

HyCal Cluster Reconstruction

- Algorithm: Island (Cellular Automaton)
- Pictorial description:
 - Each local maximum is being treated as virus
 - The virus spread until it reach module with no energy deposition, or a valley between two clusters
- Technically:
 - Sort the module energy array from high to low energy
 - Add the modules one by one along the sorted array
 - Before adding a module to a cluster, check its 8 neighbors, if none of those has been added, then the module is itself a local maximum
 - If some of the neighboring module has been added to clusters, find the maximum among them and add the module to the cluster that own the maximum

Cluster ID identified from Island

Energy from the module

0: 5.68862 0: 10.8856

0: 16.4403 0: 15.1614 0: 1.51049

0: 22904.5 0: 4.30.34 0: 47.5099 0: 6.9994.2

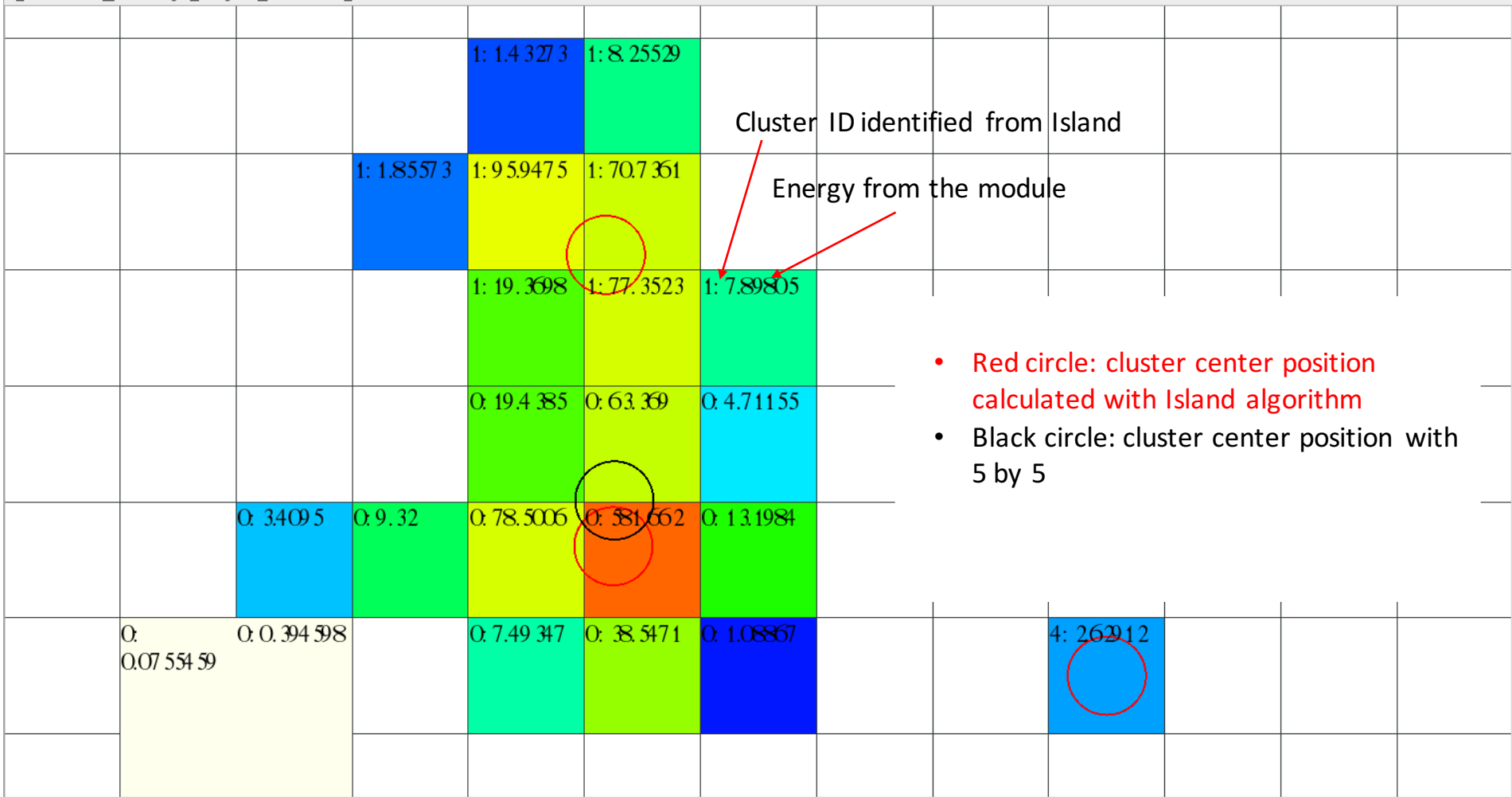
0: 2.55638 0: 31.4785 0: 68.0862 0: 9.9784.3

