

COULOMB EXCITATION OF ^{140}Sm

by

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THESIS

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Abstract

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Chapter 1

Introduction

+ Motivation

kinsim [1]

The experiment has been done before, with lower energy (and another target), Malin Klintefjord. <http://urn.nb.no/URN:NBN:no-56121>

Experiment conducted 8th - 14th of August 2017.

Tilbakemelding:

old REX-ISOLDE post-accelerator limited to 2.8 MeV/u (low Coulomb excitation cross section, low probability for multi-step excitation). Mo target was chosen to maximize cross section at this energy, and to normalize $B(E2; 0^+ \rightarrow 2^+)$ value in ^{140}Sm to the well-known $B(E2)$ value for the target.

New HIE-ISOLDE: energies up to 10 MeV/u \implies we can choose high-Z target (Pb) \implies high Coulex cross section, especially for multi-step. Also: $B(E2)$ for ^{140}Sm now known from previous experiment (and a lifetime measurement) \implies no need for normalization: we can use the known $B(E2; 0^+ \rightarrow 2^+)$ to normalize the transition probabilities for the higher-lying transitions. Chosen 4.7 MeV/u as the highest possible energy that is safe for Pb (distance of closest approach large enough to exclude nuclear interaction.)

Chapter 2

Theory

Quadrupole deformation of nuclei.

Shape coexistence possible for certain regions of N and Z .

- triaxial shape / shape coexistence
- benchmark for theoretical models
- transition probabilities and quadrupole moments between several excited states are not known
- fundamental research

COULEX:

- nucleus excited by electromagnetic interaction.
- de-excitation \rightarrow gamma

Tilbakemelding:

shape coexistence often found near closed shells. Example: neutron deficient Hg nuclei ($Z = 80$ just below 82 shell closure, $N \sim 104$: neutron mid-shell).

^{140}Sm : $N = 78$, just below $N = 82$ shell closure, $Z = 62$: mid-shell.

Typical indication for shape coexistence: 0^+ states (often at low energy).

^{140}Sm was thought to have a low-lying 0^+ state [Firestone], but this state was shown to be 2^+ [Suoranczyk?]. Indication for 0^+ states around 1.5 MeV.

One of the objectives of this experiment: clarify the nature/structure of these 0^+ states.

Shape transition: Sm-144 ($Z = 62$, $N = 82$) spherical. Adding neutrons: transition of $N = 90$ from spherical to prolate deformed \rightarrow shape-phase transition, so called X(5) critical-point symmetry.

Taking out neutrons: very neutron-deficient Sm nuclei are also prolate deformed (e.g. Sm-132), but for ^{140}Sm : indication for triaxiality/ γ -softness [Klintefjord] \rightarrow another form of shape-phase transition/critical point behavior \implies E(5) [Iachello?]. ^{140}Sm could be one of the best examples for E(5) symmetry \implies

need transition probabilities from higher-lying states to confirm.

Some suggestions:

- general things about nuclei shapes
 - multipole expansion, shape parameters (5 parameters, 3 for space, 2 for deformation β, γ), ...
 - quadrupole moments: intrinsic (body-fixed frame), spectroscopic (lab frame)
 - transition probabilities, el.magn. matrix elements
 - rotations and vibrations \rightarrow energy spectra, $B(E2)$ values
 - Casten triangle (spherical vibrator, deformed rotor, γ -soft + X(5), E(5)), expected spectrum for E(5) nuclei
- the basics of Coulomb excitation

NOTES TO BE REMOVED!!

2.1 Oppgaveteksten (skal fjernes!)

Oppgavens mål:

The ISOLDE facility at CERN has been upgraded to provide higher energies and intensities for radioactive ion beams. A new experiment to study ^{140}Sm was performed in the summer of 2017. The goal of the experiment was to measure electromagnetic transition probabilities and electric quadrupole moments for several excited states in ^{140}Sm by measuring Coulomb excitation probabilities. A large data set was obtained using silicon detectors to determine the energies and angles of scattered particles, and germanium detectors to measure gamma rays from excited states in ^{140}Sm .

The goal of the master thesis is to analyze the data from this experiment. The required tasks include development and improvement of data analysis software to determine Coulomb excitation yields. These yields will then, in a second step, be compared to theoretical calculations and transition probabilities and quadrupole moments will be extracted using chi-square minimization procedures.

Prosjektbeskrivelse (omfang 60 studiepoeng):

The shape of an atomic nucleus is determined by a delicate interplay between macroscopic (liquid drop) properties and microscopic shell effects. Nuclei with filled proton or neutron shells (i.e. magic nuclei) are generally spherical in shape, whereas nuclei with open shells gain energy by assuming a deformed shape. Depending on the occupation of specific orbitals, the nuclear shape can change drastically by adding or removing protons or neutrons. Certain nuclei exhibit shape coexistence, i.e. the coexistence of quantum states that correspond to different shapes. Because the shape of a nucleus is so sensitive to the underlying nuclear structure and to changes of the proton and neutron numbers, the excitation energy, or the angular momentum, observables related to the nuclear shape are used as benchmarks for theoretical models.

Nuclei in the rare earth region, and in particular the chain of samarium isotopes, exhibit a variety of shape effects. The Sm isotope with closed neutron

shell at N=82, ^{144}Sm , is spherical in shape. Adding neutrons to ^{144}Sm changes the deformation to an elongated (prolate) quadrupole shape. The transition from spherical to prolate shape, which occurs for ^{152}Sm at N=90, can be interpreted as a shape-phase transition. Flattened (oblate) quadrupole shapes are predicted by theory to occur below the N=82 shell closure. An earlier experiment studying ^{140}Sm at CERN-ISOLDE found triaxial shape for this isotope, i.e. a shape where all three principal axes of the ellipsoid have different lengths. ^{140}Sm can therefore be considered to lie at the critical point of a phase transition from spherical to deformed, and from prolate to oblate shape.

Foreløpig tittel:

Coulomb excitation of ^{140}Sm

Metoder som tenkes benyttet:

Multi-step Coulomb excitation with radioactive beam, isotope separation on-line technique, nuclear spectroscopy, particle-gamma and particle gamma-gamma coincidence analysis, advanced chi-square minimization procedures.

2.2 Information sources

- CD: <https://www.ikp.uni-koeln.de/~warr/doc/cd.pdf>
- Why CoulEx? https://iks32.fys.kuleuven.be/wiki/brix/images/5/58/10_20151123_Illana_BriX15_web.pdf
- 2017: <https://iopscience.iop.org/article/10.1088/1361-6471/aa5c4e#jgaa5c4es2>
- 2017: <http://iopscience.iop.org/article/10.1088/1361-6471/aa990f/pdf>
- http://publications.lib.chalmers.se/records/fulltext/175494/local_175494.pdf
- https://www.euroschoolonexoticbeams.be/site/files/nlp/LNP700_contrib2.pdf
- 2004: <http://accelconf.web.cern.ch/AccelConf/e04/PAPERS/TUXCH01.PDF>
- 2003: https://ac.els-cdn.com/S0168583X02018864/1-s2.0-S0168583X02018864-main.pdf?_tid=64f42a8d-b37c-42a6-a3c5-f01dcee73366&acdnat=1545049646_8918b985af428e17
- 2002: https://ac.els-cdn.com/S0168900201009548/1-s2.0-S0168900201009548-main.pdf?_tid=71a410a3-6554-4268-ac1a-1b43cae4039d&acdnat=1545056166_15ff5318affd89c7e

Post-accelerated beams ISOLDE <http://iopscience.iop.org/article/10.1088/1361-6471/aa78ca>

PSB <https://home.cern/science/accelerators/proton-synchrotron-booster>

Sjekk sensorveiledning!!

Chapter 3

Coulomb excitation experiment

3.1 ISOLDE at CERN

The acronym ISOLDE stands for Isotope Separator On Line DEvice. ISOLDE is a Radioactive Ion Beam (RIB) facility at CERN in Meyrin, Switzerland. [Figure 3.1](#) shows the CERN accelerator complex [2], where ISOLDE is located beside the Proton Synchrotron Booster (PSB). The facility can produce over 1000 different radionuclides to be used in a wide variety of experiments in nuclear physics, atomic physics, solid state physics, life sciences and fundamental interactions. Experiments have been performed at ISOLDE since 1967 and since 2001 experiments with post-accelerated RIBs have been conducted. The high intensity and energy upgrade (HIE-ISOLDE) have made it possible to deliver energies up to 10 MeV/u in 2018 [3–5].

Most of the around 4000 known nuclides are radioactive. In many cases it is not possible to make radioactive nuclei targets and perform an experiment because of the short half-life of the nucleus of interest. To study these radioactive nuclei, RIBs are used on stable targets. One way of obtaining a RIB is to use the Isotope Separator On Line (ISOL) method. In the ISOL method, two accelerator systems is needed. The first accelerator is used to produce the radioactive atoms at rest, and the second accelerator is used to accelerate these atoms [6].

