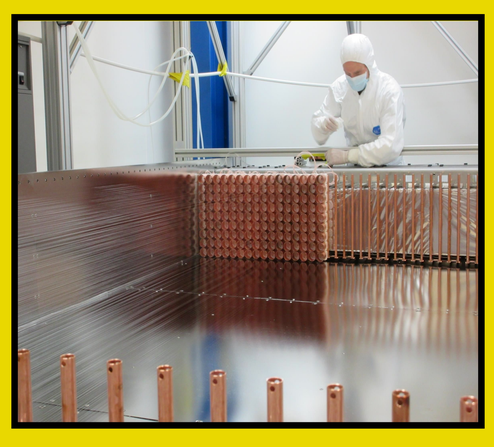
SuperNEMO

Pattern recognition and track reconstruction

Federico Nova (nova@physics.utexas.edu) on behalf of the SuperNEMO Collaboration

University of Texas at Austin

The unique technique pioneered by NEMO-3 is employed in the SuperNEMO experiment. The detector is designed to discover the neutrinoless double beta decay of enriched isotopes by measuring energies and trajectories of each emitted electron. Identifying the characteristic topology of the electron tracks is critical. The SuperNEMO Collaboration has developed two new tracking algorithms which we present in this poster.

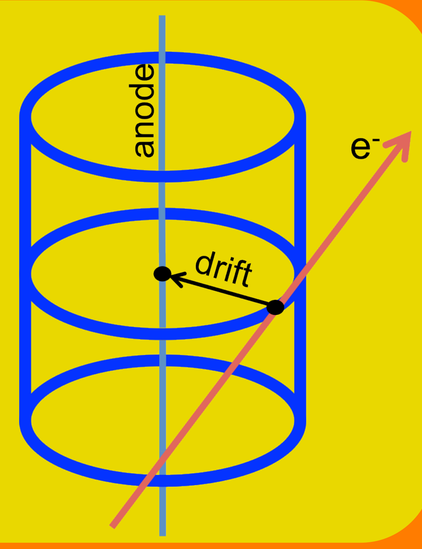


The tracking detector

The SuperNEMO tracking chamber consists of 2016 drift cells operated in the Geiger mode and aligned vertically on both sides of the source foils. The chamber is filled with He gas and immersed in a vertical uniform magnetic field of 25 gauss.

Each cell has a central anode wire surrounded by 12 ground wires. When a charged particle flies through the chamber gas, its ionization products are drifted to the nearest electrode providing the detection signal. The drift time is converted into position information.

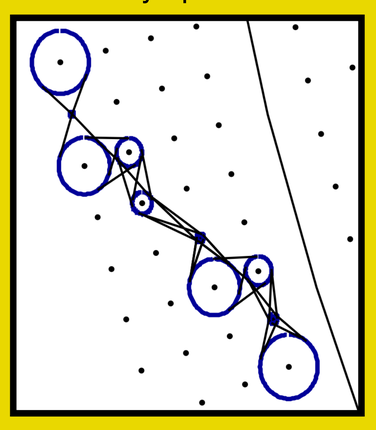
One hit cell localizes the electron on a cylindrical surface, the height and thickness corresponding to experimental errors. The track is constrained to be tangent to the cylinder.

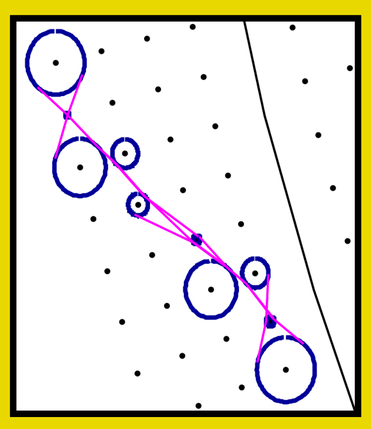


Cellular automaton tracking

Cellular automatons perform tracking by repeating elementary operations.

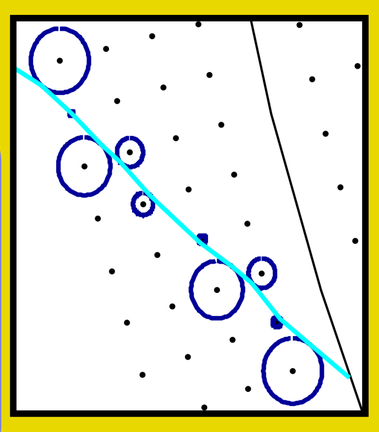
In the first step, the input hits are combined to calculate all possible tangent lines between adjacent cells.



