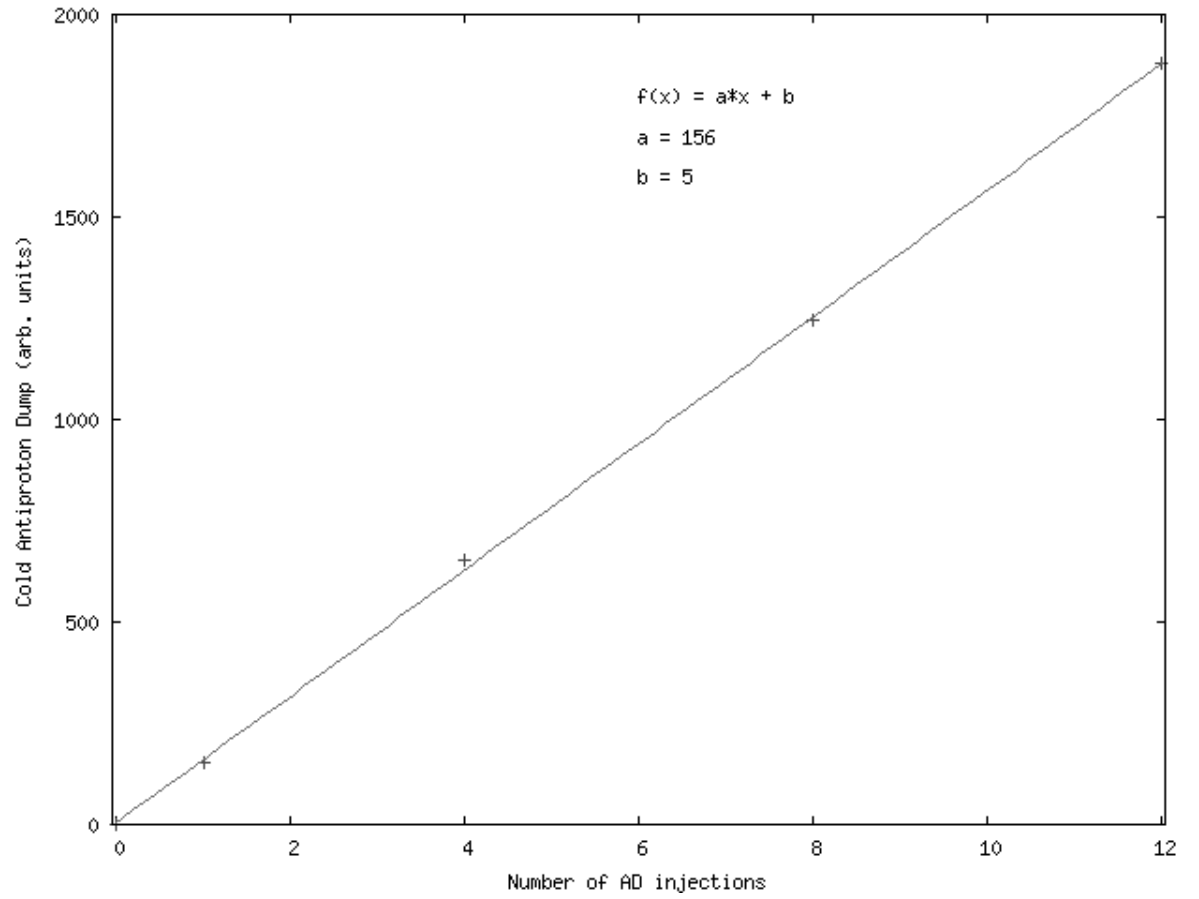


Figure 4.11: Antiproton stacking measurement (values taken from runs 1134-1138). Values are taken from single measurements and no errors given.

Chapter 5

Summary, Conclusions, and Future Work

This final chapter provides a climax to the thesis, outlining the final ALPHA experimental results from the 2006 physics run, prospects for the future of the ALPHA project, and a final overview of the thesis as a whole. This chapter is meant to both summarize the results presented through this thesis and communicate to the reader some of the excitement that exists in the ALPHA collaboration of the experimental runs for 2007 and beyond.

5.1 Results with the ALPHA apparatus

The commissioning process described in Chapter 4 demonstrated the operation of the ALPHA antihydrogen apparatus and provided a detailed understanding of the output obtained through its use. Moreover, all of the measurements taken had a specific purpose with regards to the optimization of the various aspects of the experimental setup with the intent to produce trappable antihydrogen. With the operation of the apparatus confirmed, the ALPHA project can advance into unknown territory and conduct new experiments where the outcome is yet to be determined. What follows is a short description of the results of the 2006 physics run.

An innovative aspect of the ALPHA apparatus is the inclusion of several superconducting magnets surrounding mixing region (Fig. 3.1), the combination of which constitutes a magnetic, neutral atom trap. The inhomogeneous magnetic fields provided by the superconducting magnets creates a magnetic minimum along the trap axis in the region where the antiparticles are mixed. Those antihydrogen atoms that are formed in

this region with low-field seeking magnetic moments may be confined within the neutral atom trap. The trapping of antihydrogen atoms is a major goal of the ALPHA project and the focus of most of the experimental effort.

To create the magnetic minimum potential, mirror coils are placed on the edges of the mixing region to provide confinement along the axis, while a multipole magnetic field is used to provide radial confinement. However, there have been concerns that since the multipolar field will break the radial symmetry, the positrons and antiprotons may be directed into the trap wall where they will annihilate [82]. The ALPHA magnetic neutral atom trap employs a octupole magnet to reduce the perturbation of the magnetic field near the axis of the trap while still providing radial confinement [57]. Survival of both positrons (Fig. 5.1) and antiprotons (Fig. 5.2) was demonstrated over times necessary for antihydrogen studies in the presence of the octupole field.

Given the interaction between the magnetic field and the magnetic moment of the antihydrogen atoms, as described by $U = -\vec{\mu} \cdot \vec{B}$, the well depth of the neutral atom trap is

$$U = 0.67K \times \Delta B, \quad (5.1)$$

where ΔB is the difference between the maximum and minimum applied magnetic fields (in units of T). In the radial direction the change in magnetic fields can be written as

$$\Delta B = \sqrt{B_z^2 + B_w^2} - B_z, \quad (5.2)$$

where B_z is the axial solenoid field strength and B_w is the radial multipole field strength.

To increase well depth in the radial direction, the solenoid magnetic field strength was lowered from 3 T to 1 T. However, the antiproton catching efficiency is reduced as a function of solenoid field strength (Fig. 5.3). To overcome the reduced catching efficiency, the ALPHA apparatus includes an internal solenoid in the catching region that can be

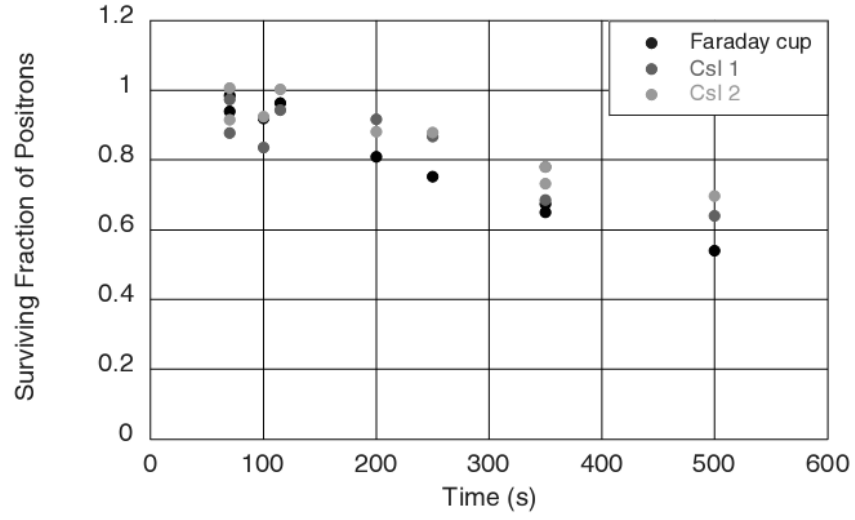


Figure 5.1: Ratio of the number of positrons in the octupole field to the number without the octupole field as a function of holding time (reproduced with permission from [7]). The number of positrons is measured using a Faraday cup and two CsI detectors. For clarity, error bars (usually $\sim 10\%$) are omitted.