3.1.1 Beam production

A continuous flow of accelerated proton beam bunches from the PSB comes into the ISOLDE facility and collide with a thick production target. The proton beam has an energy of 1.4 GeV and an intensity up to $2 \mu\text{A}$. Two proton beam bunches is separated by 1.2 s. ISOLDE typically takes 50% **REF?** of all proton bunches form the PSB, the rest goes to the LHC and other experiments shown in [Figure 3.1](#). In the reaction between the proton beam and the production target, radioactive nuclides are produced in spallation, fission or fragmentation reactions

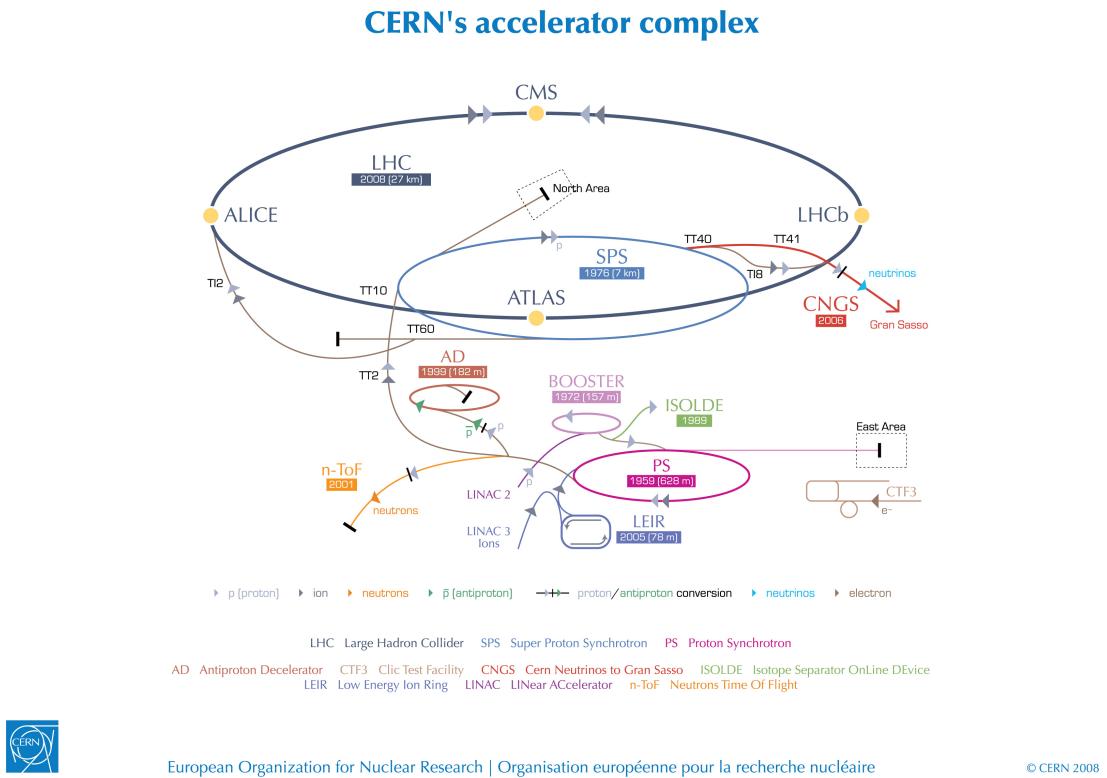


Figure 3.1: The CERN accelerator complex. ISOLDE gets accelerated protons from LINAC 2 and the PS BOOSTER.

(basically smashing the target into pieces) [4]. The production target is chosen from a stable region heavier than the nucleus of interest. In our experiment, a production target of tantalum (Ta) was used, producing the elements in the chart of nuclides up to tantalum. A large amount of different isotopes is produced in this way, and the challenge is to extract the nucleus of interest.

find other refs as well! forklare figuren mer?

Tilbakemelding:

A large amount of different nuclei/isotopes is produced in this way. Challenge: extract the nuclei we are interested in. Idea: selective ionization → use HV (electrostatic field) to extract Sm ions electronic transitions are characteristic for each chemical element. use laserlight to excite an electron to a specific excited (electron) state in Sm, use another laser to excite electrons further to another excited state, 3. laser to to kick out the electron → only Sm atoms are ionized. There could be contaminants from surface ionization (atoms that collide with the walls of the ion source).

*bruker laser on/off for å se hva annet som kommer ut av beamen

RILIS:

The resonance ionization laser ion source (RILIS) is based on the method of

step-wise excitation and ionization of the atom. It is an element-selective process which is used to produce ion beams of the correct element [7]. In this experiment RILIS was used to select samarium with atomic number $Z = 62$.

* 2-3 step ionization * also other elements come through

Other refs: <http://rilis.web.cern.ch> and https://www.research.manchester.ac.uk/portal/files/60831252/FULL_TEXT.PDF and <https://www.sciencedirect.com/science/article/pii/S0168583X13008914?via%3Dihub>

GPS:

Tilbakemelding:

at this point we have a continuous beam of Sm ions of 60 keV energy (the target is on a 60 kV HV platform).

next step: we need to have mass separation, and we need to give this continuous beam a fine structure, because the post-accelerator cannot accept a continuous beam coming in, it also accelerates bunches.

The beam can collide in one of two target stations, either the general purpose separator (GPS) or the high resolution separator (HRS). The GPS has one bending magnet and can deliver beams of different masses simultaneously into three beam lines, while the HRS has two bending magnets with high mass resolving power which delivers the beam into the main beam line [8]. In this experiment the GPS was used to select the isotope of samarium with mass number $A = 140$.

Tilbakemelding:

now we have a continuous beam of ^{140}Sm . The mass separator gets also rid of contaminants that come out of RILIS but have different mass. There could still be isobaric contaminants from surface ionization but luckily there is very little surface ionization for the neighboring elements of Sm. Laser ON/OFF.

Other refs: <http://isolde.web.cern.ch/targets-and-separators> and Klintefjord's PhD

REXTRAP:

REXTRAP is a penning trap which has the tasks of accumulation, bunching and cooling of the RIB. [3] The ions are released in bunches and transferred to the REXEBIS.

Tilbakemelding:

In REXTRAP we collect the ^{140}Sm ions, so that we can release them in bunches that are matched to the fine structure of the LINAC.

Other refs: <https://www.sciencedirect.com/science/article/pii/S0168900204020169> and <https://www.sciencedirect.com/science/article/abs/pii/S0375947401016426>

REXEgis:

REXEgis is a charge breeder where the RIB is bred to a high charge state [9], with a mass-to-charge (A/q) ratio typically between 2.5 and 4.5 [10]. REXEBIS

releases the beam with a certain energy through a mass separator and into the HIE-ISOLDE LINAC (LINear ACcelerator) [3].

Tilbakemelding:

go from $^{140}\text{Sm}^{+1}$ to $^{140}\text{Sm}^{+33}$ (I think, check log book), anyway we need a highly charged ion to accelerate to high energies. The electron beam of EBIS just blasts off more electrons from Sm. The longer the ions stay in EBIS, the higher the charge state → distribution of charge states → we loose those that have the wrong charge state. LINAC can only accept one.

excites the nucleus in three steps ionizing the atom, which leaves the nucleus in a high charge state. ?

Other refs: <http://cds.cern.ch/record/478399/files/> and <http://rex-isolde.web.cern.ch>

HIE-ISOLDE LINAC:

The HIE-ISOLDE LINAC accelerates the beam through the beam line and magnets bend the beam into MINIBALL.

* one of the first Miniball experiments with the new accelerator

Tilbakemelding:

Accelerates ^{140}Sm to 4.65 MeV/u

HIE-ISOLDE (Superconducting LINAC Upgrade): Linear accelerator, HIE-LINAC

HIE-ISOLDE <http://hie-isolde-project.web.cern.ch>, technical design <http://cds.cern.ch/record/2635892?ln=en>, direct to doc: http://cds.cern.ch/record/2635892/files/HIE-ISOLDE_TDR.pdf

MINIBALL:

Cite: https://ac.els-cdn.com/0168583X92959079/1-s2.0-0168583X92959079-main.pdf?_tid=0ccb0647-5870-48f9-ac38-df8c0077981c&acdnat=1545216224_d359ddcc40ea1f94369c85 and https://cds.cern.ch/record/2025701/files/epjconf_inpc2013_11005.pdf and <http://isolde.web.cern.ch/targets-and-separators>

Magnets....

ISOLDE actually uses the most protons at CERN [ref?].

ISOLDE <http://iopscience.iop.org/article/10.1088/1361-6471/aa5f03/pdf>

Very pure beam (did we have statistics of this?) - resultat til avhandling. sjekk etter doppler-korrigering. Nd-contaminasjon? i så fall veldig lite, 1-2 prosent?

Tilbakemelding:

we would have to look at the γ -spectra to identify any contaminants. There may

be a little bit of Nd-140 in the beam, but if so, it is very little (judging from on-line spectra).

MINIBALL <http://isolde.web.cern.ch/experiments/miniball> and https://www.miniball.york.ac.uk/wiki/Main_Page

ENSAR2 <http://www.ensarfp7.eu>

Beam production http://tuprints.ulb.tu-darmstadt.de/4599/1/TUDthesis_Christoph%20Seiffert.pdf

Test [2], copyright: <https://copyright.web.cern.ch>

CERN Document Server <https://cds.cern.ch>

3.1.2 Target

Kan skrive om dette i motivasjonen.

^{208}Pb was chosen as a target. Want high Z so that the probability of excitation is high.

Tilbakemelding:

Thickness, etc.

It is very hard to excite ^{208}Pb (doubly magic). We might see a little bit of the 2.6 MeV state (octupole vibration), but not sure.

Since we don't need normalization (because we have the $B(E2, 0^+ \rightarrow 2^+)$ from the previous experiment and from lifetime measurement [Bello], we have chosen a target that is very hard to excite, so transitions from the target will not complicate the spectrum.