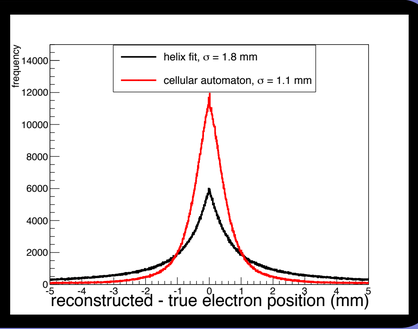


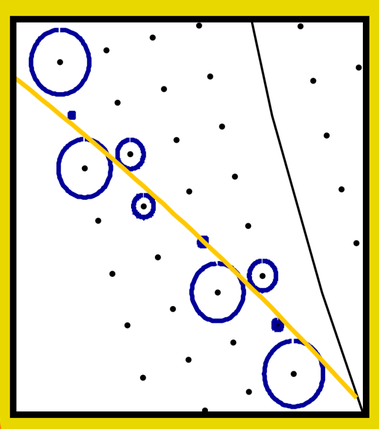
In the next step, adjacent segments are paired into sets of broken lines extending over three cells. Each broken line is required to form a small kink angle.

Broken lines are then merged to form a unique continuous track which is tangent to all circles associated with hit cells in the cluster.



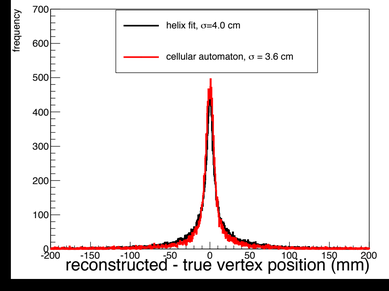
Monte Carlo studies show this step gives the most accurate reconstruction of the electron position in each cell.





Finally, a global helix fit can be performed using the previous points as seeds.

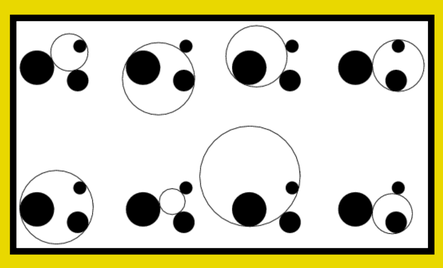
The helix extrapolation is used to find the vertex on the source foil and the impact point on calorimeter blocks.



Legendre transform tracking

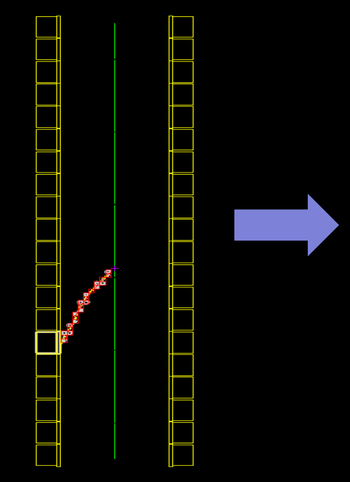
In this tracking method, input cells are first combined to form all possible triplets of cells.

By Apollonius theorem, there are at most 8 helices which can be tangent to all three cells. They can be analytically constructed through Legendre transform.

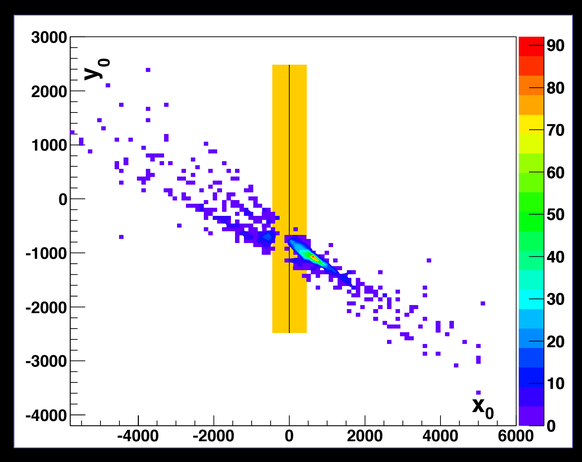


All calculated helices are mapped into points in the 5D space of helix parameters: (x_0, y_0, z_0,) for the center position, plus the radius R and pitch H. The highest peak in this space identifies the helix which activates the largest number of cells, thus providing clustering and fitting at the same time.