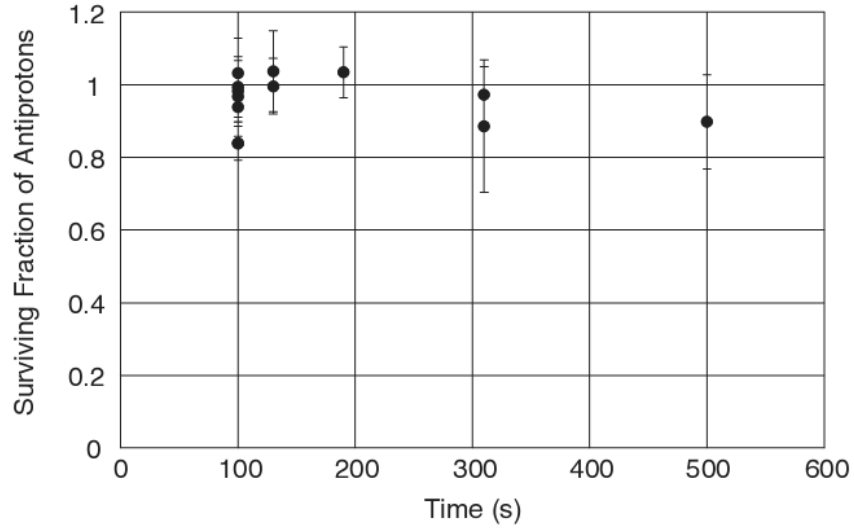


Figure 5.2: Ratio of the number of antiprotons in the octupole field to the number without the field (reproduced with permission from [7]). Error bars represent the standard deviation of one set of measurements.

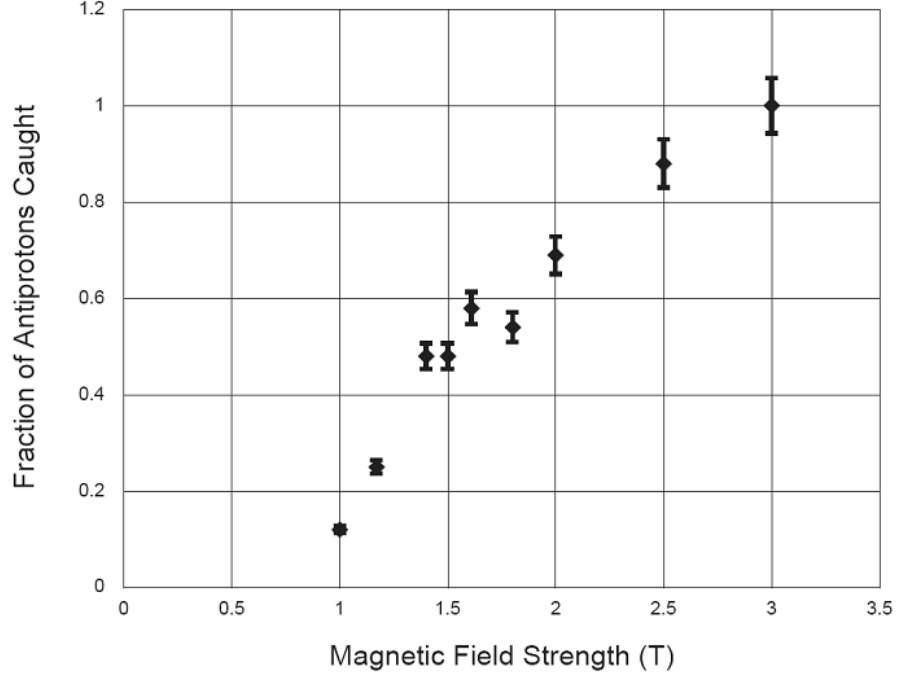


Figure 5.3: Antiproton catching efficiency relative to the value for the 3 T field (reproduced with permission from [10]). The error bars reflect the shot-to-shot variation ($\sim 6\%$) in the measurement.

ramped up 2 T to provide an overall 3 T catching field.

The next step is then to demonstrate antihydrogen production in the reduced solenoid magnetic field (previous antihydrogen production being done at 3 T or greater). One prerequisite for antihydrogen production is the positron cooling of antiprotons, observed by both ATHENA [1] and ATRAP [83]. Antiprotons injected into a positron plasma will slow through Coulomb interactions and eventually cool to the positron energy. Fig. 5.4 shows the positron cooling of antiprotons in the ALPHA apparatus at 1 T. The antiprotons remain at their injection energy when there are no positrons (Fig. 5.4b), but with positrons the antiprotons cool to an energy close to that of the potential at which the positron plasma is being held (5.4c). Fig. 5.4d shows that the antiprotons cool inefficiently when mixed with positrons that are heated through the RF interaction with the plasma's axial dipole moment.

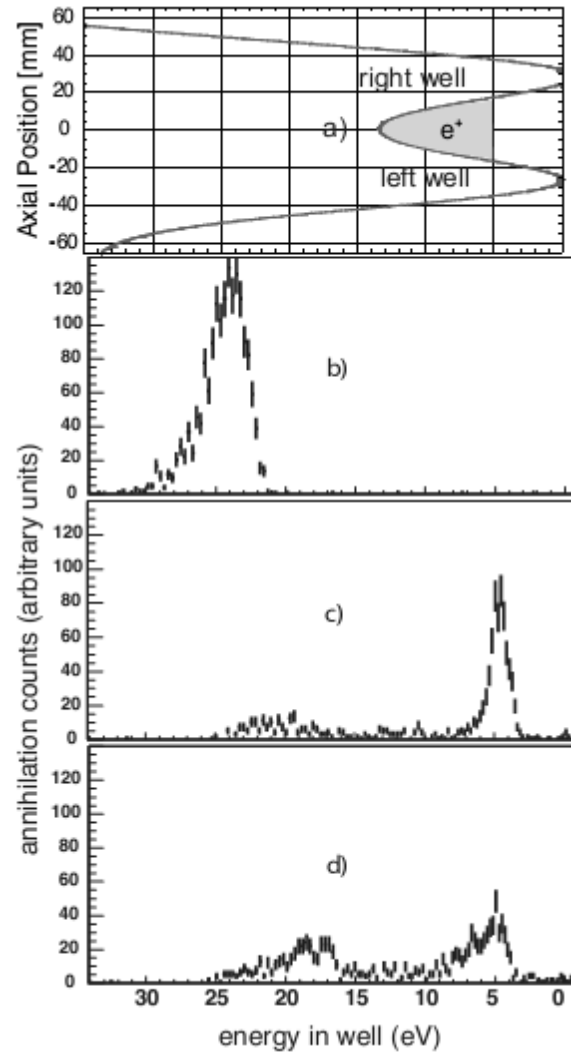


Figure 5.4: Positron cooling of antiprotons at 1 T (reproduced with permission from [10]). Fig. a) shows the on-axis trap potential. Fig. b) shows the energy distribution for only antiprotons in the trap, c) shows a normal mixing between positrons and antiprotons, and d) shows a mixing between antiprotons and heated positrons.

Fig. 5.5 shows the annihilation signal during the mixing of antiparticles as observed by internal scintillation detectors (Fig. 3.1). This signal is produced as the antihydrogen forms, leaves the trap, and annihilates on the trap walls. Two data sets are shown: normal mixing between positrons and antiprotons, as well as mixing where the positrons are electromagnetically heated by application of an RF driving field. During normal mixing, there is a well defined peak in the annihilation signal immediately following positron-antiproton mixing. However, with RF heating of the positron plasma this peak is suppressed when the positron kinetic energy exceeds the positron-antiproton binding energy (antiproton ionization potential), similar to the experience in ATHENA [4, 52]. Taken together, the positron cooling of antiprotons (Fig. 5.4) and distinctive annihilation signature (Fig. 5.5) demonstrate antihydrogen production in the ALPHA apparatus.

5.2 Future Work: Towards the Trapping of Antihydrogen

The demonstration of antihydrogen production in the ALPHA apparatus is a significant accomplishment. However, the goal still remains to trap and hold antihydrogen atoms for precision measurements. The ALPHA experiment is making steady progress towards this goal by making every effort to produce extremely cold antihydrogen and operating in a parameter range conducive to the trapping of antihydrogen.