Doubly magic, very hard to excite. No quadrupole deformation/excitation.
Need quadrupole for first state (see nndc)

ja og nei: Not enough beam energy to excite ^{208}Pb .

Highest Z for maximum excitation probability.

Contamination... finger print [[picture](#)]

3.2 Miniball

Testcite (Nigel Warr) [11]

Pictures <https://cds.cern.ch/record/844871?ln=en>

3.2.1 Particle detector, DSSSD (CD)

DSSSD: Double sided silicon strip detector

16 rings, 12 strips effectively (24 strips, 12 pairs with two strips making a pair)

Rings = annular strips, strips = radial strips or sector strips

CD distance: 26.98 mm, Inner angle (min): 9 mm, Outer angle (max): 40.9 mm

Angle coverage: [18.4°, 56.6°]

See [Table 3.1](#)

Table 3.1: CD angles in laboratory frame. Adjacent (CD distance): 26.98 mm. The centroid energy is from simulation with kinsim3.

Ring number	Opposite (mid ring) [mm]	Angle	E_t [MeV]	E_b [MeV]
0	40	56.0°	139.62	273.80
1	38	54.6°	151.51	286.78
2	36	53.1°	164.55	299.11
3	34	51.6°	182.41	312.31
4	32	49.9°	198.95	326.87
5	30	48.0°	219.53	342.40
6	28	46.1°	240.36	358.75
7	26	43.9°	262.77	376.35
8	24	41.7°	287.31	395.31
9	22	39.2°	313.65	414.84
10	20	36.5°	340.64	435.42
11	18	33.7°	369.54	456.71
12	16	30.7°	398.95	478.33
13	14	27.4°	428.87	499.72
14	12	24.0°	457.53	520.55
15	10	20.3°	484.86	539.89

SKAL TABELLEN VISE MeV eller MeV/u??

Vis en figur/tegning av "trekanten" i detektoroppsettet? Skjematiske figur?

$$\theta = \tan^{-1} \left(\frac{\text{opposite}}{\text{adjacent}} \right)$$

3.2.2 γ detectors, HPGe

24 six-fold segmented. 8 clusters of 3 crystals each. Each crystal segmented in 6 parts (144 segments in total).

Cryo-modules

3.3 Experimental setup

^{140}Sm Coulomb excitation experiment.

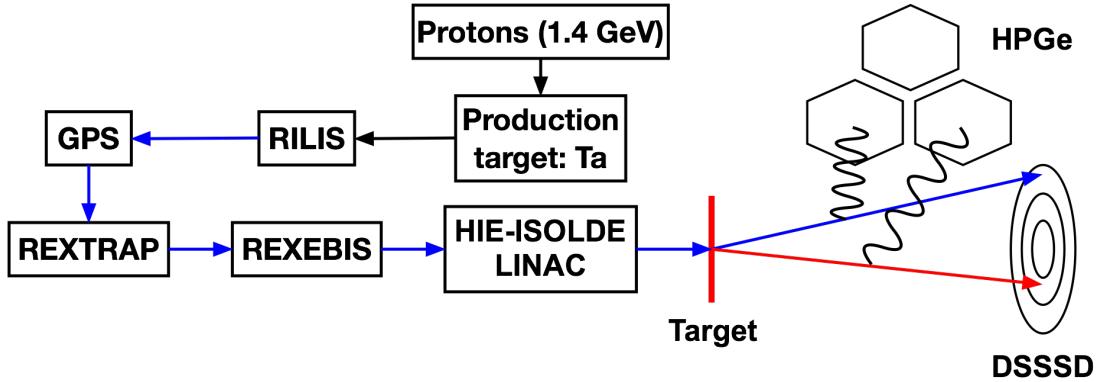


Figure 3.2: The Coulomb excitation setup at ISOLDE. Adapted from Malin Klintefjord's PhD thesis [12].

Show where Sm is made + ionized (+1) + bred (+33 or +34?) in the figure?

Experiment code: IS558

Ta: tantalum ($Z = 73$)

Sm: samarium ($Z = 62$)

Pb: lead ($Z = 82$)

Beam: ^{140}Sm ($T_{1/2} = 14.82$ min, $4.65 \text{ MeV}/u$, total 651 MeV), excellent purity

Target: ^{208}Pb (Thickness: $1.4 \text{ mg}/\text{cm}^2$)

Small angle: Forward scattering: Larger distance, weaker EM-field, less excitation probability.

Large angle: Backward scattering: Closer distance, stronger EM-field, higher excitation probability.

Expect to measure transition probabilities $B(E2)$ and quadrupole moment (nuclear deformation).

Chapter 4

Data analysis

Tilbakemelding:

First: explain the tasks and give the bigger picture of what needs to be done:
starting point: Raw data in list mode: ID, E, T, ID, E, T, ... (basically)
what you want: Doppler-corrected γ -spectra with various conditions on particles, angles, etc.

procedure: 3 steps:

1. convert raw data to ROOT format
2. event-building:
 - calibrate detectors, apply thresholds, etc.
 - use correlations to build events: particle- γ coincidences
 - store everything in a tree structure for easy access
3. apply gates on particles and perform Doppler correction

Could be nice to have a "cook book", i.e. step-by-step explanation of this procedure.

ROOT: analysere data

kinsim3 <https://github.com/lpgaff/kinsim> + SRIM <http://www.srim.org>

Table 4.1: Computer used for data analysis

Model	MacBook Air (13-inch, 2017)
Processor	1.8 GHz (Intel Core i5)
Memory	8 GB (1600 MHz DDR3)

Run time for sorting data:

TreeBuilder (online calibration): \sim 40-45 min

AQ4Sort (online calibration): \sim 120 min

Table 4.2: Run time for sorting data.

Executable	Run time [min]
TreeBuilder	~ 45
AQ4Sort	~ 120

The run time of the bash script was done with the built in script time

```
$ time ./AQ4S.sh Sm online TB
...
real 45m19.265s
user 42m49.653s
sys 0m39.665s
```

```
$ time ./AQ4S.sh Sm online Q4
...
real 121m40.830s
user 116m18.361s
sys 1m17.809s
```

```
$ time ./AQ4S.sh Sm user TB
...
real 41m11.282s
user 39m45.592s
sys 0m27.777s
```

```
$ time ./AQ4S.sh Sm user Q4
...
real 143m47.600s
user 128m6.174s
sys 1m50.921s
```

particle-gamma and particle-gamma-gamma coincidence
sjekk opp om energi fra online kalibrering passer med simuleringen.

4.1 Data and sorting

The analysis code for Miniball data is named MiniballCoulexSort and is available on GitHub at <https://github.com/Miniball/MiniballCoulexSort>. The main steps of how to download, install and use it is outlined in the README.md file in the GitHub repository.

Data from Miniball comes in the form of .med-files (Miniball Event Data). In order to analyze this data in ROOT¹ the first part of the sorting is just to convert the .med-files into .root-files with the script MedToRoot.

To get useful information out of the converted .root-files, the Treebuilder script is used. The .root-file(s) and a calibration file is given to the Treebuilder so it can make event trees that can be used for analyzing the Coulomb excitation events.

One script that is mentioned in the Miniball GitHub repository, but not showed how to use, is the AQ4Sort. It is used in the same way as the TreeBuilder script, but it sorts the histograms in another way. This script is used before and during the calibration of the detectors, because it gives information about every single ring and every single back strip. The one thing to note here, is that the numbering of the detector rings and strips are different from the ones used in Treebuilder.

The histograms sorted by Treebuilder starts counting from 0 and the AQ4Sort starts counting from 1.

The ADC spectras from the file sorted by Treebuilder have a naming convention of adc_q_s , where q corresponds to the quadrant and s corresponds to the channel. The front energy is saved in $\text{adc}_{[0-3]}_{[0-15]}$ and the back energy from strips 1-12 from all 16 rings (the whole quadrant) is saved in $\text{adc}_{[0-3]}_{[16-27]}$.

Tilbakemelding:

useful with a table that explains all the different channels and assigns the various detector segments/???? ? (???? conventions) (appendix?)

adc_{0_0} in the file sorted by Treebuilder is the same as fE_Q1_f1 sorted by AQ4Sort. All the front detectors can be found in the Treebuilder-sorted file, but when it comes to the back detector, the single pixels from the strips are not shown. These are available through the AQ4Sort sorted file. For the front detectors the histograms $\text{adc}_{[0-3]}_{[0-15]}$ and $\text{fE_Q}[1-4]_{.f}[1-16]$ are the same. For the back detectors, we have that $\text{adc}_{[0-3]}_{[16-27]}$ and $\text{bE_Q}[1-4]_{.b}[1-12]$ are the same. In addition in AQ4Sort we can see the different pixels. The histograms $\text{fE_Q}[1-4]_{.f}[1-16]_{.b}[1-12]$ shows the front energy of quadrant 1-4 gated on ring 1-16 and back strip 1-12, while the $\text{bE_Q}[1-4]_{.f}[1-16]_{.b}[1-12]$ shows the same, only for the back energy.

Tilbakemelding:

a little confusing: is it correct that the treebuilder sort individual spectra for the front and back strips, but if you want coincidences between front and back (\rightarrow pixels) you use AQ4Sort?

In the naming convention of adc_q_s or fE_Qu_fv , where $q \in [0, 1, 2, 3], s \in [0, 1, \dots, 27]$ and $u \in [1, 2, 3, 4], v \in [1, 2, \dots, 16]$, the $s = 0$ and $v = 1$ is the outermost ring, while $s = 15$ and $v = 16$ is the innermost ring. In our case, the innermost ring was so destroyed that we have to remove it from the data analysis.

