# NPS Software Analyzer Development NPS Collaboration Meeting



Carlos Yero Steve Wood







### What has been done ?

- created NPS analysis software
- tested NPS analysis software
   (See <u>Hall C Doc-DB NPS Software Update (Yero 2021)</u>)
- developed NPS calorimeter cluster algorithm
- S. Wood added code infrastructure to facilitate fADC sample (mode) data readout

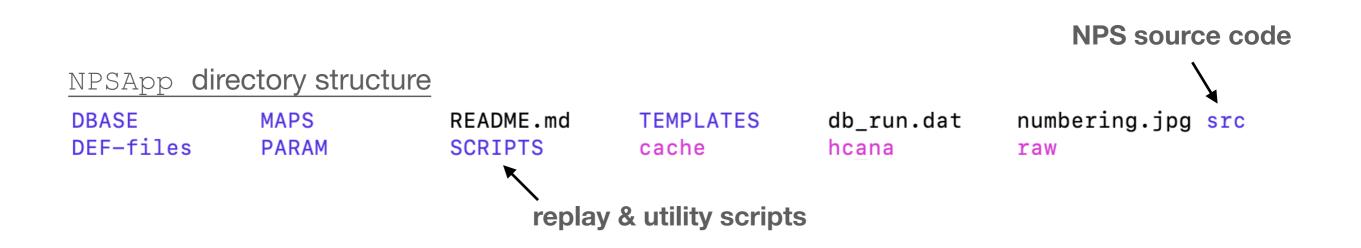
What needs to be done?

- develop NPS calorimeter calibration code
- test the software when NPS assembly is completed (on test bench)

Follow us on GitHub to contribute: https://github.com/sawjlab/NPSApp/tree/main

### What has been done?

- created NPS analysis software
  - NPS C++ classes adapted from HCANA/podd to the NPSApp repository
    - ► -> THcNPSAnalyzer
    - ► -> THcNPSApparatus
    - ► -> THcNPSCalorimeter
      - ← → THcNPSArray
      - ← -> THcNPSShowerHit

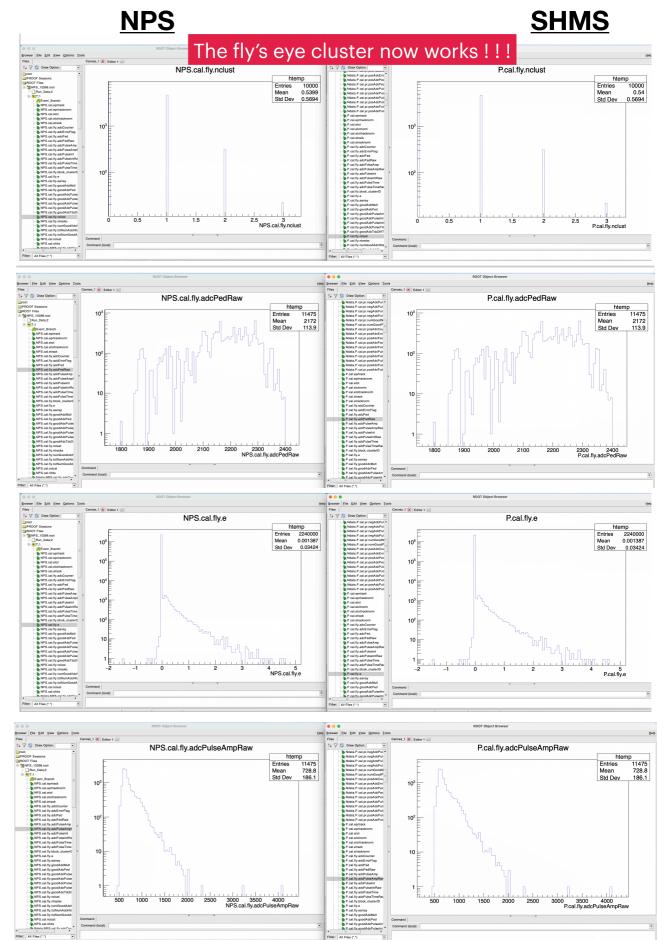


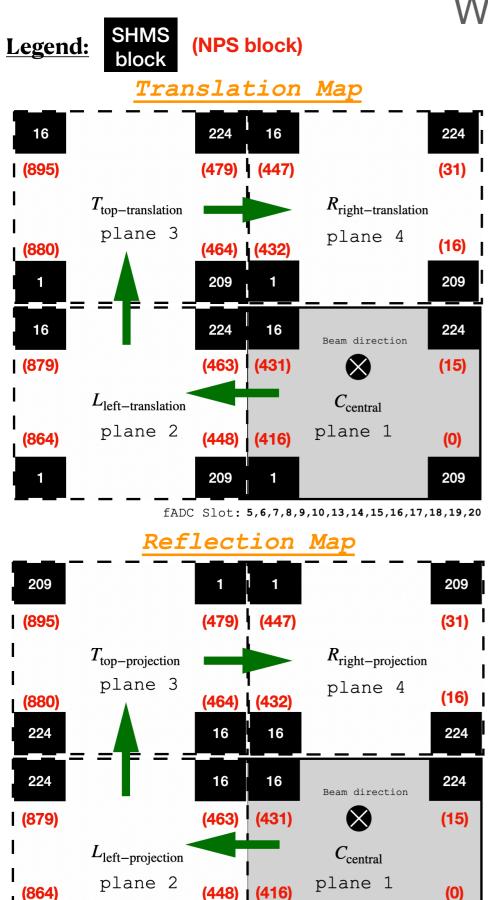
### What has been done ?

- tested NPS analysis software
  - NPS replay script adapted from hallc\_replay
    - parameters, maps & database structure also adapted and re-named accordingly
  - NPS does **NOT** have tracking detector
    - tracking removed from code
    - tested NPS source code using actual SHMS data (see right plots)

#### • mimic NPS geometry:

- use translation, reflection maps
- use nps\_cal\_replicate option
- simulate higher multiplicities:
  - use SetNevMerge(N) method





(864)

209

### What has been done?

#### mimic NPS geometry: 0

use translation, reflection maps

#### What was done? 0

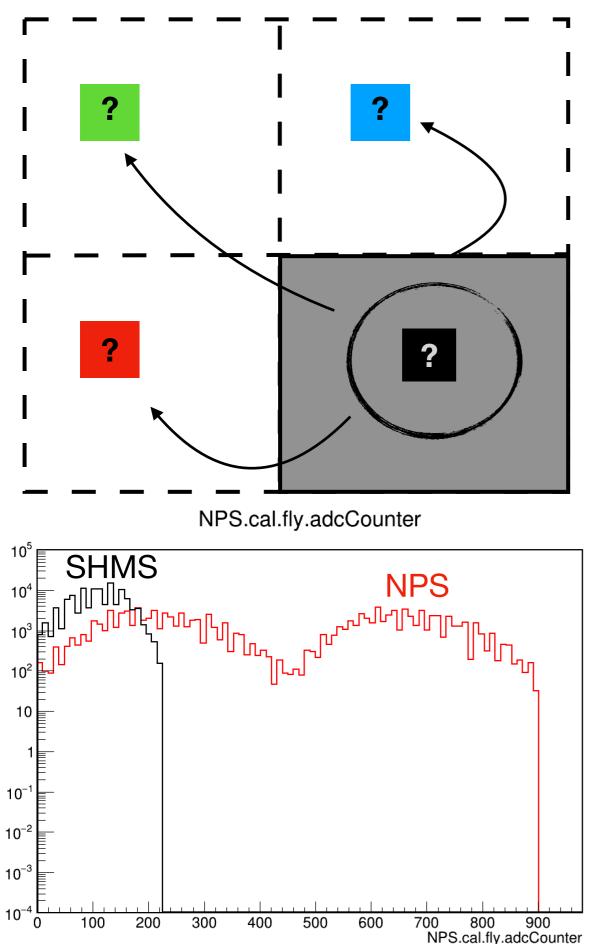
- 1. modify geometry/signal maps to include the 3 "fake" calorimeter planes
- 2. calibration/cuts parameters were copied (x3) to generate 896 parameters "fake" NPS
- 3. events translated or reflected onto 3 remaining "fake" planes (generate higher x4 multiplicity)

fADC Slot: 5,6,7,8,9,10,13,14,15,16,17,18,19,20

(0)

209

What has been done?