Some additions and improvements are scheduled for the ALPHA apparatus to aid in the effort to trap antihydrogen. A significant addition is the inclusion of a silicon vertex detector for the recording and reconstruction of the antihydrogen annihilation signature. This detector is comprised of several layers of segmented silicon microstrip wafers that surround the antiparticle mixing region. By recording the passage of charged pions (resulting from antiproton annihilation) through the silicon wafers, the path of the pions can be calculated and their origin extracted. Since the pions result from antiproton

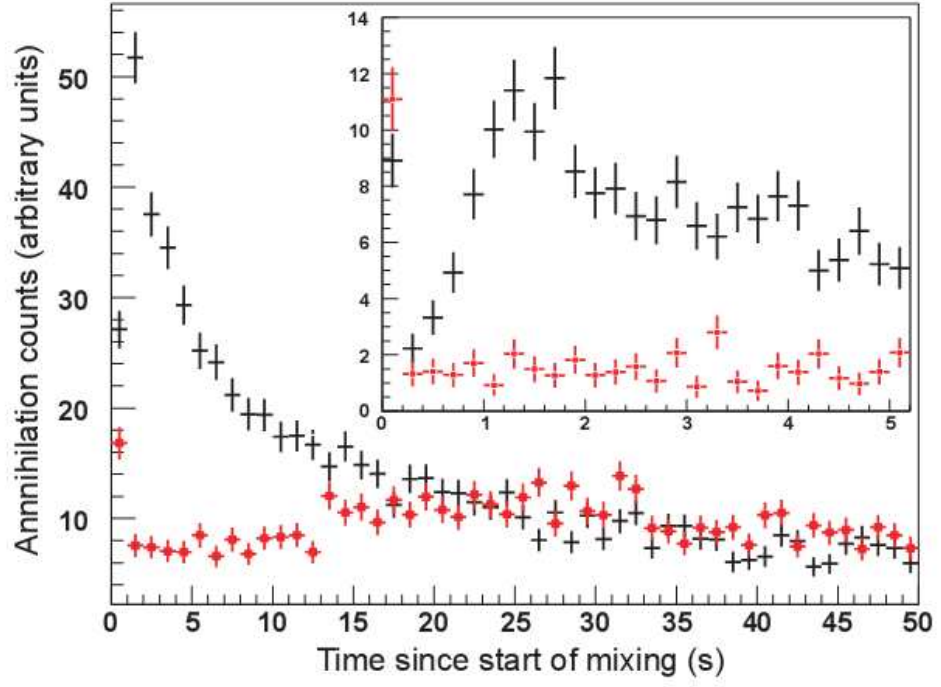


Figure 5.5: Time evolution of the scintillator events during the mixing of positrons and antiprotons (reproduced with permission from [10]). The data set marked by (black) crosses shows the evolution during a normal mixing, while the data set with (red) circles shows the mixing where the positrons are being heated to suppress antihydrogen formation. The inset shows the first 5 s of the same data with re-binning into 200 ms bins.

annihilation, by locating their origin, the position of annihilated antihydrogen atom can be inferred. This gives an accurate and extremely useful picture of the antihydrogen behaviour in the apparatus. The annihilation vertex detector will be an invaluable tool in the attempt to trap antihydrogen by providing insight into the antihydrogen produced within the apparatus.

Given the shallow trap depth of the magnetic neutral atom trap described in Sec. 5.1, producing very trappable antihydrogen atoms may prove a significant challenge. The atoms must be formed at very low energies so as to remain within the magnetic trap. By reducing the energy of the constituent positrons and antiprotons, the antihydrogen atom may be produced at lower energies. Thus, care is taken to keep the antiparticles as cold as possible and minimize heating sources, such as RF noise on the trap electrodes or thermal radiation from the surrounding environment. New techniques and approaches may be required to further cool the antiparticles and insure that the antihydrogen atoms indeed trappable.

With the innovative and sophisticated ALPHA apparatus, the magnetic confinement of antihydrogen is much closer to reality. The availability of trapped antihydrogen would permit experiments on neutral antimatter that were not previously possible. Such measurements would deeply probe matter-antimatter symmetry and the *CPT*-theorem in the largely unexplored antiatomic regime.

5.3 Summary

Effectively, this thesis is divided into two sections: a theoretical part and an experimental part. After a short introductory chapter outlining the study of antihydrogen, Chapter 2 describes three models of short-time antihydrogen production. By investigating the antihydrogen signal immediately follow the mixing of positrons and antiprotons, some insight

may be gained in regards to the onset of antihydrogen formation. It is concluded that the temperature equilibration is the important factor in the short-time production. These three models constitute the theoretical part of the thesis and demonstratably follow the short-time behaviour of antihydrogen production. These models can then be used to examine, in a simple way, properties of antihydrogen production, such as the calculation given of the percentage of antihydrogen atoms formed with axial energy less than 0.1 eV (Sec. 2.5). This calculation shows that the antihydrogen formation energy is strongly dependent upon the initial antiproton energy (injection energy), and therefore a very low initial antiproton energy is desirable in the attempt to produce low-energy antihydrogen.

Chapters 3 and 4 make up the experimental section of this thesis and deal with the ALPHA antihydrogen apparatus. The details of the apparatus and its operation are given in Chapter 3, along with descriptions of important processes for the capture and manipulation of antiprotons. Chapter 4 outlines the commissioning of the ALPHA apparatus with emphasis on the antiproton capture and handling. The series of measurements described follows the procedure intended to maximize the number of antiproton trapped in the apparatus and available for antihydrogen production. After optimizing the various apparatus parameters for antiproton trapping and manipulation, it is shown that antiprotons in the apparatus are suitable for mixing with positrons for antihydrogen production (that is, remain confined within the traps for times suitable for antiparticle mixing). This constitutes a successful commissioning of the apparatus.

Chapter 5 provides an overview of the results found with the ALPHA apparatus and describes the direction of the future experimental study of antihydrogen. The demonstration of antihydrogen production in the ALPHA apparatus is described as well as the survival of antiparticles in an octupolar magnetic field. This is an important step towards the goal of trapping neutral antihydrogen. Finally, Appendix A gives a technical description of the ALPHA data acquisition system and the software used to record and

analyze data collected from the apparatus.

Bibliography

- [1] ATHENA Collaboration, M. Amoretti *et al.*, Phys. Letts. B **590**, 133 (2004).
- [2] G. Baur *et al.*, Phys. Lett. B **368**, 251 (1996).
- [3] G. Blanford *et al.*, Phys. Rev. Lett. **80**, 3037 (1998).
- [4] ATHENA Collaboration, M. Amoretti *et al.*, Nature **419**, 456 (2002).
- [5] ATRAP Collaboration, G. Gabrielse *et al.*, Phys. Rev. Lett. **89**, 213401 (2002).
- [6] ATHENA Collaboration, M. Amoretti *et al.*, Phys. Letts. B **583**, 59 (2004).
- [7] ALPHA Collaboration, G. Andresen *et al.*, Phys. Rev. Letts **98**, 023402 (2007).
- [8] ATHENA Collaboration, M. Amoretti *et al.*, Nucl. Instrum. Methods Phys. Res. A **518** (2004).
- [9] M. Charlton and J. Humberston, *Positron Physics* (Cambridge University Press, 2001).
- [10] ALPHA Collaboration, G. Andresen *et al.*, Submitted to Phys. Letts. B (2007).
- [11] P. A. M. Dirac, Proc. Roy. Soc. A **126**, 360 (1930).
- [12] C. D. Anderson, Science **76**, 238 (1932).
- [13] S. Chu, A. P. Mills, and J. L. Hall, Phys. Rev. Lett. **52**, 1689 (1984).
- [14] M. S. Fee *et al.*, Phys. Rev. A **48**, 192 (1993).
- [15] R. J. Hughes and B. I. Deutch, Phys. Rev. Lett. **69**, 578 (1992).
- [16] B. Müller and M. H. Thoma, Phys. Rev. Lett. **69**, 3432 (1992).