0: 4.29976 0: 6.72709

0: 10.5703

0: 2.1809.2

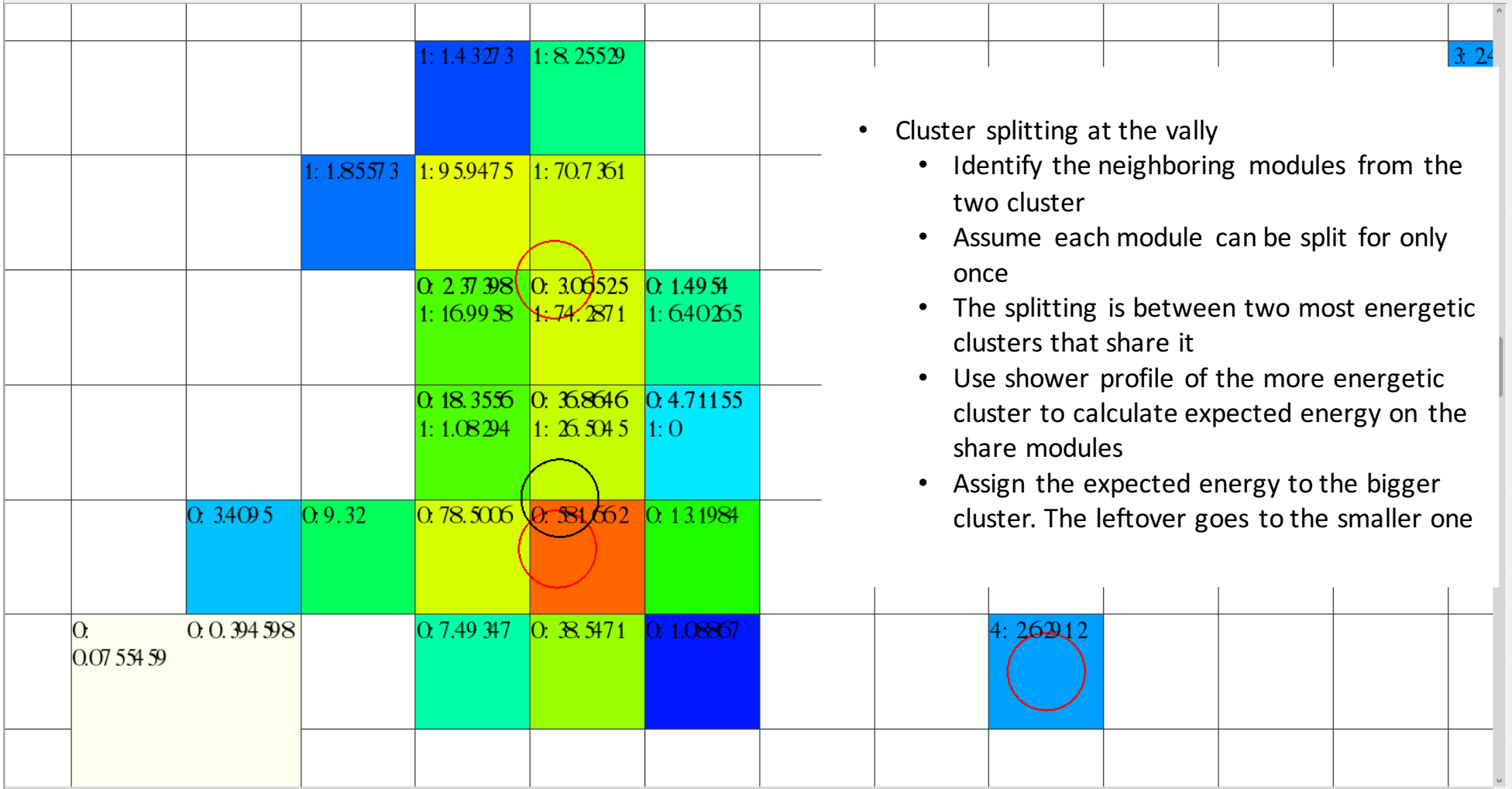
- Red circle: cluster center position calculated with Island algorithm
- Black circle: cluster center position with 5 by 5
- The red circle is underneath the black circle for this cluster