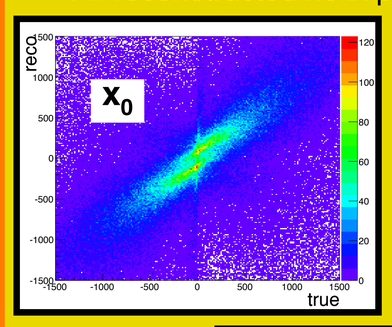
event display of a single electron emerging from the source foil and reaching a calorimeter block

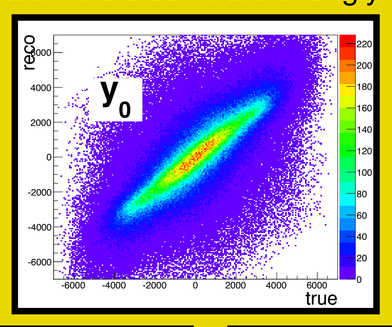


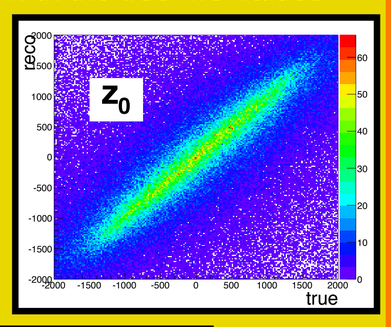
2D projection of the 5D helix space. Each point is a helix tangent to 3 cells. The peak shows the most likely position of the helix center.

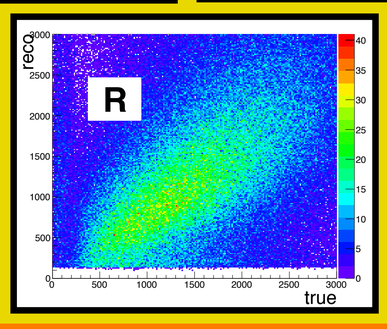


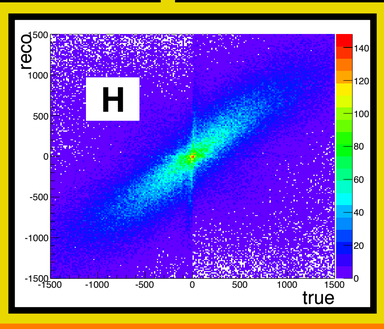
All reconstructed helix parameters correlate strongly with the true MC values.



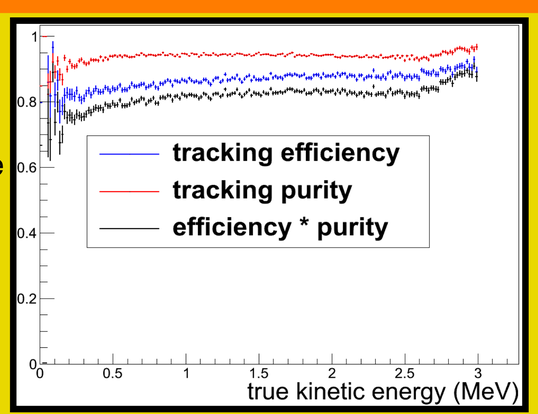




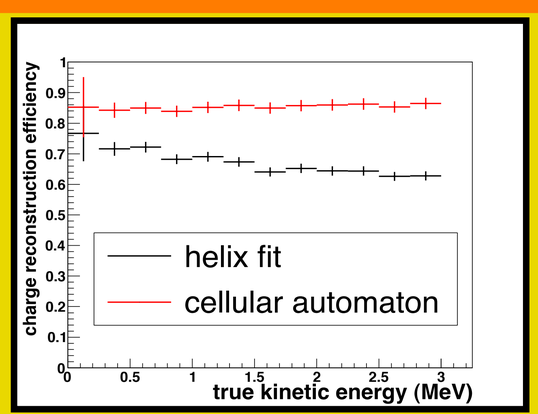




Tracking efficiency and purity are stable over the range of true kinetic energy, maximizing at the end-point value.



By sampling points throughout the track, the cellular automaton method improves the reconstruction of the electron charge.



Both tracking techniques can be run sequentially on the same event providing a precise position and charge reconstruction as well as a valuable helix fit.

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