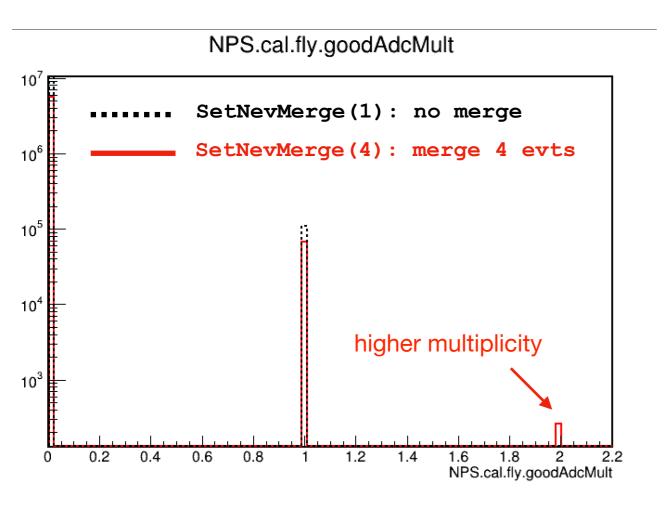
#### • mimic NPS geometry (improved):

• use nps\_cal\_replicate option

#### • How does it work ?

- 1. per trigger (physics event), select a quadrant at random and move the event to that quadrant by translation" (nps\_cal\_replicate=1) or "reflection" (nps\_cal\_replicate=2)
- 2. requires ONLY signal map from standard SHMS calorimeter since mapping done internally (in NPSApp source code)
- 3. still need 896 elements (param), as these will be used depending on which quadrant the event lands in

### What has been done ?



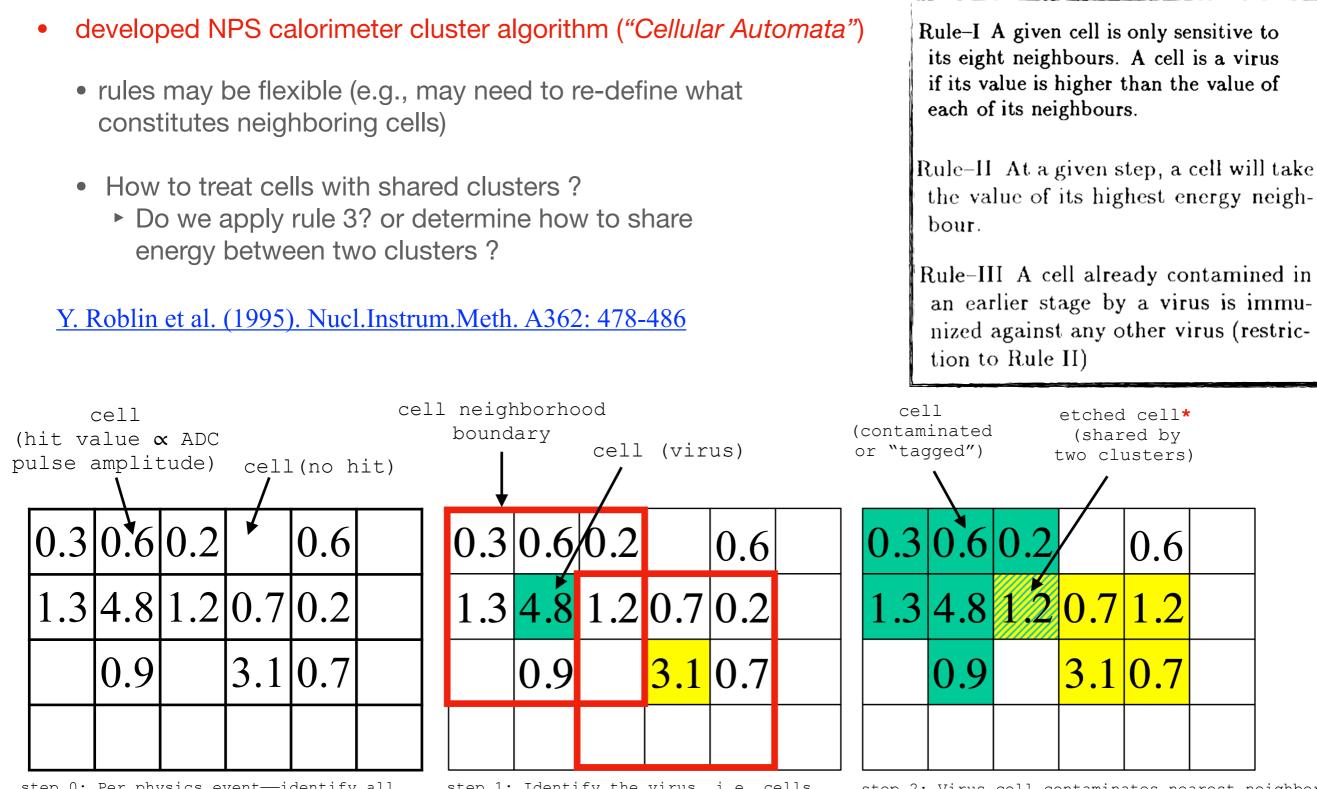
#### • simulate higher multiplicities:

• use SetNevMerge(N) method
 (call THcNPSAnalyzer::SetNevMerge(N)
 in replay script)

#### • How does it work ?

- "merge" hits every N events into hit list
- at Nth event, all hits from previous events are analyzed as if they were from the Nth event
- hit list cleared before analysis of next N events

### What has been done ?



step\_2: Virus cell contaminates nearest neighboring cells, which are "tagged" with the same color as the virus to form clusters. Cells with multiple tags (etched) are shared between their respective clusters, and a determination of how to handle these cases must be made. The contamination will spread iteratively over secondary, tertiary, etc. neighbors provided these have not been "tagged"

step\_0: Per physics event—identify all blocks with ADC amplitude > ADC\_threshold. Only the hit blocks will form part of the clustering algorithm later on.

step\_1: Identify the virus, i.e. cells
with a local maxima or larger energy
deposit than their neighbors.

Cellular Automata Evolution

8

#### What has been done?

O Currently, both HCANA and NPS "Good Hit" Selection Criteria is as follows:

- 1. ALL ADC Pulses for ALL calorimeter blocks hit are analyzed per event. (Includes blocks with Multiple Hits\*\* per event)
- 2. To be considered a 'Good ADC Pulse Hit' (per block):
- ✦ Require Pulse Amplitude [mV] > 0 && Raw Pulse Integral [Chan] > 0
- Require Pulse Time Difference [ns] (ADC Pulse Time StartTime\*\*) to be within an upper and lower bound (set by external per-block parameters)
- ✦ Require Raw Pulse Integral [Chan] > Threshold (based on pedestal peak)
  - \*\*If there are still multiple pulses per block per event that passed These conditions, then the 1st hit within the Pulse Time Difference Window will be chosen as the 'Good ADC Pulse Hit'
- 3. The 'Good ADC Pulse Hits' are added to a HitSet (to be discussed) which is used by both clustering algorithms to make clusters of hits.

\*\*Multiple Hits: I have not yet fully developed the handling of multiple hits. So far, I have made 2D vectors to store the multiple hits per block, however, it is not clear yet how to re-distribute the multiple hits per block in the clustering algorithm. Maybe we can simply add up the pulse integral of multiple hits per block, and consider that when forming clusters?