- [17] A. Schäfer and J. Reinhardt, Phys. Rev. A **51**, 838 (1995).
- [18] P. B. Schwinberg, R. S. Van Dyck, and H. G. Dehmelt, Phys. Rev. Lett. **47**, 1679 (1981).
- [19] R. S. Van Dyck, P. B. Schwinberg, and H. G. Dehmelt, Phys. Rev. Lett. **59**, 26 (1987).
- [20] O. Chamberlain, E. Segrè, C. Wiegand, and T. Ypsilantis, Phys. Rev. **100**, 947 (1955).
- [21] P. Roberson *et al.*, Phys. Rev. C **16**, 1945 (1977).
- [22] G. Gabrielse *et al.*, Phys. Rev. Lett. **82**, 3198 (1999).
- [23] M. Hori *et al.*, Phys. Rev. Lett. **91**, 123401 (2003).
- [24] G. Lüders, Annals of Physics **2**, 1 (1957).
- [25] D. C. Cheng and G. K. O'Neill, *Elementary Particle Physics* (Addison-Wesley Publishing Company, 1979).
- [26] D. H. Perkins, *Introduction to High Energy Physics* (Addison-Wesley Publishing Company, 1982).
- [27] R. P. Feynman, *The 1987 Dirac memorial lectures* (Cambridge University Press, 1987).
- [28] M. Holzschneider, M. Charlton, and M. Nieto, Phys. Rep. **402**, 1 (2004).
- [29] C. S. Wu, E. Ambler, R. W. Hayward, D. D. Hoppes, and R. P. Hudson, Phys. Rev. **105**, 1413 (1957).
- [30] A. Angelopoulos *et al.*, Phys. Lett. B **444**, 43 (1998).

- [31] C. L. Cesar *et al.*, Phys. Rev. Lett. **77**, 255 (1996).
- [32] M. Niering *et al.*, Phys. Rev. Lett. **84**, 5496 (2000).
- [33] C. M. Will, *Theory and experiment in gravitational physics* (Cambridge University Press, 1981).
- [34] R. J. Hughes and M. H. Holzscheiter, J. Mod. Opt. **39**, 263 (1991).
- [35] M. H. Holzscheiter, M. Charlton, and M. M. Nieto, Physics Reports **402**, 1 (2004).
- [36] L. Brillouin, Phys. Rev. **67**, 260 (1945).
- [37] M. M. Nieto, M. H. Holzscheiter, and T. J. Phillips, Journal of Optics B: Quantum and Semiclassical Optics **5**, S547 (2003).
- [38] M. Nieto, M. Holzscheiter, and S. Turyshev, eprint arXiv:astro-ph/0410511 (2004).
- [39] C. Munger, S. Brodsky, and I. Schmidt, Hyperfine Interactions **76**, 175 (1993).
- [40] C. T. Munger, S. J. Brodsky, and I. Schmidt, Phys. Rev. D **49**, 3228 (1994).
- [41] A. Müller and A. Wolf, Hyperfine Interactions **109**, 223 (1997).
- [42] H. Bethe and E. Salpeter, *Quantum Mechanics of One- and Two-Electron Systems* (Springer, Berlin, New York, 1957).
- [43] M. Holzscheiter and M. Charlton, Rep. Prog. Phys. **62**, 1 (1999).
- [44] M. E. Glinsky and T. M. O'Neil, Phys. Fluids B **3**, 1279 (1991).
- [45] P. J. Schultz and K. G. Lynn, Rev. Mod. Phys. **60**, 701 (1988).
- [46] M. Charlton, Phys. Letts. A **143**, 143 (1990).
- [47] E. A. Hessel, D. M. Homan, and M. J. Cavagnero, Phys. Rev. A **57**, 1668 (1998).

- [48] G. Gabrielse, S. Rolston, L. Haarsma, and W. Kells, Phys. Lett. A **192**, 38 (1988).
- [49] ATHENA Collaboration, L. V. Jørgensen *et al.*, Physical Review Letters **95**, 025002 (2005).
- [50] ATHENA Collaboration, N. Madsen *et al.*, Physical Review Letters **94**, 033403 (2005).
- [51] ATHENA Collaboration, M. Amoretti *et al.*, Physical Review Letters **97**, 213401 (2006).
- [52] ATHENA Collaboration, M. Amoretti *et al.*, Phys. Rev. Lett. **91**, 055001 (2003).
- [53] ATRAP Collaboration, J. Estrada, T. Roach, J. N. Tan, P. Yesley, and G. Gabrielse, Phys. Rev. Lett. **84**, 859 (2000).
- [54] ATRAP Collaboration, G. Gabrielse *et al.*, Phys. Rev. Lett. **89**, 233401 (2002).
- [55] ATRAP Collaboration, G. Gabrielse *et al.*, Physical Review Letters **93**, 073401 (2004).
- [56] ATRAP Collaboration, C. H. Storry *et al.*, Physical Review Letters **93**, 263401 (2004).
- [57] ALPHA Collaboration, W. Bertsche *et al.*, Nucl. Inst. Meth. Phys. Res. A **566**, 746 (2006).
- [58] F. Robicheaux and J. D. Hanson, Physical Review A **69**, 010701 (2004).
- [59] F. Robicheaux, Physical Review A **70**, 022510 (2004).
- [60] M. L. Wall, C. S. Norton, and F. Robicheaux, Physical Review A **72**, 052702 (2005).
- [61] F. Robicheaux, Physical Review A **73**, 033401 (2006).

- [62] S. X. Hu, D. Vrinceanu, S. Mazevet, and L. A. Collins, *Physical Review Letters* **95**, 163402 (2005).
- [63] D. Vrinceanu, S. X. Hu, S. Mazevet, and L. A. Collins, *Physical Review A* **72**, 042503 (2005).
- [64] S. X. Hu, *Physical Review A* **75**, 010501 (2007).
- [65] G. Gabrielse, S. Rolston, L. Haarsma, and W. Kells, *Hyperfine Interactions* **44**, 287 (1988).
- [66] M. Kretzschmar, *Eur. J. Phys.* **12**, 240 (1990).
- [67] D. Möhl, CERN-PS-96-034-DI (CERN Internal Document) (1996).
- [68] D. Möhl, Stochastic cooling for beginners, in *CAS - CERN Accelerator School: Antiprotons for Colliding-beam Facilities*, 1983.
- [69] J. Bossler, CERN-PS-90-65-AR (CERN Internal Document) (1990).
- [70] D. Möhl, CERN-PS-86-31-LEA (CERN Internal Document) (1986).
- [71] P. Belochitskii, T. Eriksson, and S. Maury, *Nucl. Instrum. Methods Phys. Res. A* **214**, 176 (2004).
- [72] H. Wiedemann, *Synchrotron Radiation* (Springer-Verlag, Berlin, 2003).
- [73] T. J. Murphy and C. M. Surko, *Phys. Rev. A* **46**, 5696 (1992).
- [74] R. Greaves, M. Tinkle, and C. Surko, *Physics of Plasmas* **1**, 1439 (1994).
- [75] X.-P. Huang, F. Andereg, E. M. Hollmann, C. F. Driscoll, and T. M. O’Neil, *Phys. Rev. Lett.* **78**, 875 (1997).
- [76] R. G. Greaves and C. M. Surko, *Phys. Rev. Lett.* **85**, 1883 (2000).

- [77] G. Knoll, *Radiation Detection and Measurement* (John Wiley & Sons, Inc., 1979).
- [78] P. Strehl, *Beam Instrumentation and Diagnostics* (Springer-Verlag, Berlin, 2006).
- [79] P. Riedler, J. Rochet, A. Rudge, M. Doser, and R. Landua, Nucl. Instrum. Meth. Phys. Res. A **487**, 316 (2002).
- [80] R. Medenwaldt *et al.*, Nucl. Instrum. Meth. Phys. Res. B **58**, 1 (1991).
- [81] W.-M. Yao *et al.*, Journal of Physics G **33**, 1 (2006).
- [82] J. Fajans, W. Bertsche, K. Burke, S. F. Chapman, and D. P. van der Werf, Physical Review Letters **95**, 155001 (2005).
- [83] ATRAP Collaboration, G. Gabrielse *et al.*, Phys. Letts. B **507**, 1 (2001).