¹ROOT is a data analysis framework made at CERN.

`adc_q_s`, where $q \in [0, 1, 2, 3]$, $s \in [0, 1, \dots, 27]$.

`pE_Qq_fr_bs`, where $\in [b, f]$, $q \in [1, 2, 3, 4]$, $r \in [1, 2, \dots, 16]$ and $s \in [1, 2, \dots, 12]$.

The `adc[0-3][16-27]` or `bE_Q[1-4].b[1-12]` are a combination of all the 16 rings of `bE_Q[1-4]f[1, 2, \dots, 16].b[1-12]`.

Don't blame me for the naming convention, I did not write the code. I just tried to make sense of it.

4.2 Helping scripts

All of my scripts are available in the GitHub repository <https://github.com/wiggoen/MasterThesis>.

In order to not copy and paste the sorting command in the terminal for every data file, I made two bash scripts to do this. The script **M2R.sh** is using MedToRoot to take in as many files as you want, and sort it in one go. The other script is **AQ4S.sh**, which is using either AQ4Sort or Treebuilder to sort a lot of files in one go.

Tilbakemelding:

you should have a list of all the files with comments: in-beam data, calibration, laser on-off, problems, which ones can be used and which can not.

I also made other helping scripts to get histograms, do fitting, comparison and calibration.

My scripts: MultiFit.cpp, MultiPlot.cpp, ++ (python, bash,..)

Tilbakemelding:

if you try to write this step-by-step cook book, you could introduce your scripts wherever is the right place to use them.

4.3 Simulation

To calibrate the data, we need to know the expected energy of the centroids of the peaks. This was done by simulating the experiment in a program called `kinsim3`. The program is written by Liam Gaffney² and the purpose of the program is to simulate the kinematics of the experiment. It takes into account the Silicon dead layer.

`kinsim3` generates pdf-files of the stopping powers automatically. The rest of the plots are available inside the root-file. To get the energy simulation for each ring, the function `cd_sim_plots()` from the script `MultiPlot.cpp` was used.

Tilbakemelding:

what are the ingredients for this simulation?

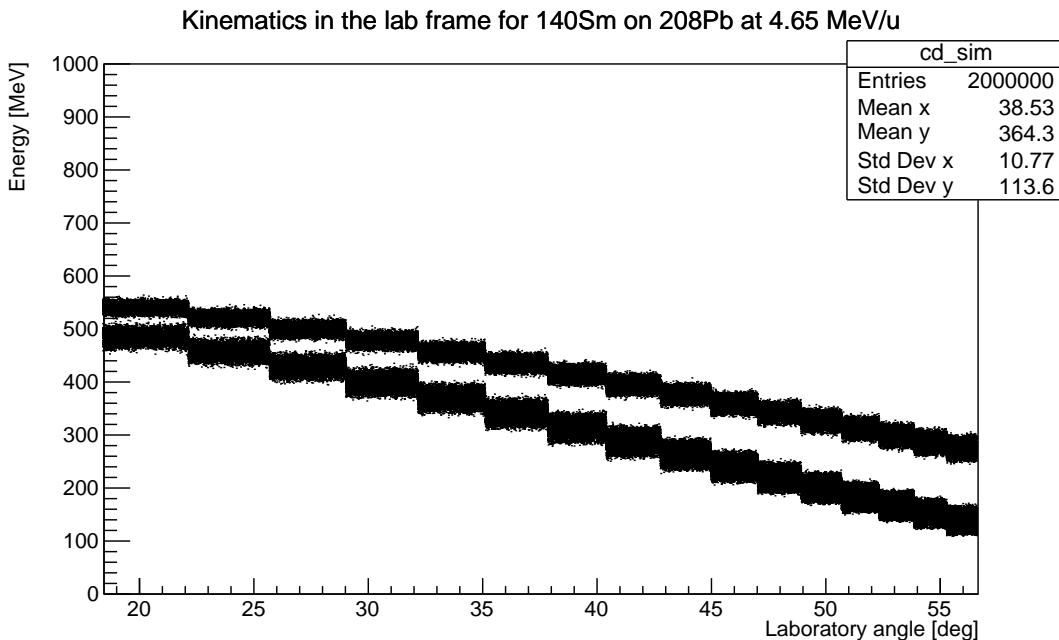
simple 2-body kinematics: energy of projectile, scattering angle of projectile \Rightarrow energy of scattered projectile, {angle, energy} of binary ???? (target recoil)

²Liam Gaffney is a fellow at ISOLDE, affiliated with MINIBALL.

Stopping powers (which models?) → SRIM
 Slowing of the particles in the target and in the dead layer of Si

CD to target distance: 26.98 mm.

Simulation done by kinsim3



Tilbakemelding:

explain figure: Sm/Pb inner ring, Sm/Pb outer ring

simulation does not consider cross sections: in simulation all angles are equally probable. The corresponding figure from your data looks therefore quite different.

— Mail from Liam started —

"the source has a thickness of 1.23 mm, which needs to be factored in so that the CD to target distance is the CD to source distance PLUS the source thickness, i.e. $25.78 \text{ mm} + 1.23 \text{ mm} = 27.01 \text{ mm}$. This is very close to the 26.98 mm you got from us in August. I think that the source data was reanalysed since the original blog entry, giving the 0.03 mm difference!"

— Mail from Liam ended —

Terminal: Simulation: 140Sm on 208Pb:

```
$ cd GitHub/Miniball/kinsim
$ root
root [0] .L kinsim3.cc+
root [1] kinsim3(62, 82, 140, 208, 1.4, 4.65, 0.02, 1.0, 0.6,
26.98, false, 1e6, "../SRIM")
```

kinsim3 function:

```
void kinsim3( int Zb, int Zt, double Ab, double At, double
    thick /* mg/cm^2 */, double Eb /* MeV/u */,
    double dEb = 0.1 /* MeV/u */, double Ex = 1.0 /* MeV */,
    double res = 0.6 /* % */,
    double cd_dist = 28.0 /* mm */, bool flat = false /* angular
        distribution? */,
    long Nevts = 1E6, string srim_dir = "../srin" )
```

Say something about SRIM files.

4.4 Calibration

Tilbakemelding:

start with explaining the general idea for the calibration:

determine centroids of peaks in spectra, compare with simulations (kinematics, energy loss) to get linear coefficients (gain + offset). You could show spectra for 2 rings: one where it is ok to get the 2 centroids for Sm and Pb, and one where it is difficult → use additional data (Ni?)

Sectors: cover wide angular range → no sharp peaks

Solution: gate on rings to see peaks in sectors and calibrate.

Idea:

1. produce spectra
2. set thresholds: example, explain criteria
3. find calibration coefficients → see above
- explain strategy, show examples...
4. time calibration

My goal of the calibration was to make a program that could automatically fit the plots I needed, but it became more and more manual labor. Because of the shape of the data peaks, it demands very much individual care. This I could not do with a automatic program. The downfall of the automatic centroid collector came when trying it on the back detectors.

The total amount particle front detectors to calibrate is 4 quadrants * 16 rings = 64 front detectors

back detectors: 4 quadrants * 12 strips = 48 back detectors

but to do this, one need all the centroids of the peaks from both sides:

front: 64 detectors * 2 peaks/ring = 128 centroids

back: 48 detectors * 2 peaks/ring * 16 rings = 1536 centroids

total centroids to collect: 1664 centroids (this I did not want to do manually)

Full calibration with 16 rings and 12 back strips. We had to remove the innermost ring.

MOVE THE BELOW TO APPENDIX?

Tilbakemelding:

up to you. I would do like this:

very technical things about scripts etc. I would move to an appendix. If it helps understanding what you did, I would leave it in the text.

For each file converted with MedToRoot, the program makes four files; OffBeam, OnBeam, OnBeamBackground and Scaler. The file we are interested in for analysis is the OnBeam file.

First all of the interesting files are converted with the M2R.sh script.

```
$ cd /Users/trondwj/GitHub/MasterThesis/Scripts/sorting
$ ./M2R.sh Sm
```

Then the OnBeam files from M2R.sh is run through using Treebuilder in the AQ4S.sh script.

```
$ cd /Users/trondwj/GitHub/MasterThesis/Scripts/sorting
$ ./AQ4S.sh Sm user TB
$ mv Sm_user-TreeBuilder-2019-04-10.root ../../Sorted_data/
```

After the sorting, I moved the file to a folder of sorted data, and gave the relative path in the setup_Sm.txt file in Scripts/plotting/ used as input in the MultiPlot.cpp script. Using the MultiPlot.cpp script, the ADC time offsets can be extracted by the following commands

```
$ cd /Users/trondwj/GitHub/MasterThesis/Scripts/plotting
$ root
root [0] .L MultiPlot.cpp++
root [1] check_ADC_time_offsets("setup_Sm.txt")
```

or they can be manually reached by

```
$ cd /Users/trondwj/GitHub/MasterThesis/Sorted_data
$ root Sm_user-TreeBuilder-2019-04-10.root
root [1] new TBrowser()
```

and in the browser, the histograms named tdiff_gp_ i (where i is a number between 0 and 3) will lie under all the folders. The peaks of these plots have the interesting x-value. Zooming into the peaks, it is very clear what value it is. These values are provided in the calibration file under ADC time offsets (ticks). These values can change depending on the amount of data sorted, so it is wise to double check them.