\*\*StartTime: This definition used the hodoscope information in the standard HCANA code however, in the NPS, the StartTime needs to be re-defined, as there are no hodoscopes in the spectrometer. Maybe we can use the HMS reference time (trigger), or the accelerator RF time instead ?

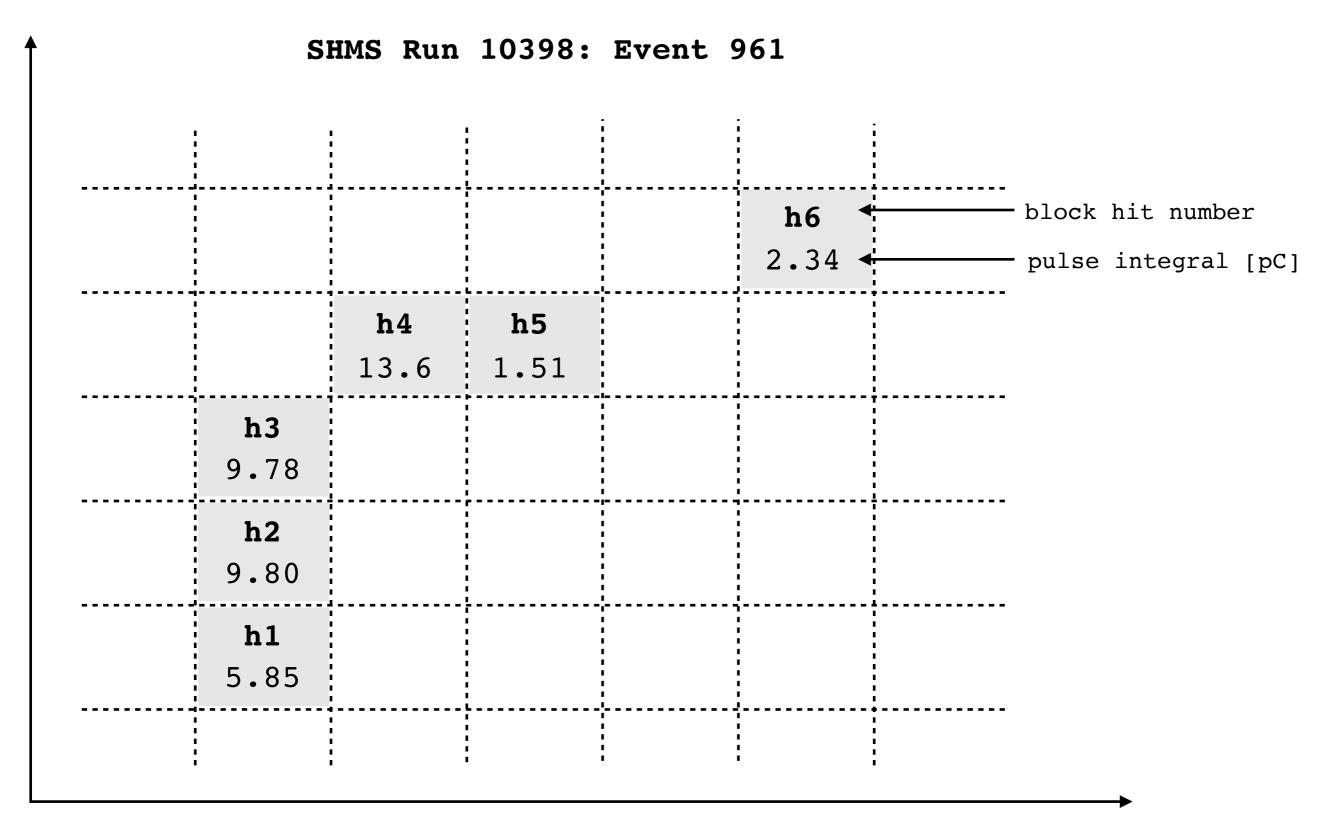
# NPSApp Calorimeter Clustering Algorithm: *Cellular Automata* Approach Animation

O The Hall C Neutral Particle Spectrometer (NPS) clustering algorithm is in development

Initial results are presented and compared to the **HCANA approach** using SHMS calorimeter data.

See <u>Hall C Doc-DB Clustering Algorithm Slides (Yero 2021)</u>

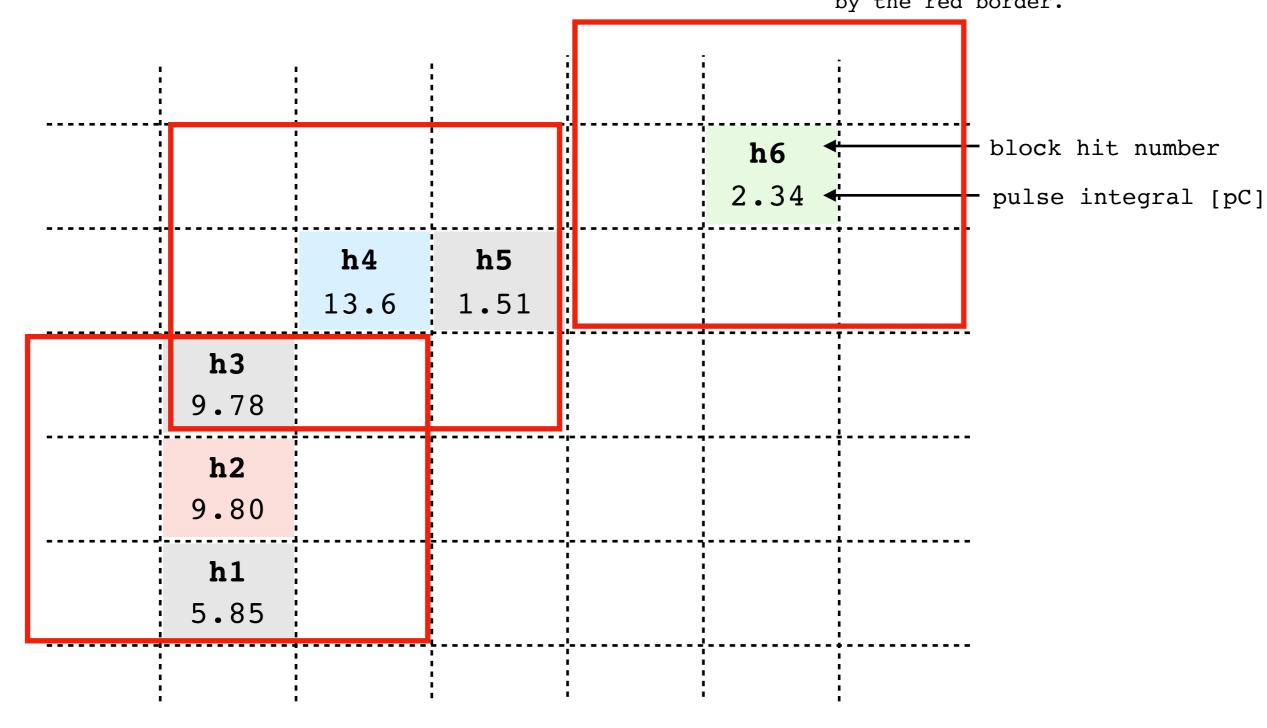
O Identify virus blocks. These are blocks that have the largest pulse integral compared to their nearest neighbors\*\*.