Appendix A

ALPHA Data Acquisition System

A major aspect of the ALPHA experiment is the accompanying acquisition system used to gather and record the data generated by the apparatus. The ALPHA Data Acquisition system (DAQ) consists of several systems that work together to acquire, distribute and record data from the apparatus and experimental support systems. This appendix will give a technical description of the DAQ system, focusing on the MIDAS framework and ALPHAROOT visualization and analysis program.

A.1 Overview

The ALPHA DAQ system (Fig. A.1) is an amalgamation of a number of different data gathering, recording and display programs. In the center is the MIDAS data acquisition framework, which occupies the primary role in collecting, recording, and sharing the data from the input devices. All data generated by the apparatus that is to be stored is passed through MIDAS to be organized and recorded. Fast data from the ADC, scaler and multiscaler modules is accessed directly by the MIDAS frontends via the VME interface. Environmental, magnet and positron data is sent to MIDAS through a TCP network connection from a LabVIEW program that interfaces directly with the instruments. Once organized by MIDAS, the incoming data is available in a shared memory buffer where it can be accessed by ancillary programs. The ALPHAROOT program fills this role, receiving the incoming data from the MIDAS buffer and performing preliminary analysis and visualization. ALPHAROOT provides online display of important parameters as well as offline analysis and the ability to histogram any of the components of the recorded data.

Module	Description
SIS3820	32 channel Multiscaler
v515	16 channel I/O module
v560	16 channel scaler
v792	32 channel ADC
VMIC 7805	VME microprocessor

Table A.1: VME Modules

The overall control of the data acquisition system is provided as part of the MIDAS web interface, which also provides monitoring and display of data with the history plotting system.

A.1.1 VME Modules

The present ALPHA DAQ system includes five VME modules, summarized in Table A.1. These include a 32-channel multipurpose counter, 32-channel ADC, 16-channel scaler, 16-channel I/O module and a VME microprocessor. All VME modules are located in the same VME crate in the ALPHA control room. Descriptions of each individual module are given below.

SIS Multiscaler

The multi purpose counter used in the ALPHA experiment is a SIS3840 multiscaler. This module has 32 channels (16 LEMO and 16 ECL) and supports 64Mbytes SDRAM. The SIS3840 module can handle 250MHz counting rates with 32-bit counter depth. For the ALPHA experiment, the SIS module is set up with a first-in-first-out (FIFO) input data buffer for primary use as a timing module for the synchronization of data from the various experimental inputs. As each instrument performs an operation, a timestamp (in the form of a NIM or TTL pulse) is sent to the SIS module. From their arrival at the SIS, the timing of the various operations can be organized and understood (as described in Sec. A.3.3). Most important is the coordination between the Sequencer and the particle

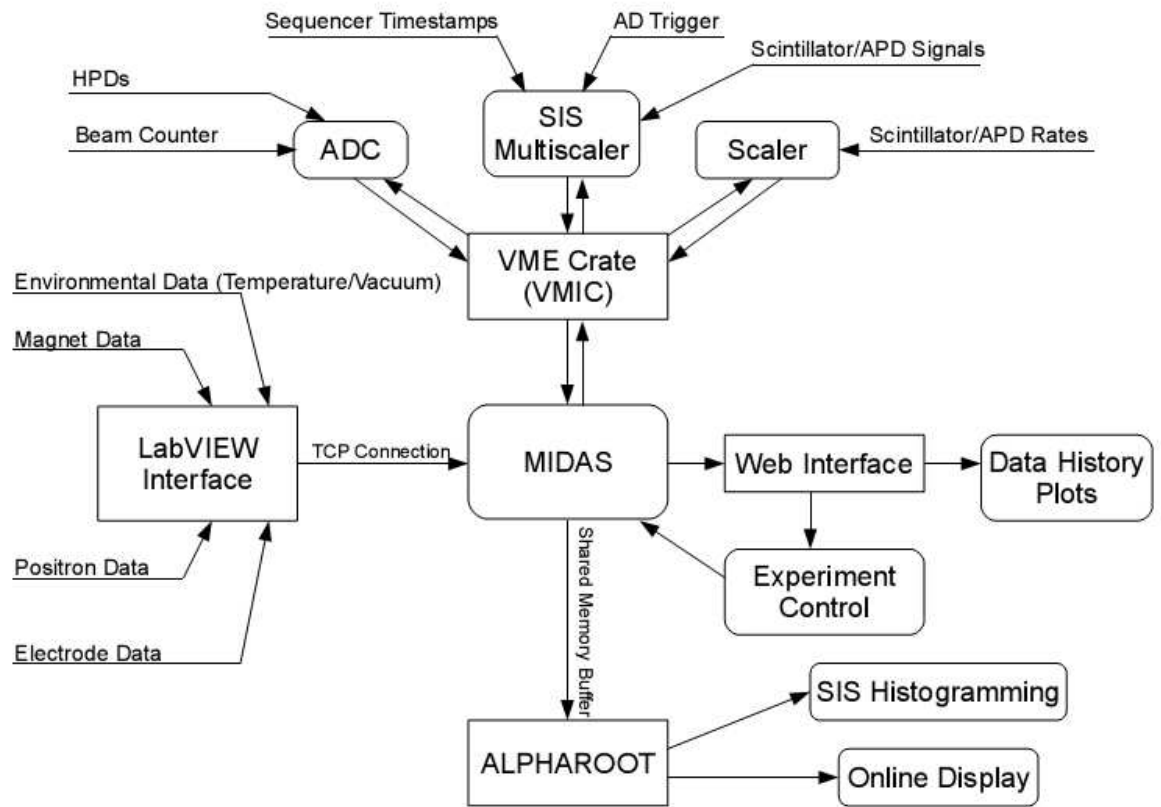


Figure A.1: Overview of the ALPHA DAQ system.

detectors, where the coincidence between operation and measurement is vital for the interpretation of particle behaviour within the apparatus. Table A.2 describes the inputs for each SIS channel.

ADC

To measure and record analog signals from various detectors, a CAEN v792 32 channel analog-to-digital converter (ADC) is employed. This unit first converts the input charge into a voltage level, then multiplexes the various input signals so they can then be converted into digital values by two fast 12-bit ADCs. The integration window of the input charge is controlled by a GATE signal provided by the NIM electronics. The GATE is carefully chosen such that the entire input signal from each channel is recorded. Each ADC channel has an associated pedestal values, which reflects the baseline integration value with no input signal. The pedestal value linearly depends upon the GATE duration length, so a small integration window that only covers the relevant signal is preferred. Table A.3 describes the ADC channels used for the ALPHA experiment. Only the silicon beam counter and HPDs are read by the ADC.

Scaler

The VME crate also includes a CAEN v560 16 channel scaler. This module has 16 independent 32-bit counting channels with a guaranteed input frequency of 100MHz. This module is used to count signals generated by the external scintillators; a description of each channel is given as Table A.4. Since the scaler module only counts the incoming signals as they are received, the DAQ software must then convert the counts to rates (which are more useful for experimental purposes).

I/O Module

A CAEN v513 16 channel general purpose I/O module is also a part of the ALPHA VME setup. Each channel of this unit can be specified either as input or output as well as

Channel	Description
1	10MHz clock
2	AD pretrigger
3	PMT OR (1 or 2 or 3 or 4)
4	APD OR (1 or 2 or 3 or 4)
5	Pbar sequencer timestamps
6	Mixing sequencer timestamps
7	Pbar sequence START
8	Mixing sequence START
9	PMT 1 and 2
10	PMT 3 and 4
11	APD coincidence (1 and 2 and 3 and 4)
12	CsI OR
13	APD 1
14	APD 2
15	APD 3
16	APD 4
17	Free
18	Mixing background START
19	Free
20	Mixing background END
21	(PMT 1 and 2) and (PMT 3 and 4)
22	Pbar chain START
23	LNE before VETO
24	LNE after VETO
25	Positron dump start
26	Ionization dump start
27	APD integrator
28	Mixing user timestamp
29	Start of mixing
30	End of mixing
31	Dump START
32	Dump END

Table A.2: SIS multiscaler channel descriptions.

Channel	Description
1	Beam counter pad 1
2	Beam counter pad 2
3	Beam counter pad 3
4	Beam counter pad 4
5	Beam counter pad 5
6	HPD 1
7	HPD 2
8-32	Free

Table A.3: ADC channel descriptions.