After the peak values have been collected, they should be written into the calibration file

```
# ADC time offsets (ticks)
adc_0.TimeOffset: 0
adc_1.TimeOffset: -2
adc_2.TimeOffset: -3
adc_3.TimeOffset: 5
```

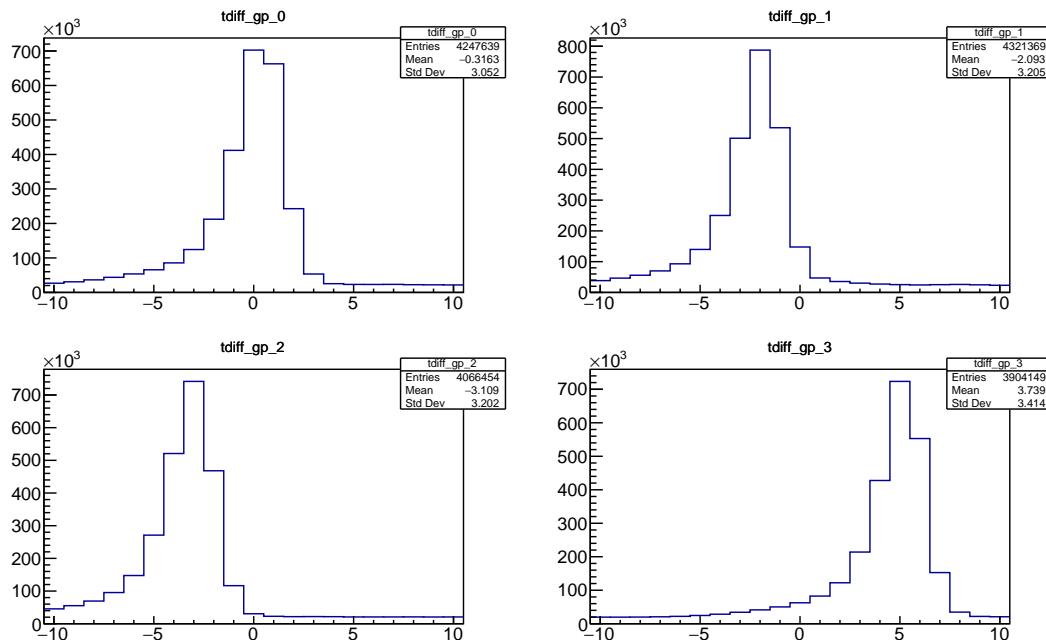


Figure 4.1: ADC time offsets.

Tilbakemelding:
one time spectrum per quadrant?

HUSK: Si noe om ADC time offsets + Threshold. Og at man må se på det tidlig, så resørtere.

M2R.sh → AQ4S.sh → check time offset → threshold → AQ4.fit() → particle-calibration.py → ADC-generator.py → copy the calibration from the terminal and paste into calibration file

Tilbakemelding:
need to explain the time spectra: start - stop
purpose: align time spectra so that you can set a prompt time gate.
→ correlate γ -rays with particles.

Simulation fit → AQ4.fit() → particle-calibration.py → ADC-generator.py → copy the calibration from the terminal and paste into calibration file

Visualize plots using ROOT and the scripts.

Skriv om scriptene som er lagd, og at det var litt vanskelig å automatisere kalibreringen. Hvis det skulle vært gjort måtte vi funnet en funksjon med ”negatively skewed distribution” or ”negative skewness” (right modal), en ”left skewed function” (most data is more than the mean).

I log-skala ser dette mer Gaussisk ut, men det er ikke det i non-log skala.

Back detector calibration: There are just too much individual differences to calibrate the back detectors with a simple script given a range for all 12 back strips. I found out this way to late. There isn’t any range to rule them all, at least since the fitting function can behave very strange given a too small or too big range.

— **Mail from Liam begins** —

”You might have to investigate the threshold a little bit. The continuum of events at low energy comes from charge sharing between the strips. For these very heavy ions, the total amount of charge deposited gets split between neighbouring strips of the CD. The code does performs some tricks to try and recover the correct energy and position, but that depends on counting the number of strips that fire. Therefore, if the threshold is too low you will include ”pedestal” events and it will get things wrong. If the threshold is too high, you will miss some events that have charge sharing and get the wrong energy for your particle.

The key spectra to look at are ”part” and ”cd_debug”. The latter counts how many particles have X strips fired on the front side and Y strips fired on the back side.

If you have too many cd_debug events = 3, then your thresholds are too low. If you have a large continuum/background in the ”part” spectrum, your thresholds are too high. Best thing to do is play about with different values.

Bin 20 is when no particle can be found, because there is no energy registered in either the front or the back strips. This can only happen when the front energy is below the software threshold that you set and the back energy is either in a broken strip or is also below the software threshold. Likely it is some noise events or charge sharing that comes below the threshold.

The major problem with the online calibration is that a number of the back strips have the wrong gains, but it otherwise looks quite good. Have you identified which strips these are, by comparing the gains between the ’online’ and ’user’ calibrations? You could maybe correct those strips as an intermediate step and see how things look.

the source has a thickness of 1.23 mm, which needs to be factored in so that the CD to target distance is the CD to source distance PLUS the source thickness, i.e. $25.78 \text{ mm} + 1.23 \text{ mm} = 27.01 \text{ mm}$. This is very close to the 26.98 mm you got from us in August. I think that the source data was reanalyzed since the original blog entry, giving the 0.03 mm difference!”

— **Mail from Liam ended** —

Tilbakemelding:

I presume that charge sharing is only considered if 2 firing strips are neighbors?

Pedestal

The pedestal is like a massive statue in front of the interesting data.

We use a threshold to cut away the pedestal.

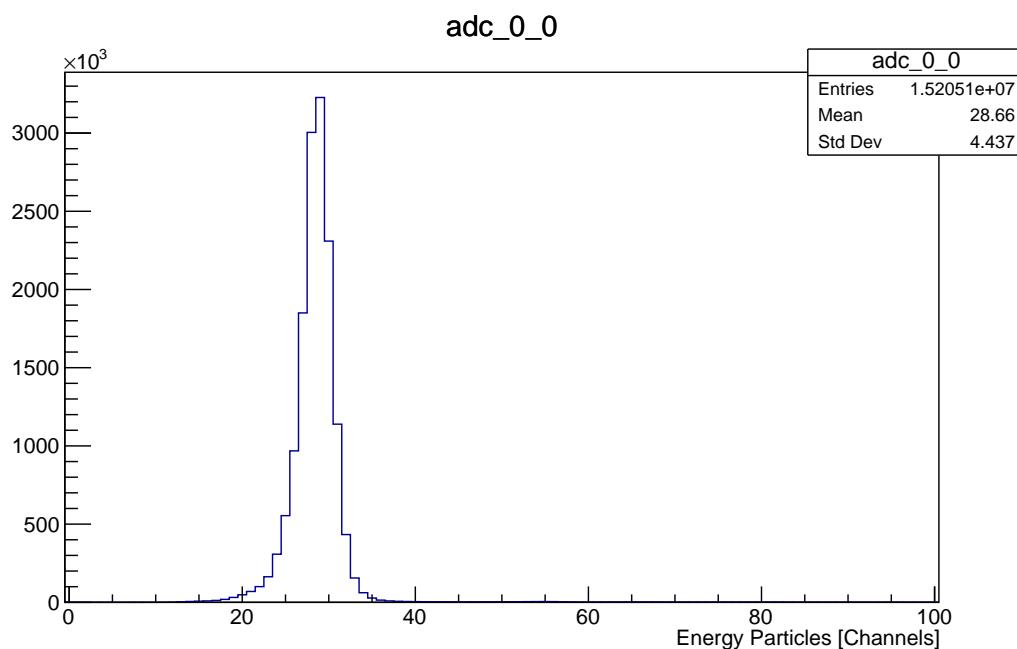


Figure 4.2: Pedestal Q1, f1.

Threshold

* Threshold (forskjellig i log/ikke-log skala)

Using a logarithmic y-axis, the threshold value will decrease very much. So don't use that.

Tilbakemelding:

easier to set thresholds on lin. scale.

Threshold: The code has a default threshold of 100, but in some cases this is too much and some cases this is not enough. So for each adc channel, the threshold can be set. We don't want to include the "pedestal". Charge sharing. Won't cut too much or too little..

CD debug:

```
$ cd /Users/trondwj/GitHub/MasterThesis/Scripts/plotting
$ root
root [0] .L MultiPlot.cpp++
root [1] check_cd_debug("setup.Sm.txt")
```

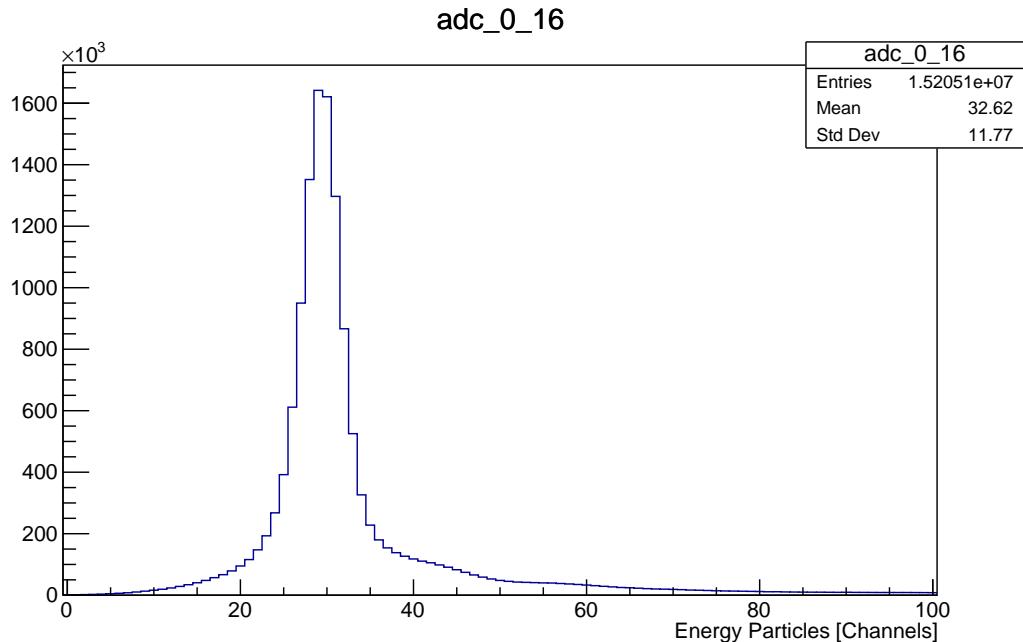


Figure 4.3: Pedestal Q1, b1.