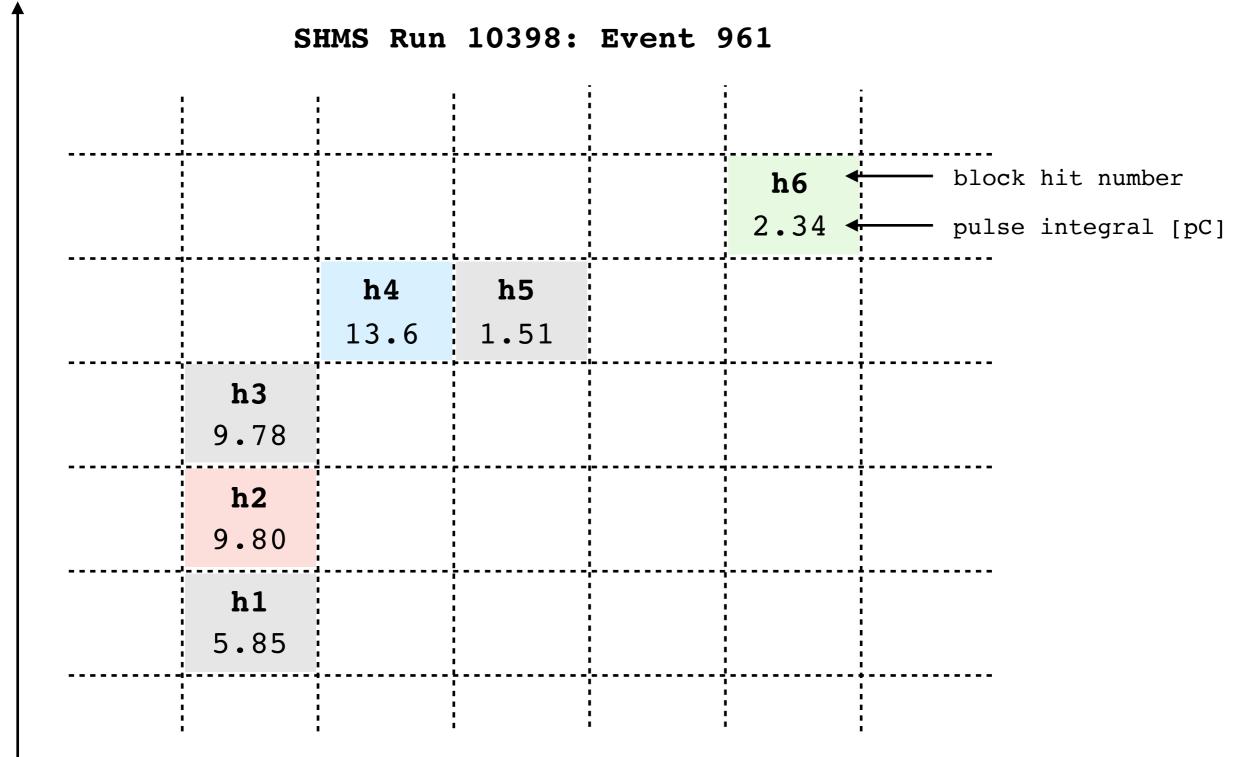
SHMS Run 10398: Event 961

\*\*NOTE:

The nearest by neighbors are identified as the adjacent blocks to the central block in question. The neighborhood of the virus blocks are represented by the red border.

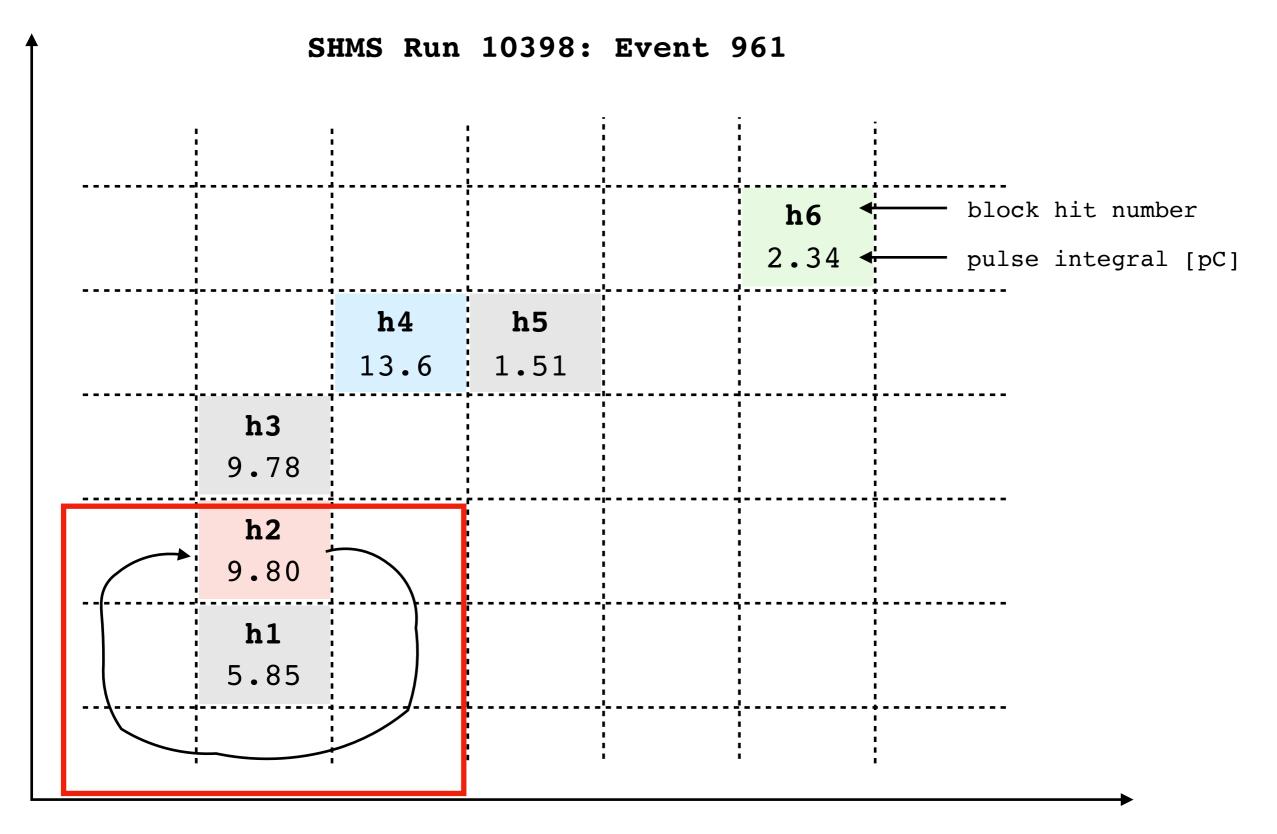


O Determine the nearest neighbor with the highest pulse integral. If this neighbor is a virus (shaded red, blue or green), then it will "contaminate" the block in question (shaded grey) and make it ill.