Channel	Description
1	Scintillator 1
2	Scintillator 2
3	Scintillator 3
4	Scintillator 4
5	Scintillator 1 and 2
6	Scintillator 3 and 4
7	Scintillator (1 and 2) or (3 and 4)
8	Scintillator (1 and 2) and (3 and 4)
9-16	Free

Table A.4: Scaler channel descriptions.

working in either positive or negative logic. For the ALPHA experiment, this module is used to generate the ‘MIDAS running’ flag, that is, channel 1 of this module is set HIGH during a experimental run, and LOW otherwise.

VMIC Microprocessor

Access to the ALPHA VME bus is provided through a VMIC VMIVME-7805 microprocessor. The VMIC module contains many of the features usually available on a desktop computer and is fully capable of running most current operating systems. The ALPHA VMIC is designated **alphavme01** and is cross-mounted with **alphacpc04** and **alphacpc05**, which all run Scientific Linux 4. The data acquisition and display responsibilities are split between these three computers, with **alphavme01** running the MIDAS software (including the web interface) and communicating with the other VME modules, **alphacpc05** running the ALPHAROOT analysis and visualization program as well as the ELOG electronic logbook, while **alphacpc04** is reserved for offline analysis. These three machines constitute the computing element of the ALPHA DAQ system.

A.2 MIDAS

MIDAS¹ (Maximum Integration Data Acquisition System) is a data acquisition system developed at PSI² and TRIUMF³, and used mostly for nuclear and particle physics experiments. MIDAS incorporates a flexible framework, which can accommodate a variety of hardware and computing components, with a powerful recording and data distribution system. The MIDAS framework is divided into a number of frontends, which collect and pass along the incoming data, and backend computers, which organize, record and analyze the data.

¹MIDAS websites: <http://midas.ph.ch> and <http://midas.triumf.ca>

²Paul Scherrer Institut: <http://www.psi.ch>

³TRI University Meson Facility: <http://www.triumf.ca>

Program	Description	Communicates with
fevme.exe	Handling of data from VME	VME Crate $\leftarrow$ VME modules
felabview.exe	LabVIEW data handling	LabVIEW interface over network
fesequence.exe	Sequencer data handling	Sequencer GUI over network
feade.perl	AD cycle information	AD computer
feadsurvey.perl	AD equipment information	AD computer

Table A.5: MIDAS Frontends.

A.2.1 Frontends

For every stream of incoming data, there is an associated frontend which acts as an intermediary between the module and MIDAS. This frontend communicates with the data input device, and relays the information to MIDAS. The frontend can also be used to control the operation of some devices (in the case where they are remotely controllable). Table A.5 gives a summary and description of the frontends used in the ALPHA experiment. All frontend programs are located in the `/home/alpha/online/bin/` directory on the **alphavme01** machine.

fevme.exe

The program **fevme.exe** handles the operation and data collection from the VME modules, including the SIS multiscaler, ADC, 16-channel scaler and multipurpose I/O module. The initialization and proper module readout are both handled by **fevme.exe**, as well as some rudimentary data processing operations like calculating data rates and maximum values for some instruments. Also handled by **fevme.exe** is the behaviour of the VME modules throughout the data collection process. **fevme.exe** defines their operation at the start and end of data collection runs, particularly the I/O module, for which the first channel is set HIGH during the collection run and LOW otherwise.

felabview.exe

Measurements performed by instruments outside of the VME rack must be sent to and recorded by MIDAS. The program that accepts the incoming data from the LabVIEW

interface, which reads out these various instruments, is **felabview.exe**. This program opens a TCP connection on port 12021 which receives data strings of the form

Label Timestamp value1 value2 value3 ...

where Label is some unique name identifying the type of data (e.g. ‘ADSurvey’), Timestamp is a time-identifying marker, and value1, value2, value3 ... are the experimental values to be recorded by MIDAS. The data is then sorted according the Label designation with all the values being recorded according to their associated device.

fesequencer.exe

All information sent by the sequencer to be recorded comes through **fesequencer.exe**. Similar to **felabview.exe**, **fesequencer.exe** receives and records TCP data, although from port 12022. However, **fesequencer.exe** simply records verbatim whatever information is sent over this connection. In practice, this frontend records only sequencer files used during a data collection run.

feade.perl

Information about the AD cycle is written to a remote CERN computer and is not directly accessible through the MIDAS equipment. In order to gather this information, the Perl script **feade.perl** is used to send the cycle information to MIDAS. First, the sh script **start.feade** is run, which copies the Perl script onto the the CERN **abcopl1** machine, then logs on and executes the script. This script will check the file containing the AD cycle information (**/ps/java/data/ade/sms/np/Last_shot.txt** on **abcopl1**) every 10 seconds. When the cycle information file is changed or updated, the new information is sent to MIDAS via the **felabview.exe** frontend. A list of the values managed by **feade.perl** is given in Table A.6.

feade.perl	feadsurvey.perl
ADE_unixtime	AD Timestamp
ADE_time	DR.SME5307S
ADE_3.5GeV	DE2.VGP45
ADE_2GeV	DE2.VGP12
ADE_300MeV	DE3.VGP17
ADE_100MeV_ramp	DE2.BHZ10
ADE_100MeV_end	DE2.DHZ15
ADE_TFA7049	DE2.DVT15
	DE2.QN20
	DE2.QN30
	DE2.DHZ35
	DE2.DVT35
	DE2.VVS42

Table A.6: List of AD values collected by **feade.perl** and **feadsurvey.perl**.

feadsurvey.perl

Information about the status of AD beamline equipment is also important to the experiment. This information is also available directly from an ALPHA computer or instrument and a Perl script similar to **feade.perl** is used. In this case, **feadsurvey.perl** is copied and executed by the sh script **start.feadsurvey**, which looks for changes in the file **/ade/data/eqpsurvey/NielsMadsem.txt_log1** on the **abcopl1** computer. Again, the script checks for changes every 10 seconds and sends any new information to MIDAS via the **felabview.exe** frontend. A list of the values managed by **feadsurvey.perl** is given in Table A.6.

A.2.2 MIDAS Backend

Once the incoming data has been collected by the frontends, it still needs to be organized, recorded and stored. These tasks are left to the MIDAS backend, which for the ALPHA experiment, resides on the **alphavme01**, **alphacpc04** and **alphacpc05** computers. These machines share the MIDAS event buffer and are cross-mounted to share the MIDAS data files. The program **mserver** acts as the MIDAS server that mediates

Event Element	Description
Event ID	Defines the type of event
Trigger Mask	Available to define sub-types of events
Serial Number	An event counter starting at one and increased by the frontends
Timestamp	Timestamp written by the frontend before readout
Event Data Size	Declares the number of bytes to follow
Total Bank Size	Size of all bank headers and data (in bytes)
Flags	Not used

Bank Element	Description
Bank Name	Four character bank identification
Data Type	Type of data used in the bank
Bank Size	Size of the following data (in bytes)
Data	Experimental data set by the frontend (all of the same data type)

Table A.7: Structure of MIDAS events and banks.

all incoming data events.

MIDAS Events

Within the MIDAS framework, an event is when a frontend sends its collected data to the MIDAS server. An event can contain any number of MIDAS banks, which contain the data from the experimental devices. MIDAS banks can only contain one type of data, although it can contain an array of values of the same type. Banks have a four character name used to identify and sort the data. A detailed description of the event and bank structure is given in Table A.7.

Logging

When the frontends send the MIDAS events to the MIDAS server, this information is relayed to the shared memory buffer which is distributed between **alphavme01**, **alphacpc04** and **alphacpc05**. At this point the MIDAS events are accessible to MIDAS applications for readout in a standard form. Here the program **logger** is used to write the events to disk. For the ALPHA experiment, **logger** writes the events in the MIDAS format (.MID files), located in the **/data/alpha/current/** directory. The .MID files

CASTOR Command	Description
<code>rfc <i>/dir1/Filename /dir2/Filename</i></code>	Copy file to, or from, the CASTOR
<code>rfr <i>/directory/Filename</i></code>	Remove file from the CASTOR
<code>rfmkdir <i>/directory/</i></code>	Create directory in CASTOR
<code>rfd <i>/directory/</i></code>	Display to contents of the CASTOR

Table A.8: A short description of some common CASTOR commands.

contain the unformatted MIDAS events, with two special event types: the begin-of-run and end-of-run events, which both contain an ASCII dump of the online database (discussed below). These two events define the beginning and end of the data collection run, with the begin-of-run event coming at the beginning, and the end-of-run at the end.