4.4.1 Particle detector

User calibration

ADC: Analog to digital converter (Mesytec)

TDC: Time to digital converter

DSSSD: Double-Sided Silicon Strip Detector \Rightarrow CD

must remove the inner ring from data analysis because of damage

$$\text{gain} = \frac{E_{\text{Sm}} - E_{\text{Pb}}}{Ch_{\text{Sm}} - Ch_{\text{Pb}}}$$

$$\text{offset} = E_{\text{Sm}} - \text{gain} \cdot Ch_{\text{Sm}}$$

in keV.

Hvis man har flere sentroider bruker man bare lineær regresjon. Gjelder spesielt for baksiden!

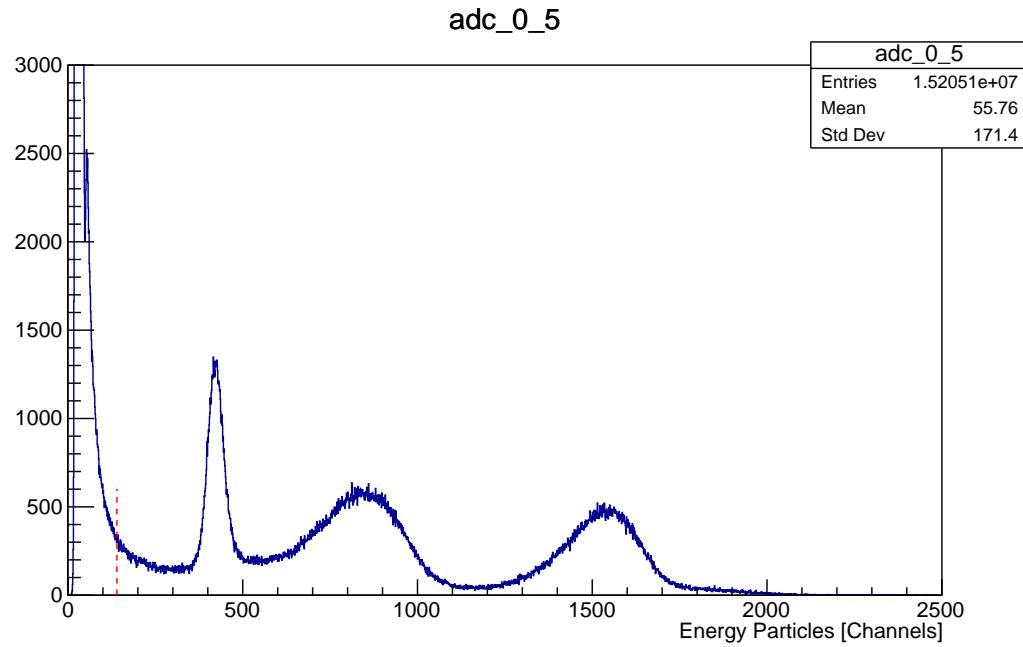


Figure 4.4: Threshold Q1, f6.

Online calibration

4.4.2 Gamma detectors

DGF: Digital γ finder
addback, singles, ...

4.5 Doppler correction

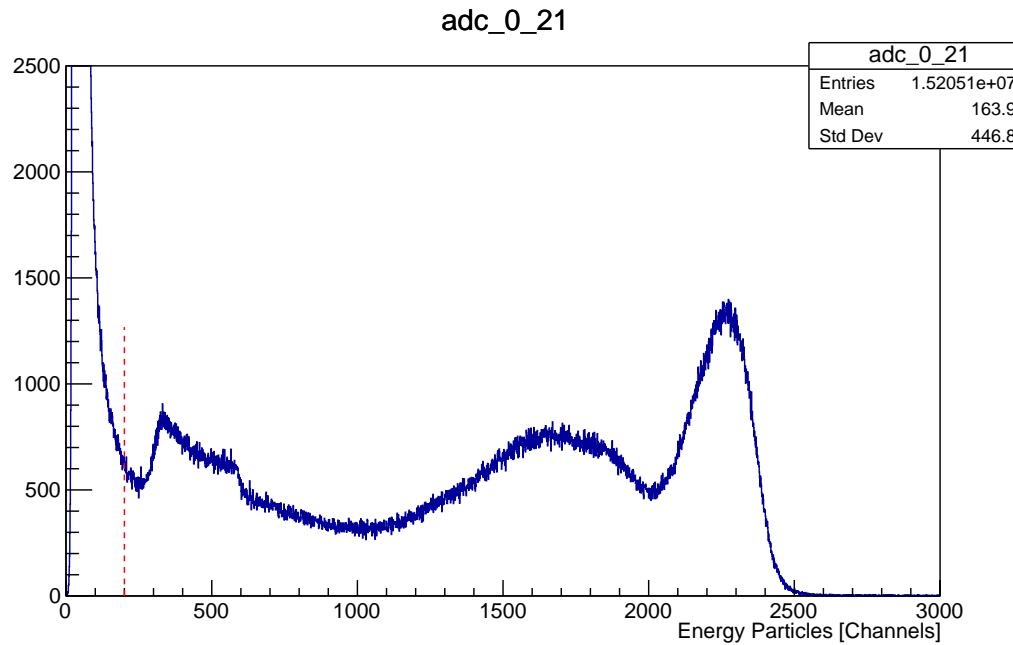


Figure 4.5: Threshold Q1, b6.

