

PHSX815 Project 1

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Introduction

For this project I will be simulating an electron-positron collision at a specified collision energy. You will be able to configure what collision energy you want and how many experiments you want to run then the program will calculate which final-state products are allowed based on their rest masses. This is a toy model, the interaction is simplified by ignoring any higher order contributions or QFT nuances, I only consider an s-channel process.

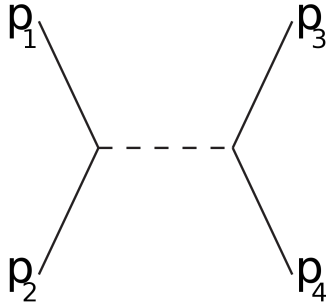


Figure 1: In my simulation, p_1 = electron, p_2 = positron, boson (dotted line) = photon

Since the initial state is neutral (total charge = 0) the final states must also have zero net charge, so our possible products are all six leptons paired with their anti particle: $\nu_e \bar{\nu}_e$, $\nu_\mu \bar{\nu}_\mu$, $\nu_\tau \bar{\nu}_\tau$, ee^+ , $\mu\bar{\mu}$, $\tau\bar{\tau}$, and then all 6 quarks paired with their anti particle: $u\bar{u}$, $d\bar{d}$, $c\bar{c}$, $s\bar{s}$, $t\bar{t}$, $b\bar{b}$. So, in figure 1, p_3 and p_4 are one of the above listed pairs. Which particles are allowed as final state products only depends on the initial state's collision energy. This is a categorical distribution with equal probability for each outcome. When it comes time to analyze the data I will hypothesize that this simulated decay prefers leptons over quarks, and I will (hopefully) be able to show that is not the case with my analysis code.

Algorithm Analysis

For the simulation code, I first initialize the default collision energy and the number of experiments. I also initialize a vector of strings, call it `product_names`, and fill it with (by order of ascending mass) the decay products possible from my above list. E-neutrino, mu-neutrino, so on and so forth. Since I'm explicitly defining this array I might as well save myself a step and sort it now. I then define an int named `name.size`, set that equal to the `product_names` array length. I then add a block that I copied from Chris Rogan's code to parse our command line and check for two key strings: `"-Ce"` and `"-Nexp"` and whatever ints follow them. This block is so I can pass this simulation different values of collision energy and/or number of experiments in the future.

I then initialize another array, this time of doubles, and name it `product_masses`. This array is also organized by way of increasing mass size, such that `product_name[0]` corresponds to `product_mass[0]`, so on and so forth. Now, I finally do the calculation of which products are allowed. I first initialize a global variable called `possible_products_size` and a global int `j`. then, in a while loop, while `j` is less than the size of our product array (`names_size`), I check if collision energy is greater than or equal to 2 times the product mass of `product_masses[j]`. If `Ce` is greater than or equal to the mass of `product_masses[j]`, then I increment `possible_products_size` by 1, then regardless of the outcome I increment `j` by 1. This while loop runs until `j` is as long as our `product_names` array (which is also the length of my `product_masses` array). When that is complete, I now know how many products are possible, everything from `product_masses[0]` up to `product_masses[possible_products_size]`.

Now, I would like to create a new array of only my possible products. I define an array `possible_products` of length `possible_products_size`. I then use a for loop to iterate through the `product_masses` array and fill `possible_products` with those values, again maintaining the order of ascending mass. Now, the simulation is as easy as rolling a dice and comparing the outcome to an evenly split distribution. To create the distribution I divide 1.0 by `possible_products_size` and store that as a double named `distribution`. I am expecting a number for distribution like .25 or .3333333, etc. Next I define a seed by using a block of code I found online for a high precesion clock (it uses your computer's clock in units of nanoseconds to get very unique seeds. The regular method of using `time(0)` was not giving unique enough seeds when run back to back). I then feed that seed into `srand`, this is a required step when using the random functions in the standard c++ libraries. Finally, I use a for loop do "roll the dice" and print the outcome as many times as you define with `Nexp`. The `rand()` function outputs a number between 0 and 1, then I divide that number by `distribution` to determine which domain it falls into in my probability distribution. For example how this works, if we have 4 possible outcomes our distribution is $0 \rightarrow .25$, $.25 \rightarrow .50$, $.50 \rightarrow .75$, $.75 \rightarrow 1.0$. Any number that falls between 0 and .25 should correspond to outcome 0, between .25 and .5 corresponds to outcome 1, and so on. So, a very easy way to check a random number and match it to the proper outcome is to divide your outcome by the value you are partitioning your distribution by, in the above example that would be .25. Whatever your outcome from the division is tells you the exact outcome that corresponds to (when indexing the outcome from 0, that is important).

Making use of this quick check trick, I then just pipe the output of `main.cpp` into a text file named "data.txt". It is imperative that you use `data.txt` as the name because the `analysis.cpp` file will be looking for that file name. From here, we have a .txt file full of integer values in a long string separated by spaces. In order to oraganize this and visualize our results I wrote another program, `analysis.cpp` that uses the ROOT library for data analysis to import this data file and interpret the results.

Running my `analysis.cpp` file requires ROOT, I prefer to launch the root interactive environment by typing

```
root
```

in the terminal. Once thats begun I load the file with the load command followed by the file name:

```
.L analysis()
```

then by running the analysis:

```
analysis()
```

The program will generate the histogram and save it to the current directory. Please note, repeated running will overwrite the previous histogram.

The generated histogram will show you the number of produced products in each category of particle that was allowed by that collision energy. There is no further analysis beyond this. An example of further analysis would be an investigation into whether the particles are equally generated with some random variation between particle types... I did not do this, though.