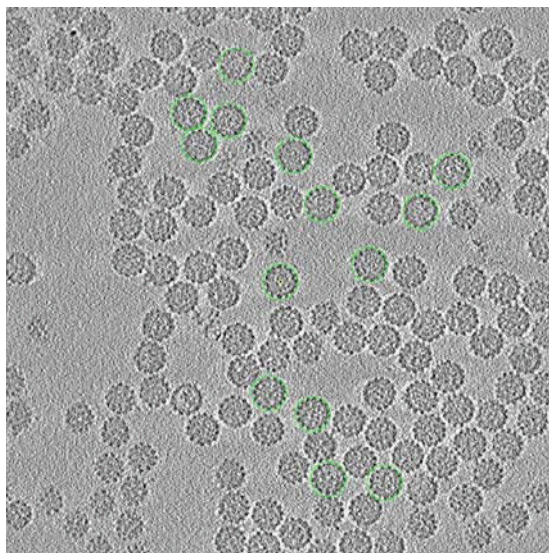


Aligning Isolated Particles: BPV

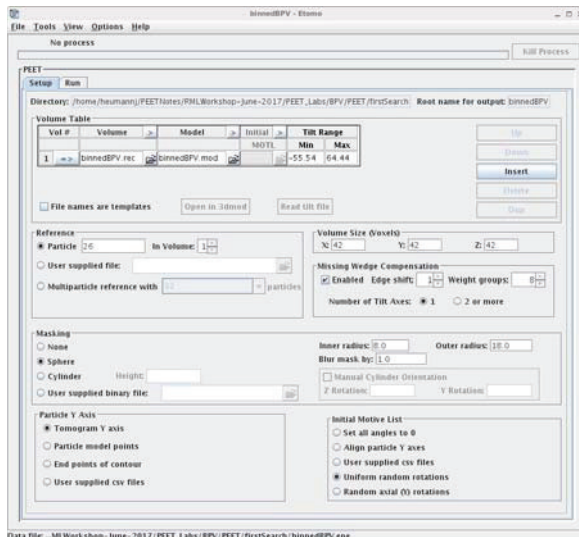
2X Binned BPV Sample -8 μm Defocus



Modeling BPV

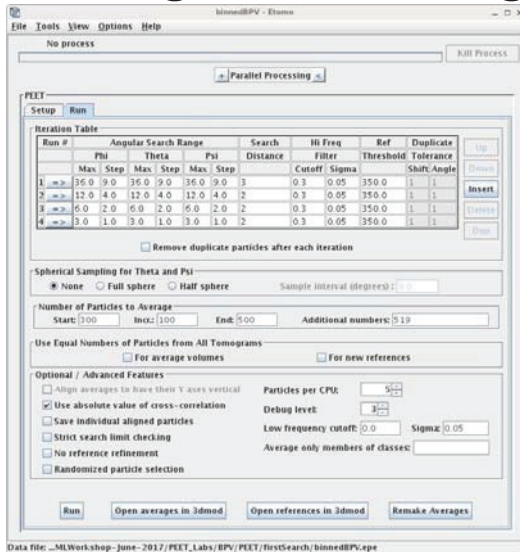
- Always try to model accurately
 - improves the odds of a good alignment / average
- Center points in XY and Z as well as you can
- Setting “Sphere Radius for Points” and paging up / down helps with centering points in Z
- May wish to start with binned or binned and NAD-filtered data

Alignment Settings – Setup Tab



- Volume(s)
- Model(s)
- Tilt range
- Reference
- Size to average
- Mask Definition
- Particle Y Axis
- Initial Motive List

Alignment Settings – Run Tab



- Parallel Processing
- Iteration Table
- Spherical Sampling
- Number to Average
- Equal Numbers?
- Optional / Advanced Features

Data file: _MLWorkshop-June-2017/PEET_Labs/BPV/PEET/firstSearch/binmodBPV.epe
 II. BPV Initial Alignment IMOD / PEET Workshop at RML, June 2017

Iteration Table

Run #	Angular Search Range						Search Distance	Hi Freq Filter		Ref Threshold	Duplicate Tolerance	
	Phi		Theta		Psi			Cutoff	Sigma		Shift	Angle
	Max	Step	Max	Step	Max	Step						
1 =>	36.0	9.0	36.0	9.0	36.0	9.0	3	0.3	0.05	350.0	1	1
2 =>	12.0	4.0	12.0	4.0	12.0	4.0	2	0.3	0.05	350.0	1	1
3 =>	6.0	2.0	6.0	2.0	6.0	2.0	2	0.3	0.05	350.0	1	1
4 =>	3.0	1.0	3.0	1.0	3.0	1.0	2	0.3	0.05	350.0	1	1

Remove duplicate particles after each iteration

- Search settings based on model uncertainty
- Iteration n Max ~ 1.5X iteration n-1 Step
- 3:1 ratio Max:Step good for speed / accuracy
- Angular settings decrease 2X row-to-row

II. BPV Initial Alignment IMOD / PEET Workshop at RML, June 2017

Finest Angular Resolution?

- $R \sin(d\theta) \approx R d\theta = 1$ [voxels]
- $d\theta \approx 1 / R$ [radians] = $180 / (\pi R)$ [degrees]
- In this case, mask radius = 18
so $d\theta \approx 3^\circ$
- Actually searched down to 1°
- Last 2 iterations shouldn't change much
- This is the case, as we'll verify in the lab

Optional / Advanced Features

Optional / Advanced Features	
<input type="checkbox"/> Align averages to have their Y axes vertical	Particles per CPU: <input type="text" value="5"/>
<input checked="" type="checkbox"/> Use absolute value of cross-correlation	Debug level: <input type="text" value="3"/>
<input type="checkbox"/> Save individual aligned particles	Low frequency cutoff: <input type="text" value="0.0"/> Sigma: <input type="text" value="0.05"/>
<input type="checkbox"/> Strict search limit checking	Average only members of classes: <input type="text"/>
<input type="checkbox"/> No reference refinement	
<input type="checkbox"/> Randomized particle selection	

- Align vertical: not available with Tomogram Y
- Absolute value: $|CCC|$ instead of CCC
 - avoid Einstein-from-the-noise
 - problematical with some pattern... *e.g.* Zebra stripes
- Strict search limits: never exceed max step
- No reference refinement: template matching

Optional / Advanced Features

Optional / Advanced Features

<input type="checkbox"/> Align averages to have their Y axes vertical	Particles per CPU: <input type="text" value="5"/>
<input checked="" type="checkbox"/> Use absolute value of cross-correlation	Debug level: <input type="text" value="3"/>
<input type="checkbox"/> Save individual aligned particles	Low frequency cutoff: <input type="text" value="0.0"/> Sigma: <input type="text" value="0.05"/>
<input type="checkbox"/> Strict search limit checking	Average only members of classes: <input type="text"/>
<input type="checkbox"/> No reference refinement	
<input type="checkbox"/> Randomized particle selection	

- Randomized selection: not based on CCC
- Particles per cpu: determines number of chunks
- Debug level: amount of detail, seldom used
- Low frequency cutoff: attenuate shading gradients, seldom used
- Average only: for use with heterogeneous data

Questions?