



Weekly Report 9/11/2018

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Task this week:

Closely examine Jack's proton labels of run_0130 by plotting the histograms of fitting results (total events & proton events) using various methods:

Monte Carlo

Differential evolution

Basin hopping

Monte Carlo

Six-dimensional parameter space: $(x, y, z, E, \varphi, \theta)$

Random generation of uniformly distributed candidate points around the seed point

The point with lowest objective function value is updated as the new seed point

Stops when the number of iteration is reached

Differential Evolution

Randomly selects n points within 6-D search space (population)

Recombines each point with other candidates in the population -> there are different strategies for this

Decides whether the mutated points will be kept as the new candidate

Stops when the point with lowest objective function value is found and/or when the number of iteration has been reached

Basin hopping

A variation of Markov Chain Monte Carlo method, combines global stepping algorithm with local minimization algorithm

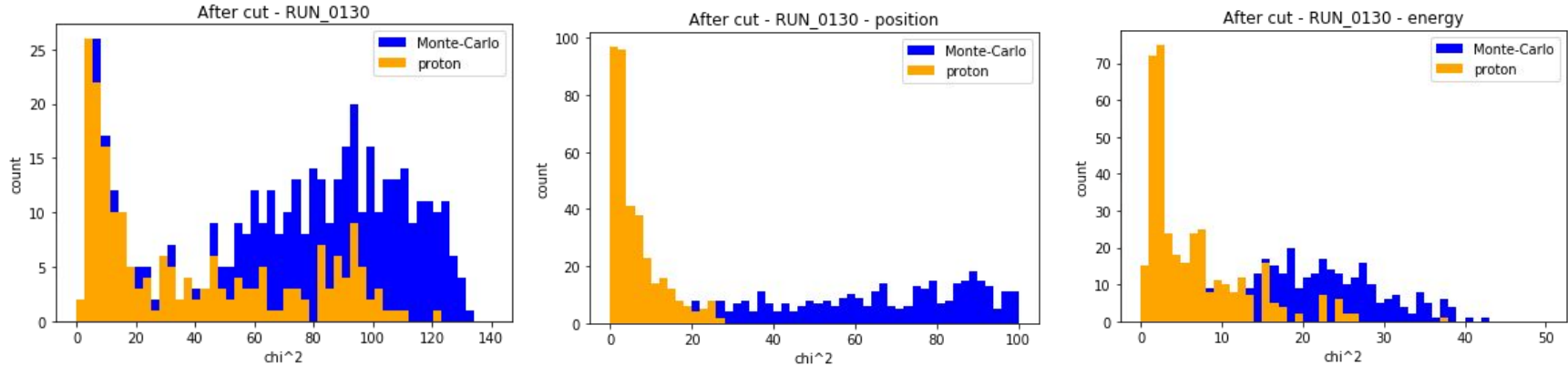
Calculates local minimum based on the starting point

Applies a random perturbation to the coordinates

Calculates candidate point (local minimum) at new location, then accepts/rejects the new candidate using Metropolis criteria.

Stops when the point with lowest objective function value is found and/or when the number of iteration has been reached

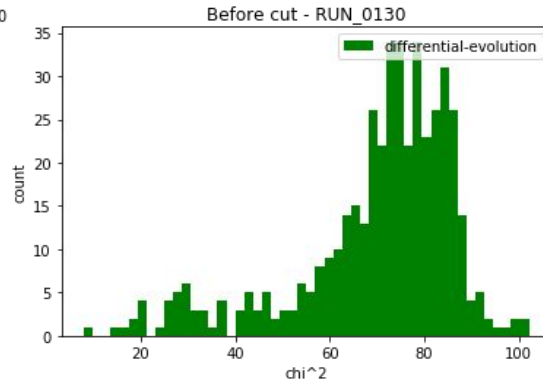
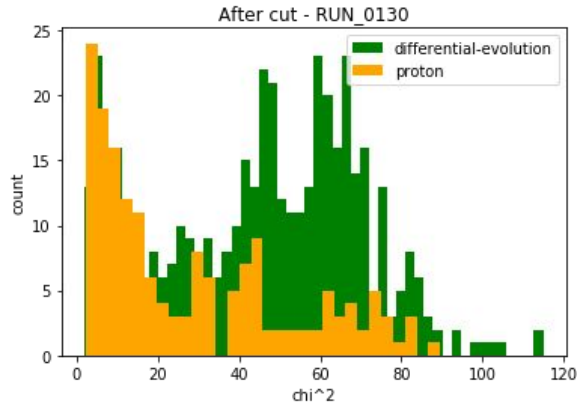
Results - Monte Carlo



Above are plots of MC fitting results of total events and proton events, with individual components of the MC fitting results

Monte Carlo is a good indicator of proton events; the position component seems to be an even better one.

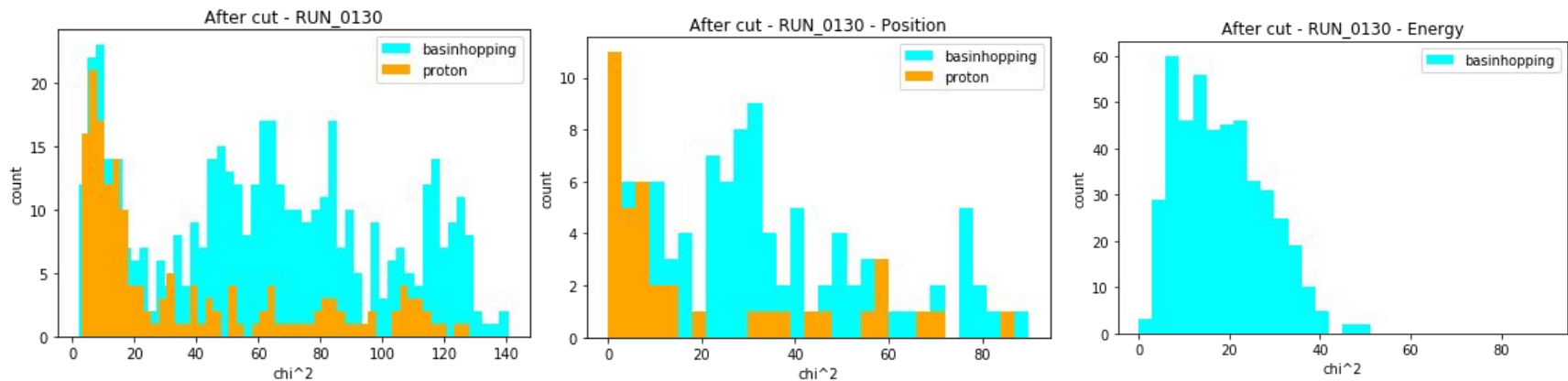
Results - differential evolution



To test my original hypothesis that differential evolution (DE) is robust to noise, I plotted χ^2 results for both cleaned and uncleaned data - it turns out that DE is not as robust as I originally thought.

DE is also good for successfully identifying proton events.

Results - basin hopping



The “energy” and “position” here is not the individual components from the minimum χ^2 value; instead, it is the result when the algorithm only minimizes the position/energy. (I have not tried minimizing a vector yet, but have figured out a way to do so)

Comparing the three methods

Differential evolution has better overall fitting and slightly better proton fitting