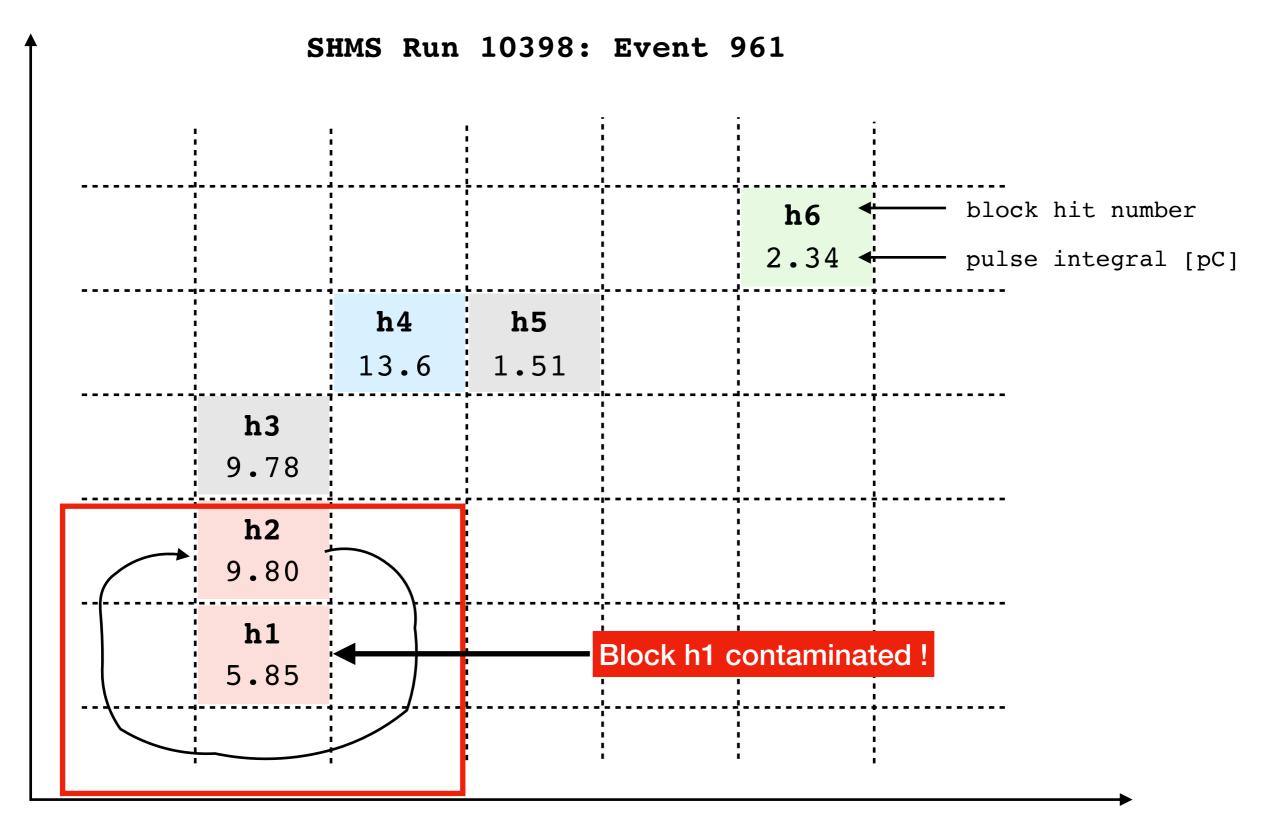
O Examine block h1: Found block h2 to be the highest pulse integral and identified as a virus, so it will "contaminate" block h1 and make it ill.

Rows



Columns

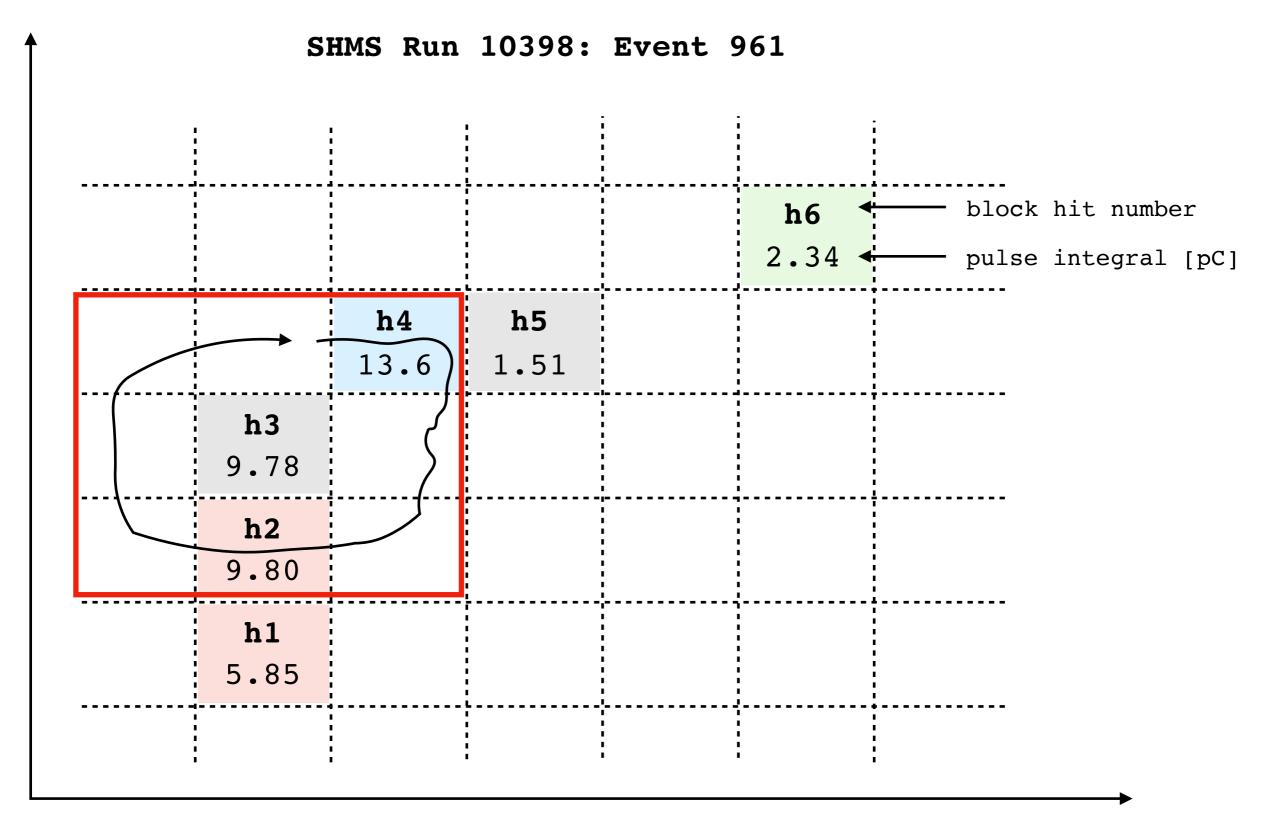
O <u>Examine block h1</u>: Found block h2 to be the highest pulse integral and identified as a virus, so it will "contaminate" block h1 and make it ill.



Columns

16

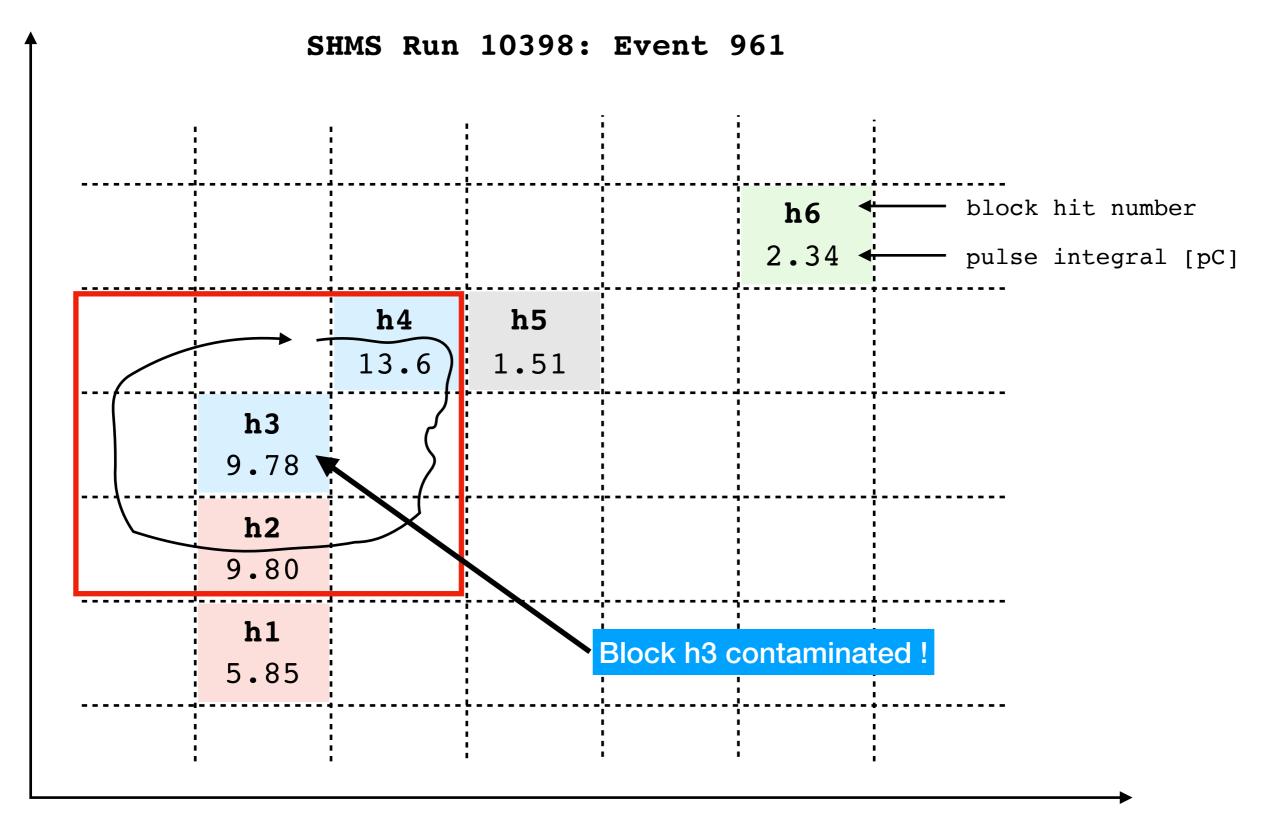
O Examine block h3: Found block h4 to be the highest pulse integral and identified as a virus, so it will "contaminate" block h3 and make it ill.