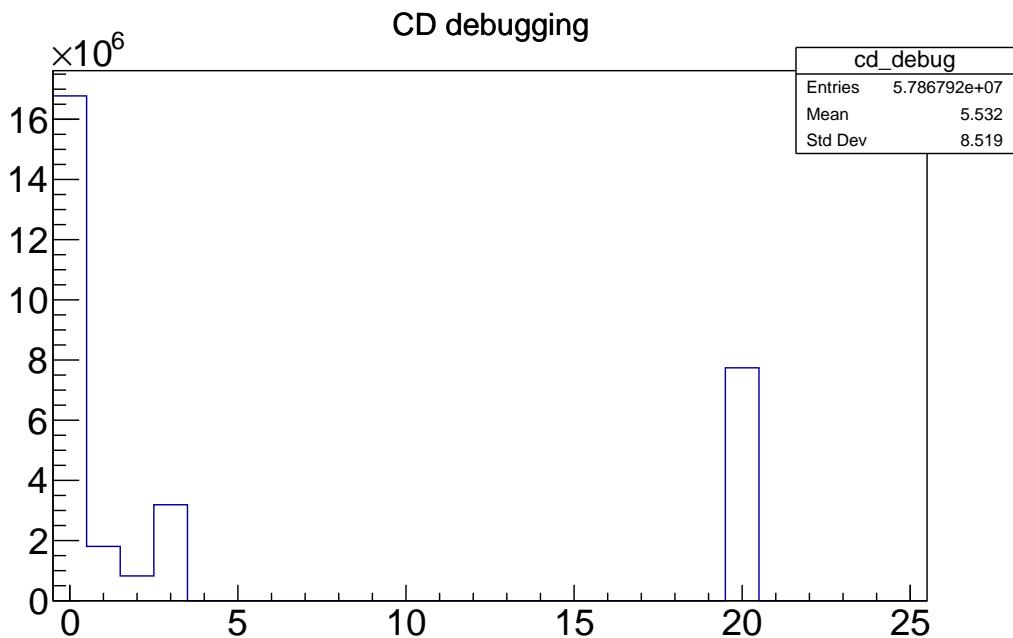
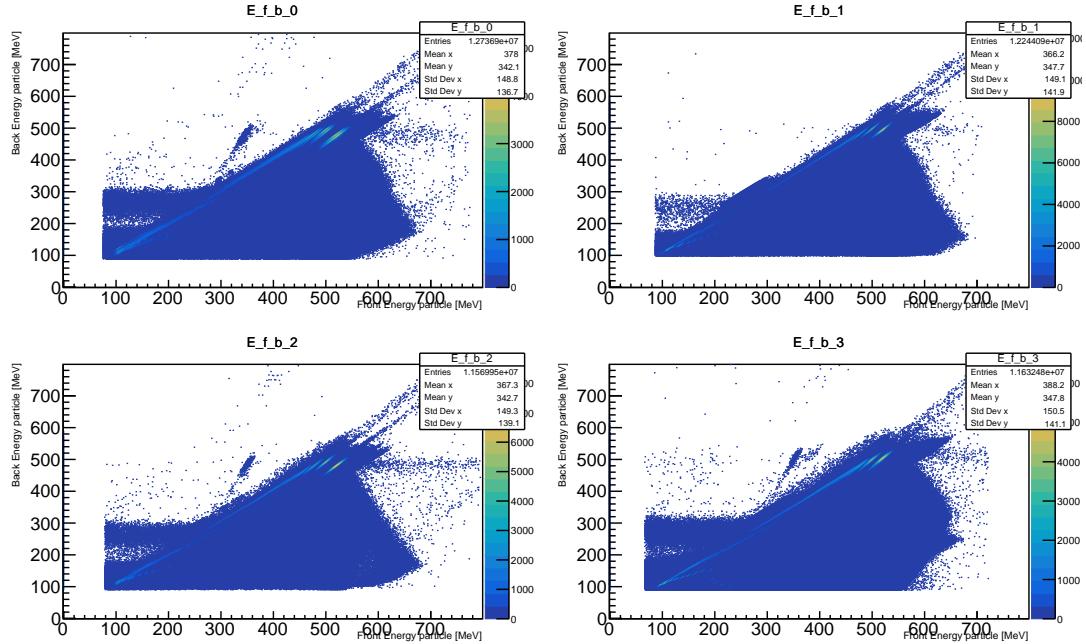
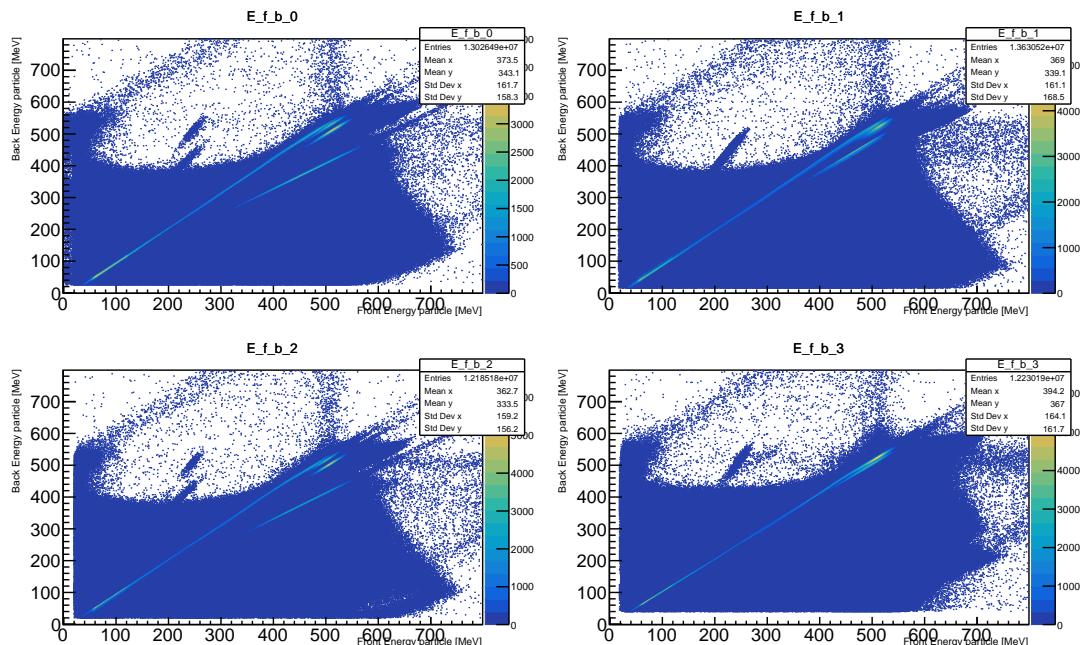


Figure 4.6: CD debugging.

Table 4.3: ADC

ADC	Quadrant	Channel	Front [F] or Back [B]
0 - 3	1 - 4	0	F
0 - 3	1 - 4	1	F
0 - 3	1 - 4	2	F
0 - 3	1 - 4	3	F
0 - 3	1 - 4	4	F
0 - 3	1 - 4	5	F
0 - 3	1 - 4	6	F
0 - 3	1 - 4	7	F
0 - 3	1 - 4	8	F
0 - 3	1 - 4	9	F
0 - 3	1 - 4	10	F
0 - 3	1 - 4	11	F
0 - 3	1 - 4	12	F
0 - 3	1 - 4	13	F
0 - 3	1 - 4	14	F
0 - 3	1 - 4	15	F
0 - 3	1 - 4	16	B
0 - 3	1 - 4	17	B
0 - 3	1 - 4	18	B
0 - 3	1 - 4	19	B
0 - 3	1 - 4	20	B
0 - 3	1 - 4	21	B
0 - 3	1 - 4	22	B
0 - 3	1 - 4	23	B
0 - 3	1 - 4	24	B
0 - 3	1 - 4	25	B
0 - 3	1 - 4	26	B
0 - 3	1 - 4	27	B
0 - 3		28	Empty
0 - 3		29	Empty
0 - 3		30	Empty
0 - 3	1 - 4	31	PAD
4		0	Ionization Chamber
4		1	Ionization Chamber

**Figure 4.7:** User calibration.**Figure 4.8:** Online calibration.

Chapter 5

Experimental results

Chapter 6

Discussion

Level scheme (from Klintefjord?)

Tilbakemelding:

at some point you should show the level scheme.

- motivation: to explain what is known, and which transition probabilities you want to measure.

Perhaps also to explain what theory predicts.

- discussion: if you get γ -spectrum for $^{140}\text{Sm} \rightarrow$ to explain what you see.

Chapter 7

Summary and outlook

Future work: Better calibration of particle detectors (online not perfect). Take into account the shape of the peaks \Rightarrow calibrate the particle detectors manually.. Takes a lot of time! But maybe less than trying to fit all in a script? Had I just known...

Fra oppgaveteksten:

determine Coulomb excitation yields. These yields will then, in a second step, be compared to theoretical calculations and transition probabilities and quadrupole moments will be extracted using chi-square minimization procedures.

GOSIA and GOSIA2 analysis?

https://www.pas.rochester.edu/~cline/Gosia/Gosia_Manual_20110609.pdf

Appendices

Appendix A

Symbol list

Table A.1: Table of symbols with explanations.

$T_{1/2}$	Half-life
-----------	-----------

Appendix B

Acronyms and abbreviations

Table B.1: Table of acronyms and abbreviations.

ADC	Analog to Digital Converter
CERN	European Council for Nuclear Research (in French Conseil Européen pour la Recherche Nucléaire)
COULEX	Coulomb excitation
DGF	Digital Gamma Finder
DSSSD	Double-Sided Silicon Strip Detector
GPS	General Purpose Separator
HRS	High Resolution Separator
HIE-ISOLDE	High Intensity and Energy upgrade of ISOLDE
ISOL	Isotope Separator On Line
ISOLDE	ISOL DEvice
LINAC	LINear ACcelerator
PSB	Proton Synchrotron Booster
EBIS	Electron Beam Ion Source
REXEgis	Radioactive beam EXperiment EBIS
REX-ISOLDE	Radioactive beam EXperiment at ISOLDE
RIB	Radioactive Ion Beam
RILIS	Resonance Ionization Laser Ion Source
TDC	Time to Digital Converter

Appendix C

Source code

The sorting and analysis code used in this thesis has been developed at CERN-ISOLDE and can be found at <https://github.com/Miniball/MiniballCoulexSort>

The code for theoretical predictions of energy used in the calibration was developed by Liam Gaffney who is working at ISOLDE and has to do with analysis of data from Miniball and ISS. kinsim can be found here <https://github.com/lpgaff/kinsim>

Some calibration code is based on the codes of Ville Virtanen and Liam Gaffney.

Other code/scripts have been written by the author. C++ / Python.

Table C.1: Table of source code.

Name/Link	Description
MiniballCoulexSort	Sorting and analysis code
	Kinematic simulation

Appendix D

Connecting MiniballCoulexSort with ROOT

To connect MiniballCoulexSort with ROOT you need them to share their libraries with each other. This is done with a dynamic loader. You can find out more here: <https://root.cern.ch/root/html/doc/guides/users-guide/ROOTUsersGuide.html#file-system.rootrc>.

You have to make a `.rootrc` file in your home folder on your computer. In the `.rootrc` file you want to write something like this

```
Unix .*. Root .DynamicPath:    .:/Users/trondwj/GitHub(ROOT-
framework/build/lib >:/Users/trondwj/GitHub/Miniball/
MiniballCoulexSort/lib :
```

This should all be in one line. The first part is to tell the system to use the dynamic loader of ROOT to connect the given paths that follow. In my case the lib folder of the ROOT install was at

```
/Users/trondwj/GitHub(ROOT-framework/build/lib
```

and the lib folder of the MiniballCoulexSort was at

```
/Users/trondwj/GitHub/Miniball/MiniballCoulexSort/lib
```

These paths is totally individual, and you will probably not have it in the same place. Therefore these paths must be changed to fit your system.