Online Database

The Online Database (ODB) contains all the DAQ parameters and run information. The ODB resides in the shared memory between the three ALPHA computers and uses the XML format to organize the entries. Since the ODB is shared and accessible from any of the DAQ computers, it is the ideal place for information and parameters required by numerous DAQ programs. The ODB can be accessed from the MIDAS web interface, which provides an intuitive graphical structure, or by using the **odbedit** program for a command line interface.

Storage

In addition to the collection and recording of data, long term storage is also necessary, as often older data needs to be revisited or reanalyzed. CASTOR (CERN Advanced STORAGE) is used to store the large MIDAS data files as well as the ODB XML files after they are not longer immediately needed on the local ALPHA computers. CASTOR allows files to be accessed or retrieved, but primarily is used as a stable and long term data storage facility. A short list of CASTOR commands is given in Table A.8. The CASTOR directory containing the ALPHA 2006 data files is `/castor/cern.ch/alpha/2006/data/`.

A.2.3 MIDAS Web Interface

The MIDAS system also includes a web-based interface for convenient monitoring and control of the DAQ system. For the ALPHA experiment, the program **mhttpd** runs the web server on the **alphavme01** computer (later on **alphacpc05**). The MIDAS web interface (Fig. A.2) contains several very useful components which are described below.

Experimental Controls

The MIDAS web interface contains the controls to Start and Stop data acquisition and recording. Each data acquisition session is called a Run and assigned an incremental number. Clicking on the ‘Start’ button on the MIDAS front page (Fig. A.2) will bring up the Start Run dialog screen, where run parameters can be set. These include run comments and the option to conduct a Pedestal run to collect the ADC baseline pedestals.

To conclude a run, a ‘Stop’ button has replaced the ‘Start’ button on the front page and is used to stop the current data acquisition run.

History Plotting

The MIDAS web interface also includes a plotting feature to display data coming into MIDAS. This feature can be accessed through the ‘History’ button on the MIDAS front page (A.2), which brings up the History display page (Fig. A.3). Histories are plots of the data collected by MIDAS versus the time it was received. Data can be displayed over different time scales, from 10 minutes to 7 days, with the option to display several variables on the same plot.

Electronic Logbook

MIDAS also includes an electronic logbook (ELog) to record and archive information about the experiment as a replacement for a physical logbook (Fig. A.4), and can be accessed through the ‘ELog’ button on the MIDAS front page (Fig. A.3). Entries can

be made under a variety of groupings with the option to reply to previous posting. Files and History plots can be attached to entries and all entries are searchable. The ELog is also configurable to send out email for certain entry types.

A.3 ALPHAROOT

The ALPHAROOT program runs in conjunction with the MIDAS system and provides preliminary analysis and data visualization. ALPHAROOT uses C++ and the ROOT⁴ framework to sort, analyze and display data received by MIDAS. In particular, ALPHAROOT displays beam counter values and makes histograms based on data received by the SIS multiscaler, both online as the data is being collected or offline from the MIDAS files. The source and parameter files used by ALPHAROOT are summarized in Table A.9. All ALPHAROOT files are located in the `/home/online/alpharoot/` directory. ALPHAROOT can be ran online using the the command:

```
./alpharoot.exe
```

in the `/home/online/alpharoot/` directory. Runs can also be reanalyzed offline with the command:

```
./alpharoot.exe /data/alpha/current/runN.mid
```

where N is the run number.

A.3.1 Data Handling

ALPHAROOT receives data from the MIDAS shared SYSTEM buffer, through which all data sent to MIDAS passes in the form of MIDAS banks. Data from different equipment arrives asynchronously and must be sorted and sent to the appropriate subroutine.

⁴ROOT website: <http://root.cern.ch/>

File	Description
alpharoot.cxx	Main file, interfaces with the MIDAS shared buffer and sorts the incoming data banks for the subroutines
alpharoot.ini	Initialization file, contains the customizable program parameters
Globals.h	Global variable file, contains the definitions for all global variables
HandleBeamADC.cxx	File containing all the subroutines dealing with ADC data (includes beam counter and HPDs)
HandleBeamADC.h	External declarations for ADC subroutines
HandleLabview.cxx	Handling subroutines for all data sent from the LabVIEW interface
HandleLabview.h	External declarations for LabVIEW subroutines
HandleScaler.cxx	Handling subroutines for all data sent from the 16 channel scaler
HandleScaler.h	External declarations for the scaler subroutines
HandleSequencer.cxx	Subroutines to handle data sent from the sequencer GUI
HandleSequencer.h	External declarations for the sequencer subroutines
HandleSIS.cxx	Subroutines to handle data from the SIS multiscaler, includes histogram triggering and online SIS monitoring
HandleSIS.h	External declarations for the SIS subroutines
config/Details.xml	File containing the parameters controlling the detailed SIS monitor
config/onlinemonitor.xml	Parameters defining the online SIS monitor
config/switches.txt	File containing the definitions for all the SIS triggered histograms

Table A.9: ALPHAROOT file structure in the `/home/alpha/online/alpharoot/` directory.

Subroutines for handling different data types all reside in separate source files dedicated to the specific equipment from where the data came (Table A.9).

Data received from the SIS multiscaler is not handled immediately, rather, it is placed in a circular buffer based on the originating SIS channel and arrival time. ALPHAROOT will then step through this buffer to create the histograms described in Sec. A.3.3.

A.3.2 Visualization

ALPHAROOT is used for the display of important values during the course of a data acquisition run. The ROOT graphical libraries are used for the Graphical User Interface (GUI) that handles the display windows, as well as the display of the data. Fig. A.5 shows a typical online screen display, including values from the beam counter, magnet current values, counts from the scintillators, and temperatures readings from on the apparatus. Values from particle dumps are also displayed through ALPAHROOT.

These images are also written to a web server so that the experimental progress is viewable from any web browser (<http://alphacpc05.cern.ch:8082/~alpha/>).

A.3.3 Histogramming

To understand the results of the experiment, the output of the detectors must be correlated with the operation of the apparatus. The SIS multiscaler module is the main timekeeping device and the means by which operation of the different equipment is related. The Sequence hardware sends a timestamp at every step of operation to MIDAS through the SIS multiscaler. Likewise, the output of the scintillating detectors is also sent to the multiscaler along with a 10 MHz clock signal from the AD. Since the multiscaler is set up with a first-in first-out memory buffer, all the incoming data is ordered and the detector output can be interpreted based on the Sequencer information.

To ease the analysis of the incoming data, ALPHAROOT is programmed to auto-

midas

PositronLog

MagnetEvents

test

ALPHA Experiment. Page 1 of 1

ELOG

New

Find

Select

Config

Admin

Login

CSV Import

Logout

Help

Type:

Routine

Full

Summary

Threaded

Collapse

Expand

Last month

Routine

-- Author --

23 Entries

2313, Mon May 21 05:23:58 2007, New URL for ALPHA ELOG, Software, Routine, K.Olchanski

2313, Mon May 21 19:28:05 2007, New URL for ALPHA ELOG, Software, Routine, K.Olchanski

2313, Fri May 25 16:03:39 2007, New URL for ALPHA ELOG, Software, Routine, K.Olchanski

2314, Thu May 24 15:39:28 2007, Test, Hardware, Routine, Niels

2314, Wed May 23 18:51:09 2007, Konstantin's travel to CERN, June 2007, Software, Routine, K.Olchanski

2314, Wed May 23 18:43:13 2007, alphapc09 new daq computer, Software, Routine, K.Olchanski

NA, Wed May 23 14:05:43 2007, Cabling of mixing and positron traps, Hardware, Routine, Niels

NA, Wed May 23 12:15:12 2007, Network Upgrades in Zone, Hardware, Routine, Niels

2313, Mon May 21 18:22:26 2007, Some updates to what labview sends, Software, Routine, Niels