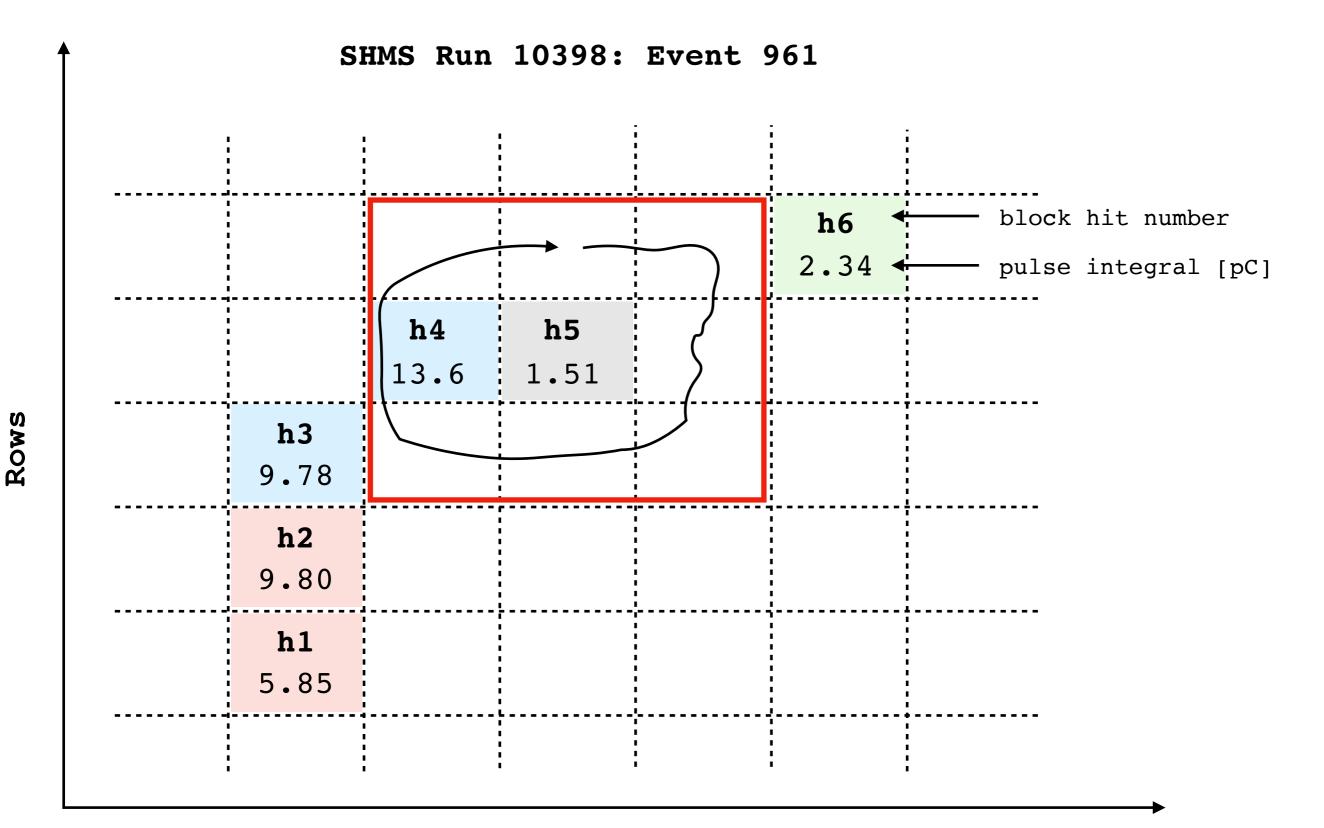
Rows

17

O Examine block h3: Found block h4 to be the highest pulse integral and identified as a virus, so it will "contaminate" block h3 and make it ill.

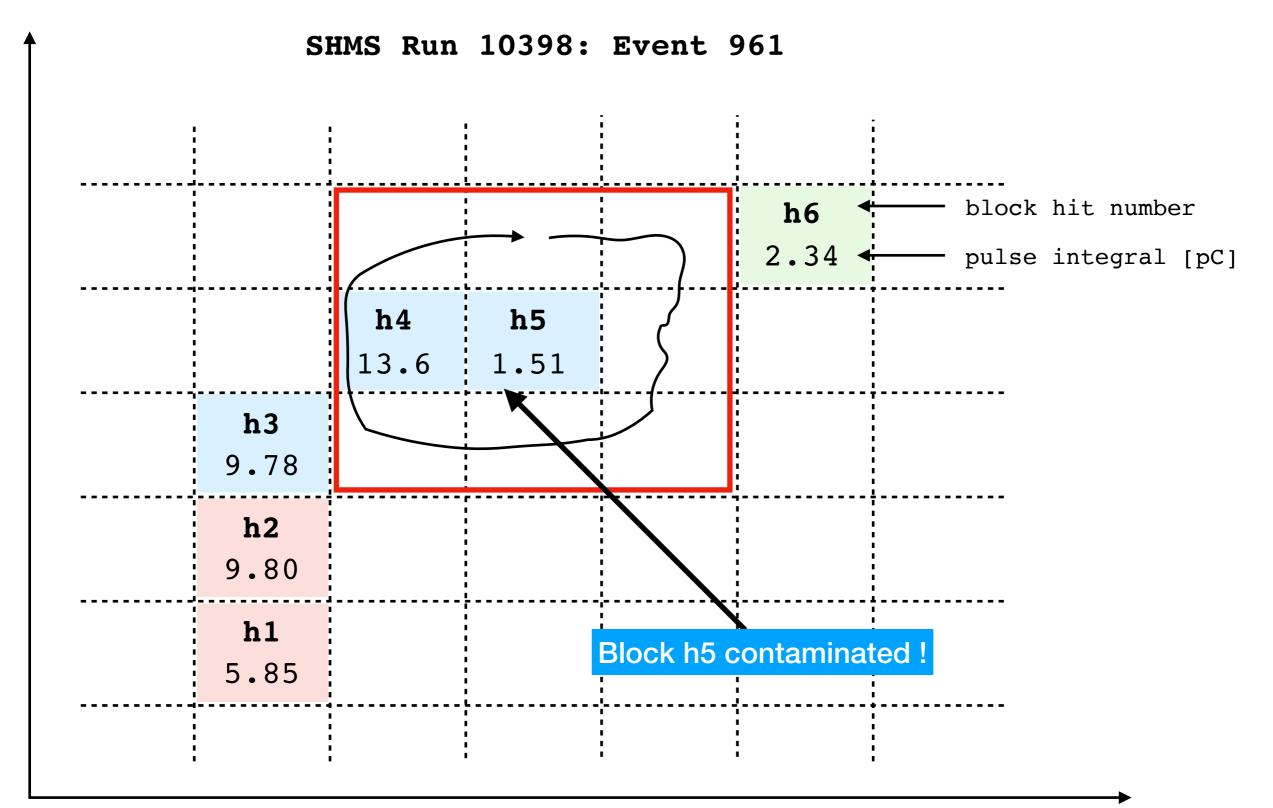


O Examine block h5: Found block h4 to be the highest pulse integral and identified as a virus, so it will "contaminate" block h5 and make it ill.