Cluster ID identified from Island

Energy from the module

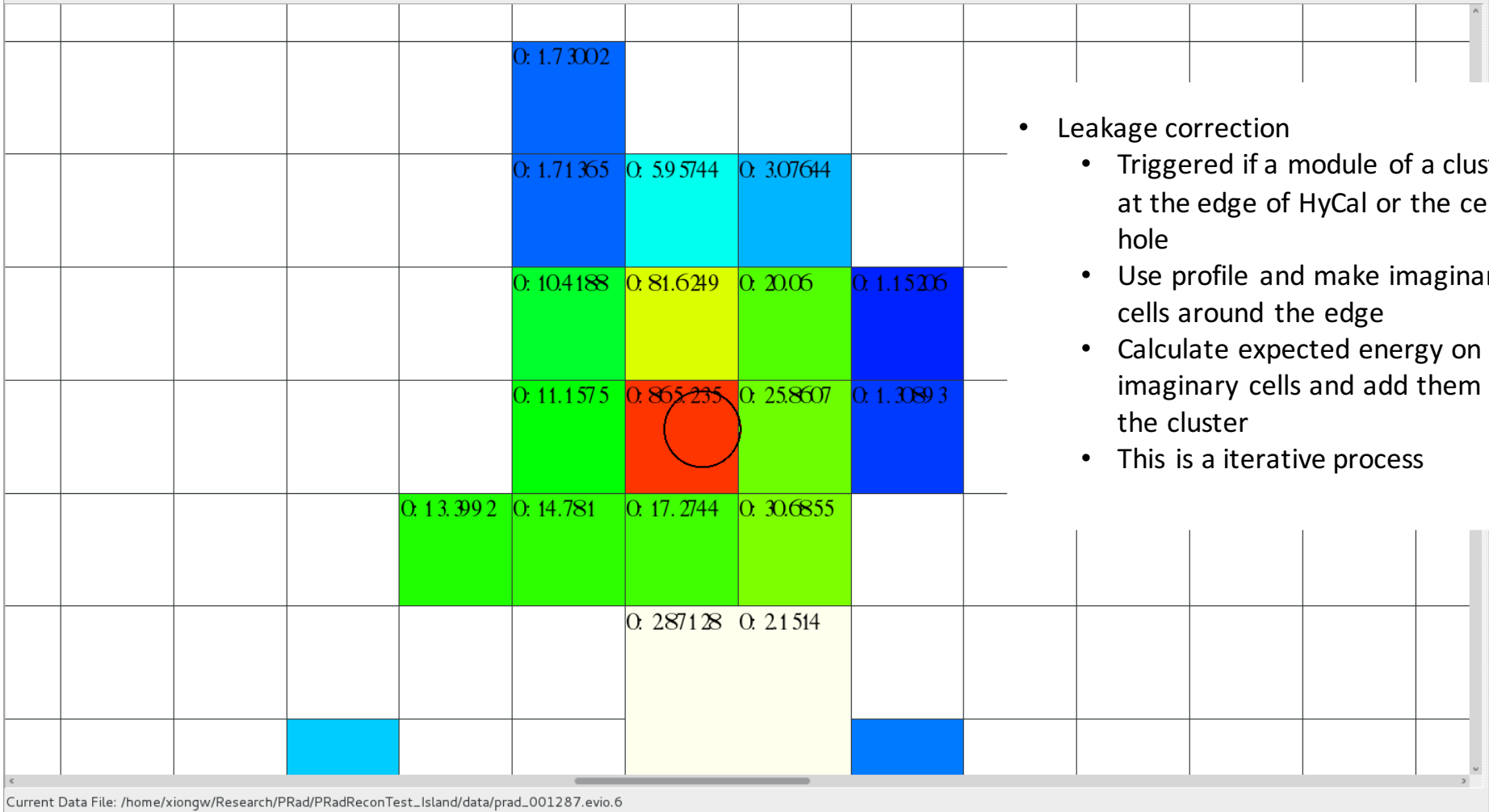
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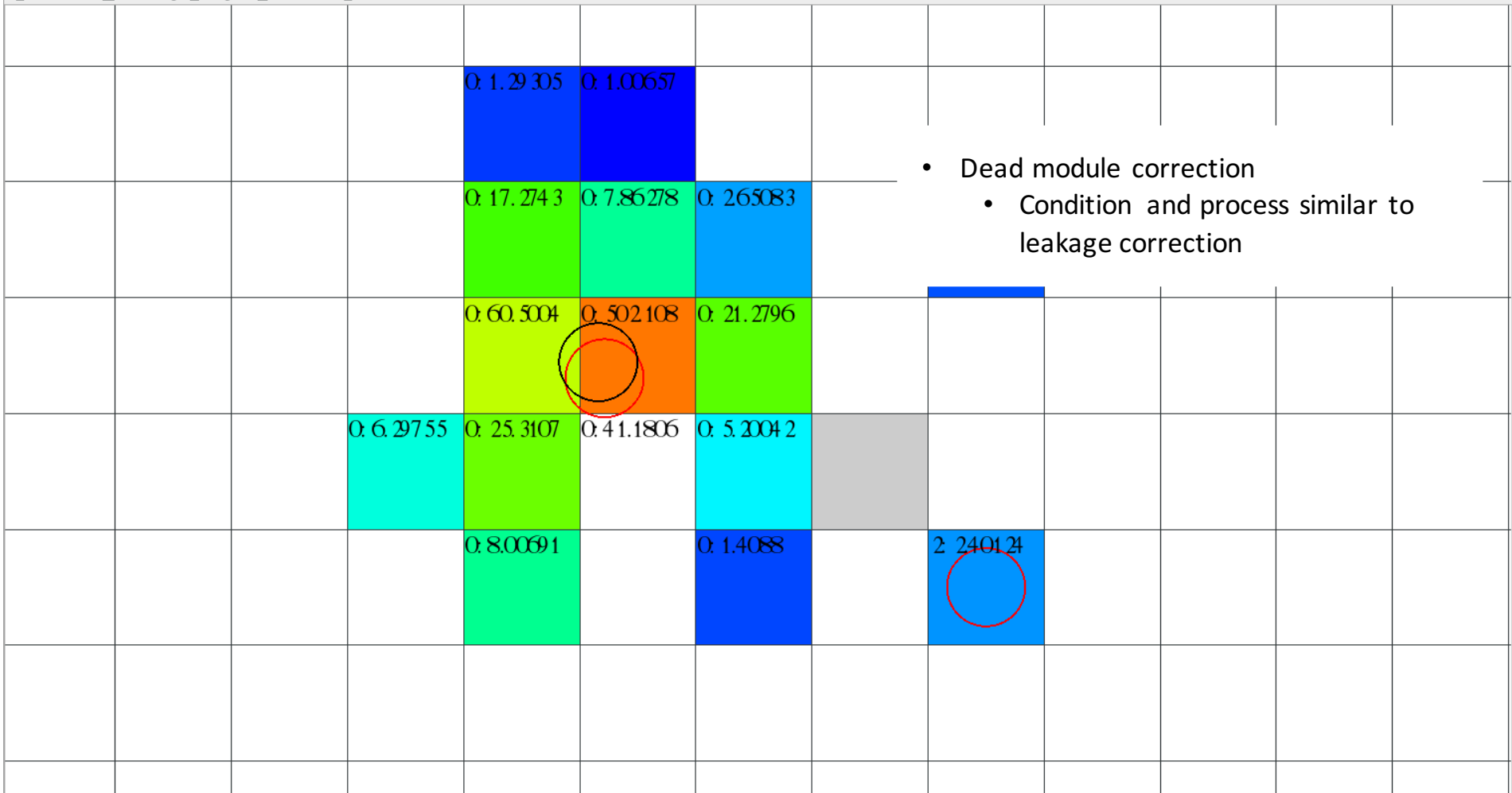
- Cluster splitting at the vally
 - Identify the neighboring modules from the two cluster
 - Assume each module can be split for only once
 - The splitting is between two most energetic clusters that share it
 - Use shower profile of the more energetic cluster to calculate expected energy on the share modules
 - Assign the expected energy to the bigger cluster. The leftover goes to the smaller one