2313, Mon May 21 22:15:37 2007, Some updates to what labview sends, Software, Routine, Niels

2313, Tue May 22 06:21:51 2007, Some updates to what labview sends, Software, Routine, K.Olchanski

2313, Mon May 21 04:57:03 2007, Request for CERN firewall exemption, Software, Routine, K.Olchanski

2313, Mon May 21 04:52:54 2007, Reconfiguration of DAQ web services, Software, Routine, K.Olchanski

2313, Mon May 21 01:43:24 2007, test elog, Analysis, Routine, K.Olchanski

NA, Thu May 17 16:04:32 2007, Cernoxes mounted on mixing trap, Hardware, Routine, Niels

NA, Thu May 17 16:02:03 2007, Linear Filament and Faraday Cup mounted on catching, Hardware, Routine, Niels

NA, Thu May 17 15:53:43 2007, Positron and mixing trap cabling and mounting, Hardware, Routine, Niels

NA, Thu May 17 15:50:37 2007, Flap device, Hardware, Routine, Niels

NA, Thu May 17 15:48:37 2007, Beam Counter Orientation, Hardware, Routine, Niels

NA, Thu May 17 15:46:42 2007, Catching trap external cabling, Hardware, Routine, Niels

NA, Thu May 17 15:16:15 2007, Voltage monitoring in MIDAS, Software, Routine, Niels

NA, Wed May 16 14:34:22 2007, Failed to start Run ?, Software, Routine, Niels

NA, Tue May 15 18:15:14 2007, New Labview->MIDAS packets, Software, Routine, Niels

NA, Tue May 15 20:05:11 2007, New Labview->MIDAS packets, Software, Routine, Richard

NA, Tue May 15 15:16:14 2007, Current Labview->MIDAS formats, Software, Routine, Niels

N.A., Sun May 13 14:19:12 2007, Positron trap and fancy flange, Hardware, Routine, Niels

2311, Sat May 12 14:47:50 2007, Images of catching and mixing traps, linear filament and faraday cup/final degrader., Hardware, Routine, Niels

2311, Thu May 10 21:29:46 2007, General Purpose Programmable Logic Module (GPPLM) Interface Documentation, Software, Routine, Richard

File 12 6.5.1844

Figure A.4: MIDAS electronic logbook (ELog).

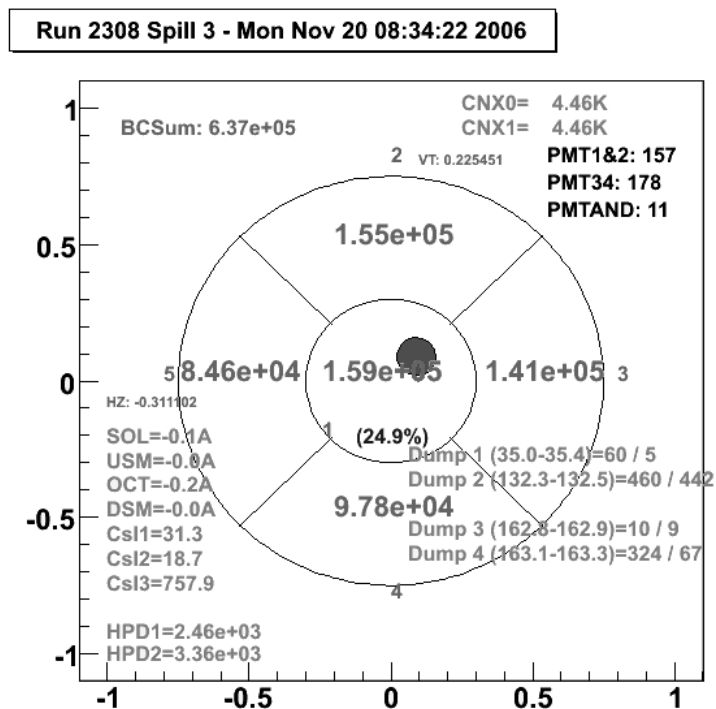


Figure A.5: Online display of beam counter and other status values.

matically create time-ordered histograms based on SIS inputs, as well as other simple preliminary data analysis. To know when to start and stop the histogram filling process, some SIS channels are dedicated as triggers to for ALPHAROOT. When stepping through the SIS data, if ALPHAROOT encounters a start histogramming trigger it will immediately create and fill the histogram from the appropriate input until a stop histogramming trigger is received. A typical histogram is shown as Fig. A.6, where the histogram starts at the beginning of the mixing between positrons and antiprotons and records the coincidence of the APD detectors.

The configuration of the ALPHAROOT histogramming is contained in the **config/switches.txt** file. This file defines which SIS channel is to be recorded, and which channels are used to start or stop. The histogram parameters are also defined in **config/switches.txt**, including the histogram name, x -axis range, and number of time bins. When complete, the histograms are written into a ROOT file (**data/runN.root**, where N is the run number) which can be viewed with a ROOT file viewer, such as ROODY, or through the file viewer included in the ROOT suite.

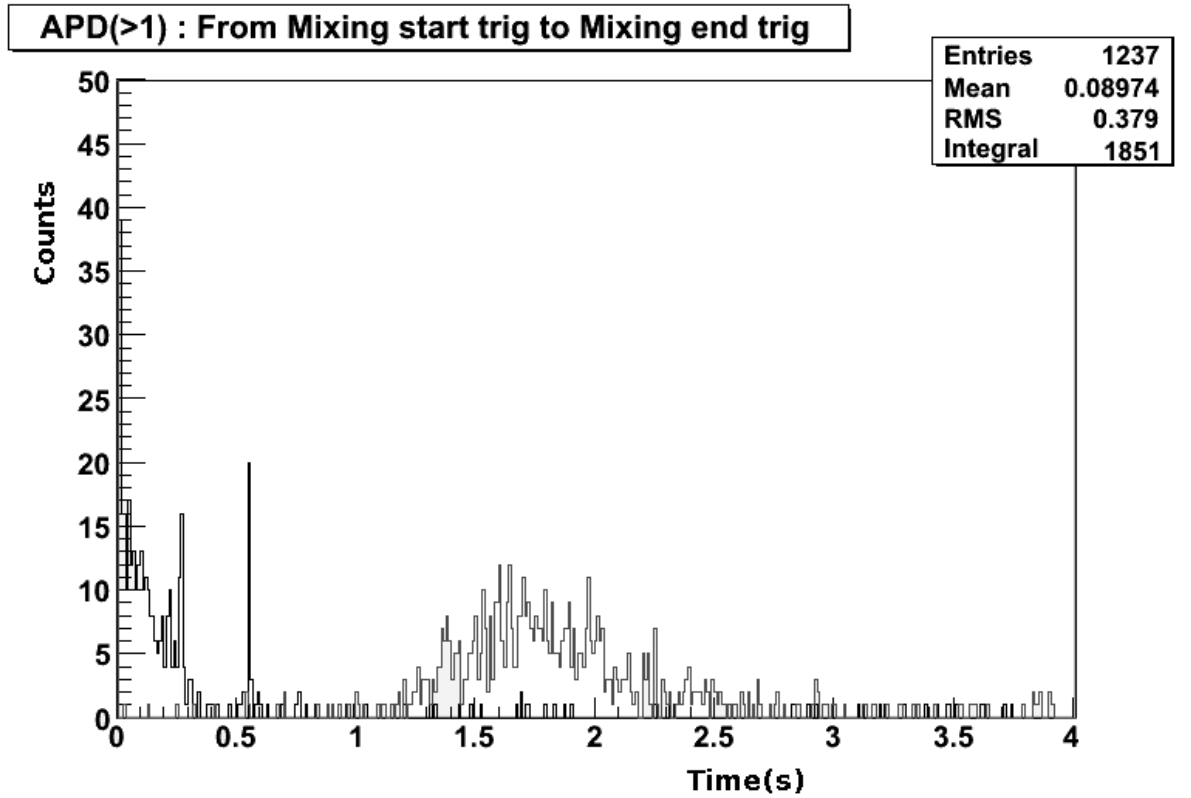


Figure A.6: Typical ALPHAROOT histogram. The histogram starts at the beginning of the mixing of positrons and antiprotons, and ends at the conclusion of mixing. Coincidence counts from the APD detectors are shown.