19

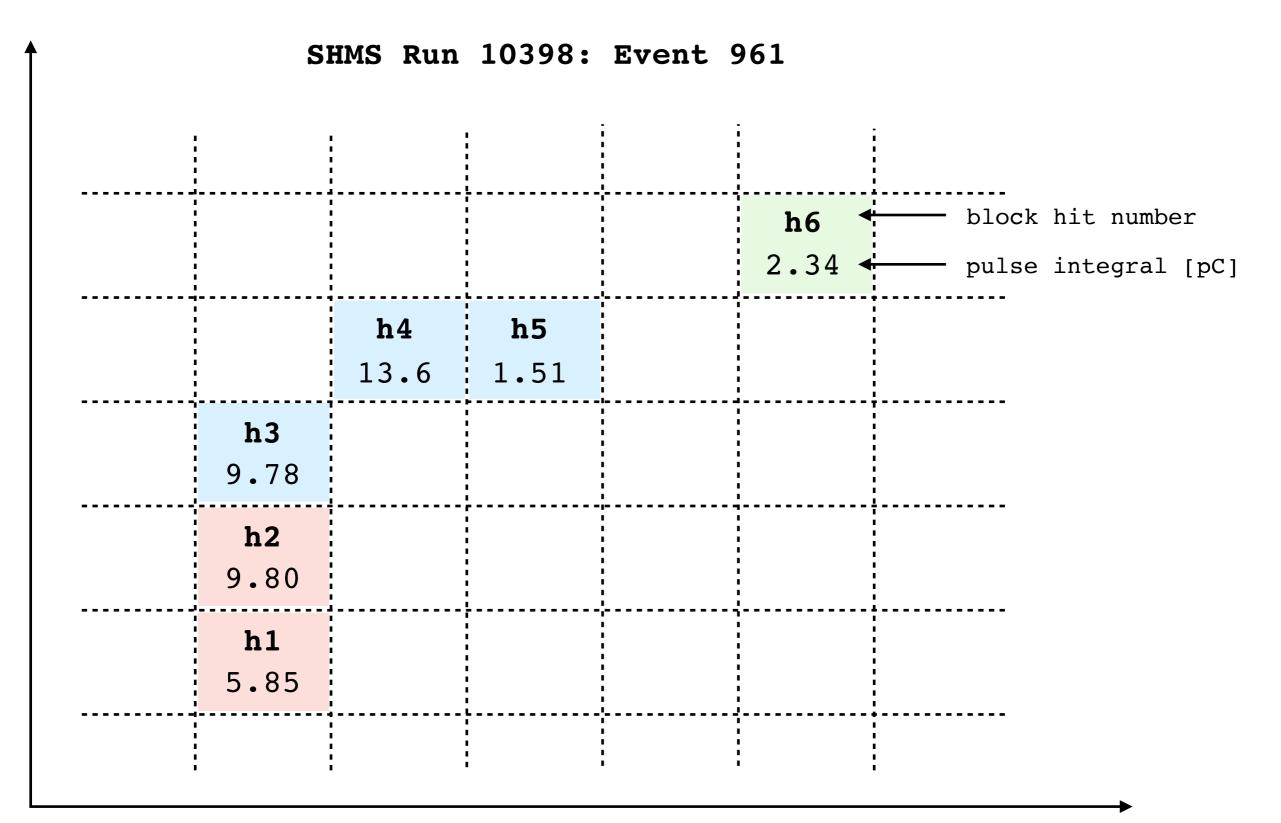
O Examine block h5: Found block h4 to be the highest pulse integral and identified as a virus, so it will "contaminate" block h3 and make it ill.



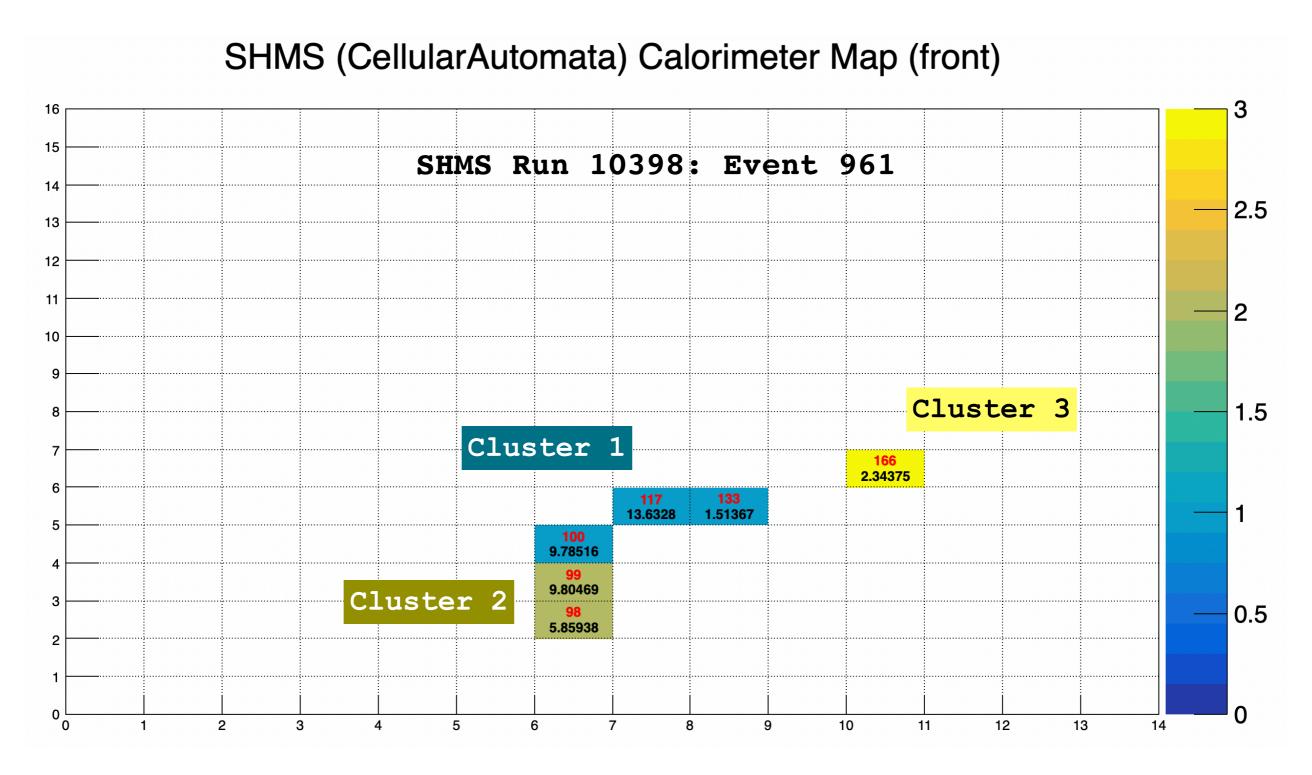
Rows

20

O Overall, there were 3 clusters found, as compared to 2 clusters in the HCANA method presented earlier.