PRad Event Viewer

File Online Mode High Voltage Calibration Tools



- Leakage correction
 - Triggered if a module of a cluster is at the edge of HyCal or the central hole
 - Use profile and make imaginary cells around the edge
 - Calculate expected energy on the imaginary cells and add them to the cluster
 - This is a iterative process



- Dead module correction
 - Condition and process similar to leakage correction

Clustering Near Transition Region

- There is no program in terms of identifying the modules of a cluster at the transition region
 - The problem comes when we are trying to use the shower profile to do various calculations (expected energy and χ^2)
 - Shower shape for both LG and PWO should be quite similar, if weighted by the Moliere radius
 - Calculate the distance between the cluster center and the destination position, split it at the transition boundary, and use the portion of the distance in each region as weight
 - Finally, to take into account the slight difference between the LG and PWO profiles, take the weighted average again between the two profiles
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- No transition region: Profile is in a form of $P_{LG}(d/R_{LG})$ or $P_{PWO}(d/R_{PWO})$
 - At transition region: Profile is in a form of $P_{LG}(a*d/R_{LG} + b*d/R_{PWO})$ or $P_{PWO}(a*d/R_{LG} + b*d/R_{PWO})$
 - To take into account the difference between the two profiles:
 - $(a/d)*P_{LG}(a*d/R_{LG} + b*d/R_{PWO}) + (b/d)*P_{PWO}(a*d/R_{LG} + b*d/R_{PWO})$