After making the file you either have restart the terminal or you can source the file by writing this in the terminal

```
$ source ~/.rootrc
```


Appendix E

Running ROOT and MiniballCoulexSort from anywhere in the terminal

To run ROOT or the different scripts of MiniballCoulexSort anywhere in the terminal, you have to edit your `.bash_profile` file [.bash_profile on MacOS, .bashrc on Linux]. In my `.bash_profile` I used this

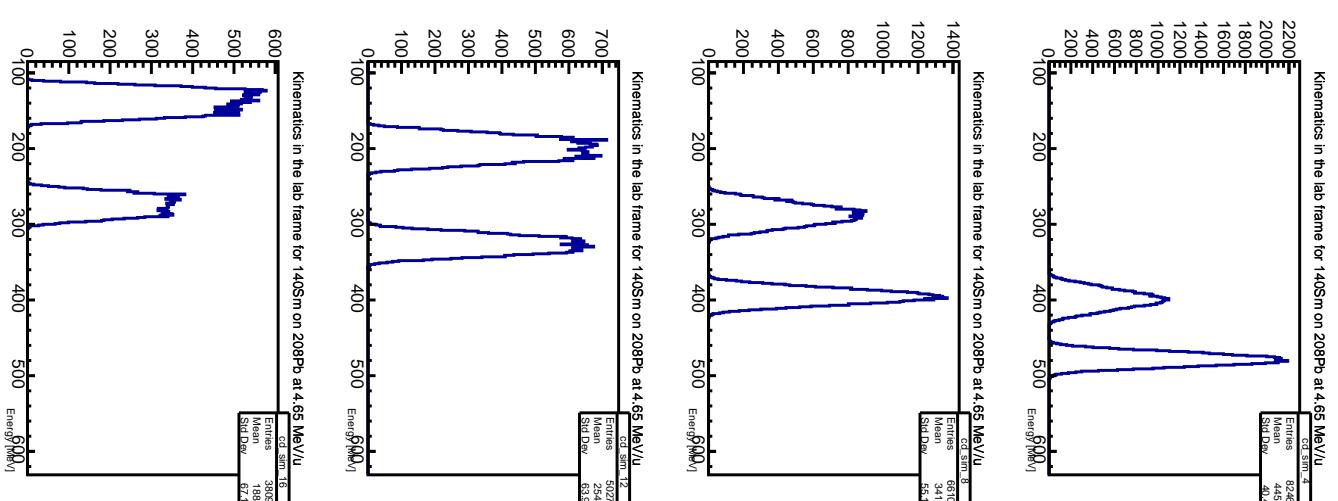
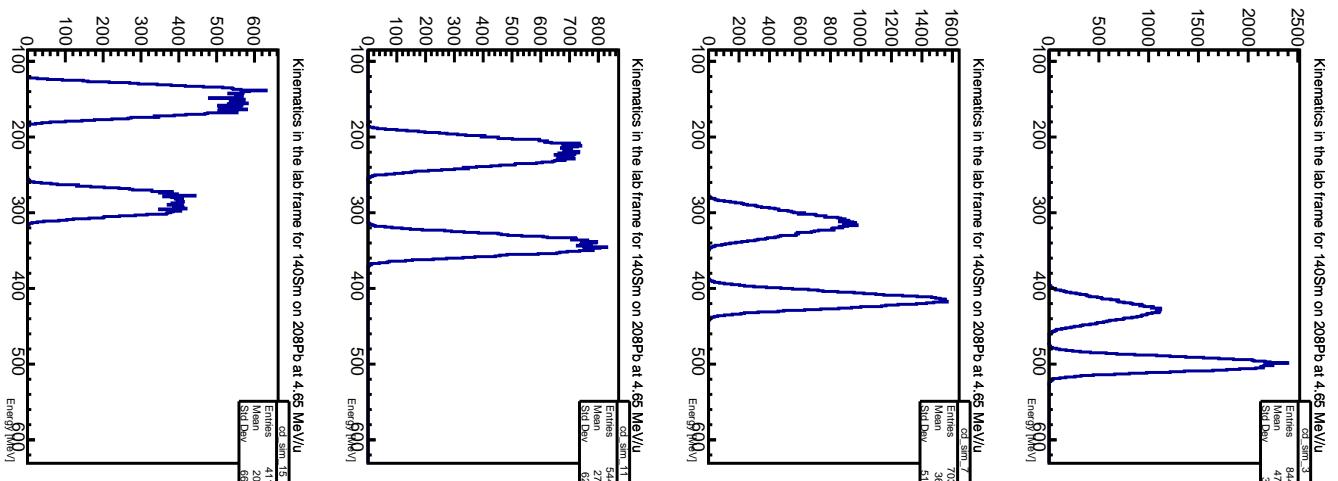
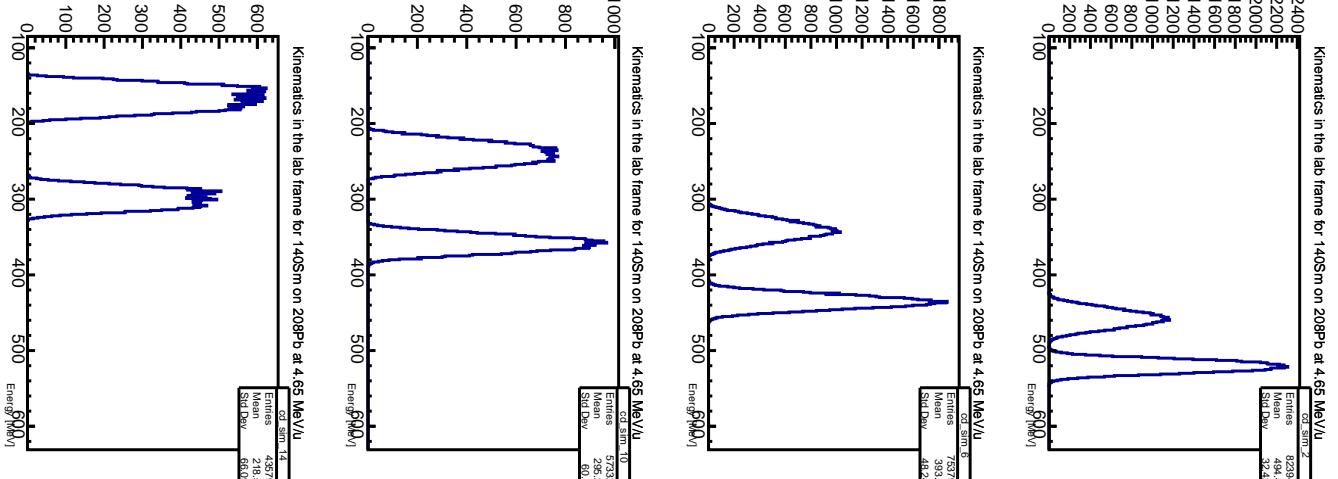
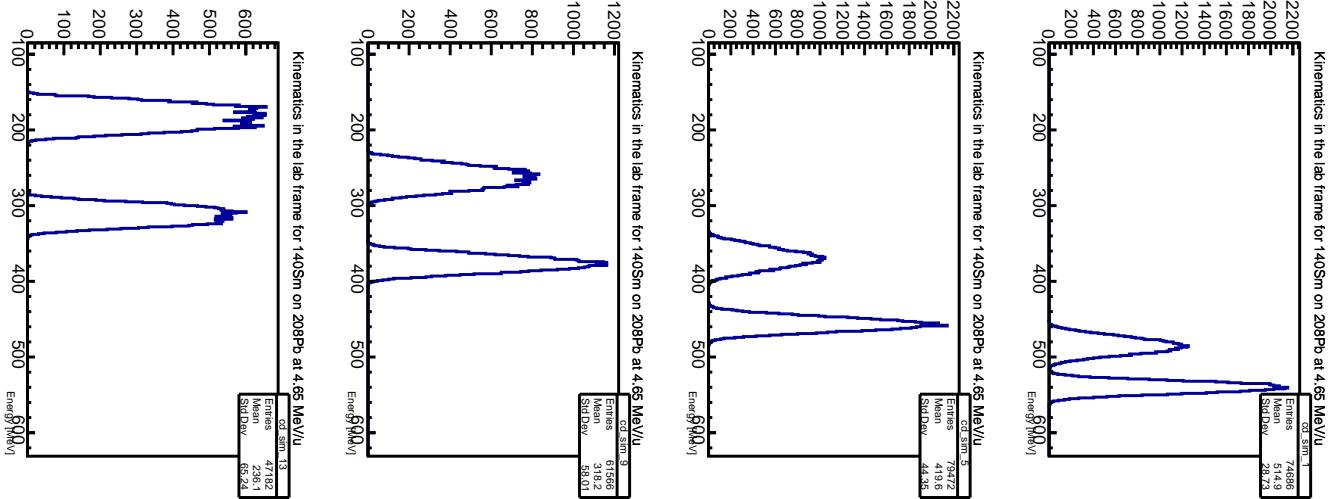
```
# Run ROOT from anywhere
export ROOTSYS=$HOME/GitHub(ROOT-framework/build
export PATH=$ROOTSYS/lib:$PATH
export PATH=$ROOTSYS/bin:$PATH
export DYLD_LIBRARY_PATH=$ROOTSYS/lib:$DYLD_LIBRARY_PATH

# Run MiniballCoulexSort from anywhere
export DYLD_LIBRARY_PATH=$HOME/GitHub/Miniball/
    MiniballCoulexSort/lib:$DYLD_LIBRARY_PATH
export PATH=$HOME/GitHub/Miniball/MiniballCoulexSort/lib:$PATH
export PATH=$HOME/GitHub/Miniball/MiniballCoulexSort/bin:$PATH
```

The DYLD_LIBRARY_PATH is used on Mac only. On other systems, use LD_LIBRARY_PATH. You need to locate the lib and bin folders for both ROOT and MiniballCoulexSort and change them to fit your system, and in addition you need the build folder of your ROOT install.

Appendix F

Other appendices



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