#### **2D** Grid of the Actual Data Clusters Used in the Example

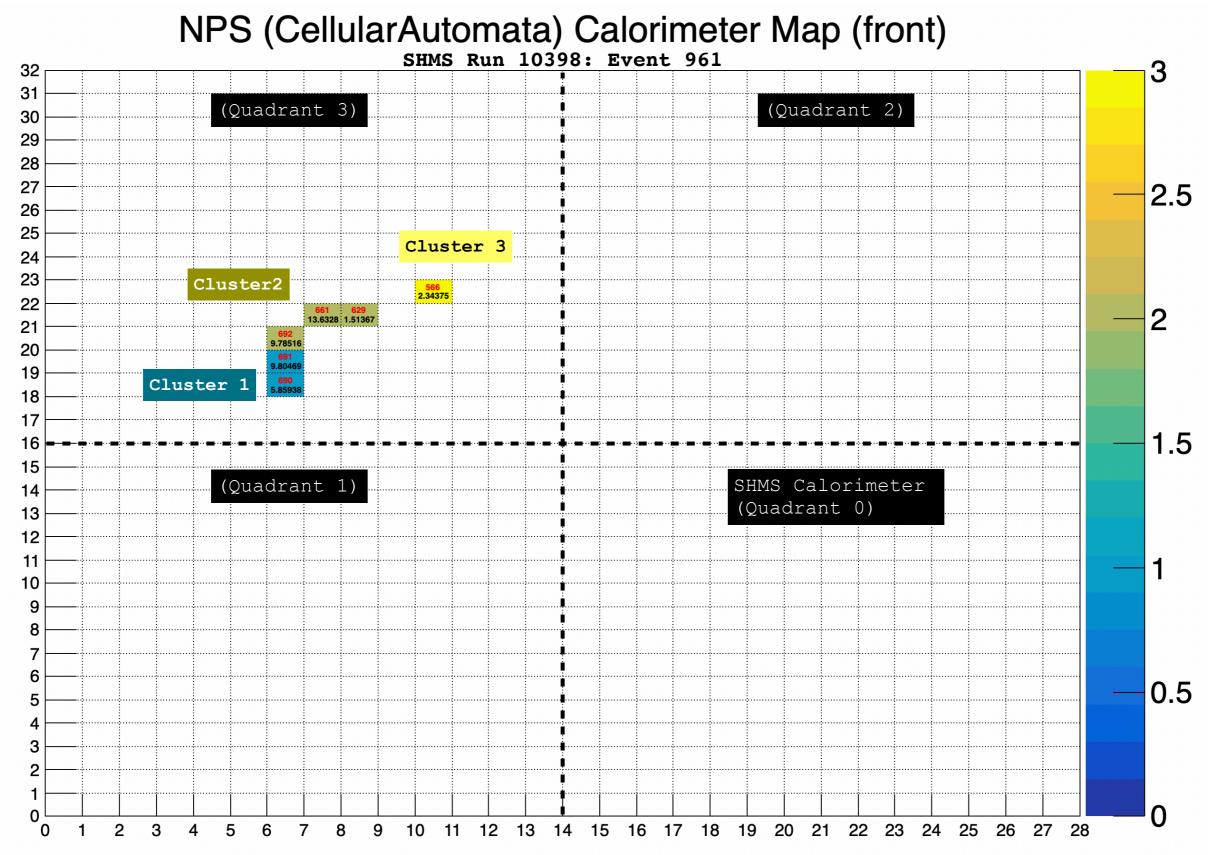


**Block ID** 

Pulse Integral [pC]

Legend:

\*\*Note: The clusters are color-coded, in integer values of 1 (for cluster 1), 2 (for cluster 2), and so on.

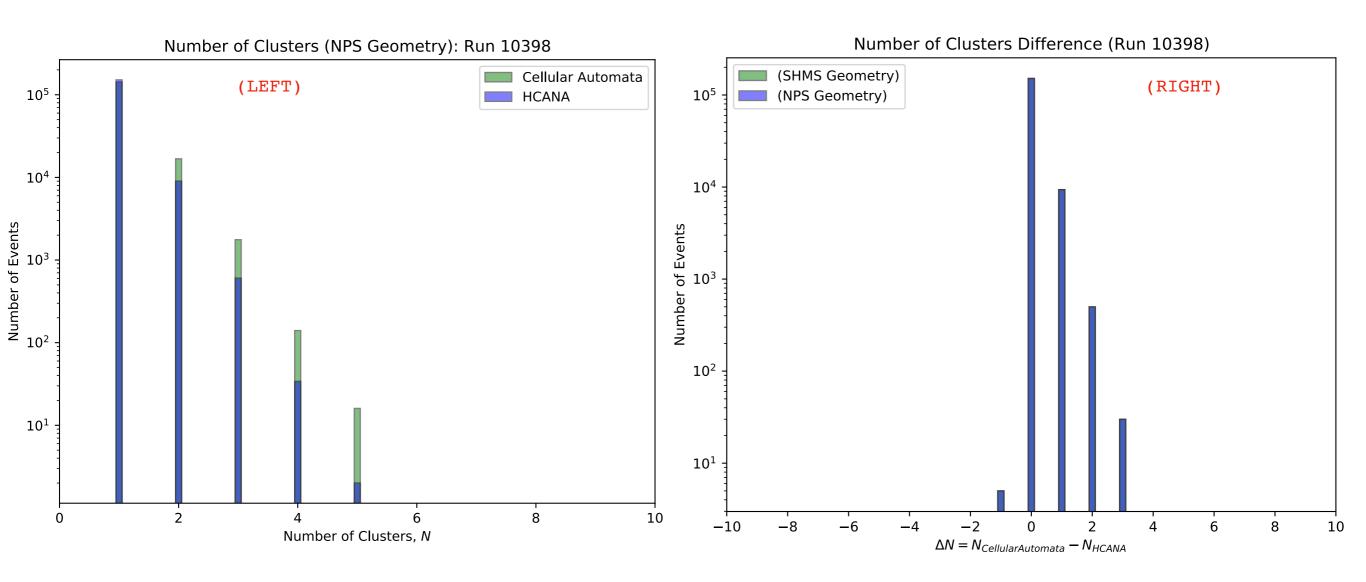


O Same event shown in previous slide, but using approximate NPS geometry which is replicates the SHMS calorimeter geometry (14x16) into three other quadrants.

O The number of clusters is the same, but has been projected at random (during the NPS analysis replay) into one of the four quadrants to simulate the NPS geometry under more realistic conditions.

22

#### **Total Number of Clusters Formed with the Different Algorithms**



O (LEFT) Total number of clusters formed using Cellular Automata or standard HCANA clustering algorithm.

**O** (RIGHT) Difference (on a per-event basis) between the number of clusters formed using "Cellular Automata" or standard "HCANA" clustering algorithm. A difference of  $\Delta N = 0$  indicates that the two algorithms formed the same number of clusters for a certain number of events, whereas a difference of  $\Delta N = n$  (n > 0) indicates that the Cellular Automata formed n more clusters as compared to the standard HCANA approach.

### Summary

- created and tested NPS analysis software using existing SHMS data
- developed NPS calorimeter cluster algorithm based on "Cellular Automata"
- S. Wood added code infrastructure to facilitate fADC sample (mode) data readout

What needs to be done?

- develop NPS calorimeter calibration code (maybe can use SHMS as starting point?)
- NPS software and cluster algorithm will need fine tuning once NPS is fully assembled and on a test bench

### NPS SOFTWARE CONTRIBUTORS NEEDED ! ! !

Follow us on GitHub to contribute: https://github.com/sawjlab/NPSApp/tree/main