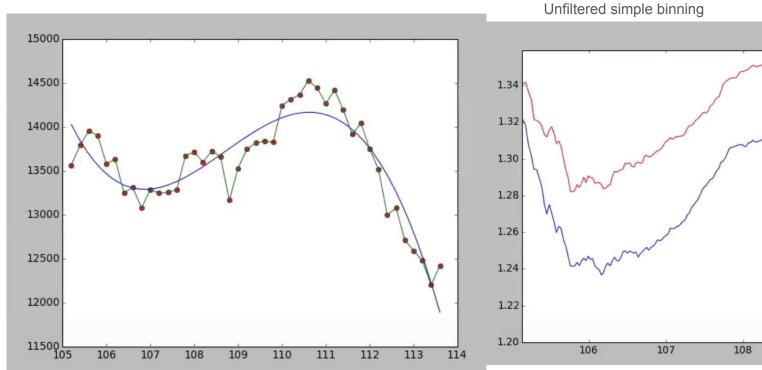
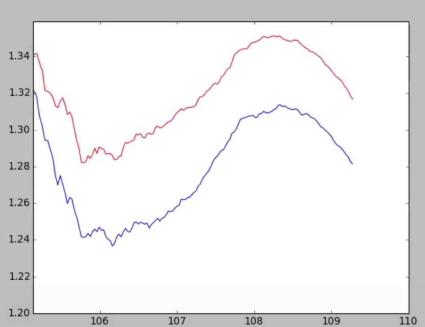
SXRI0214

For some reason using the batch system makes the data worse.

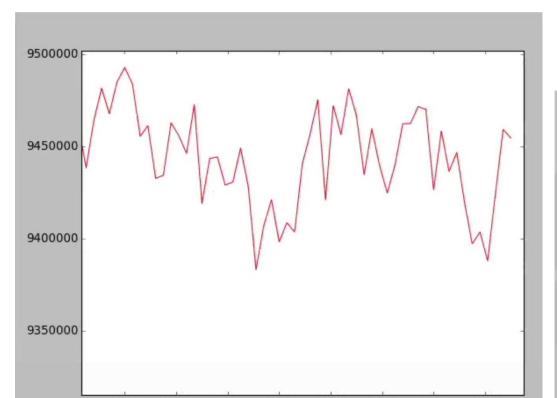
files

63 [5840:15217]	99 [478:18129]	98 [4497:18447]
64 [4803:16178]	100 [4482:18513]	101 [4631:19016]
67 [4544:13008]	95 [4601:]	102 [4420:19132]
69 [5422:16174]	91 TIME [4707:18533]	-
77 TIME [4357:12734]	97 [4533:17621]	
133- [4850:] You can ea	stimate these	
136 [4714:17342]		
137 [4615:17619]		
TIME 144 [4555:]		
145 - [4719:]		
146 - [4500:]		
<u> 149 - [445:10,000]</u>		
151 TIME [382:]		
152 TIME [454:]		
163 TIME [422:]		
164 TIME [422:]		
166 [420:]		
1		

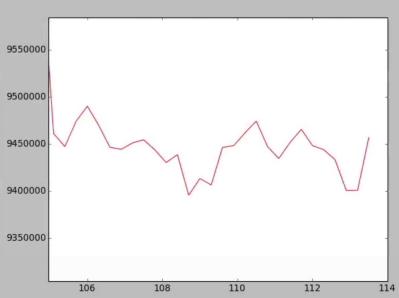




133 with batch system:

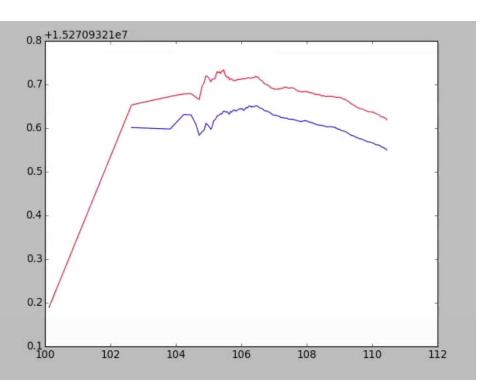


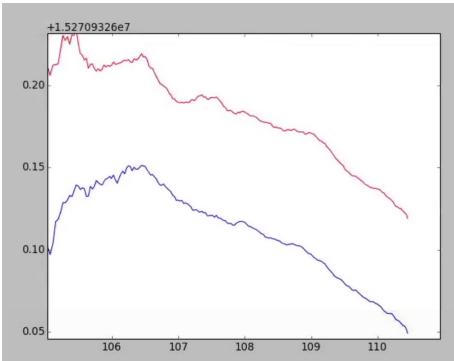
However the GMD normalization causes the data to become meaningless. (not shown)



145

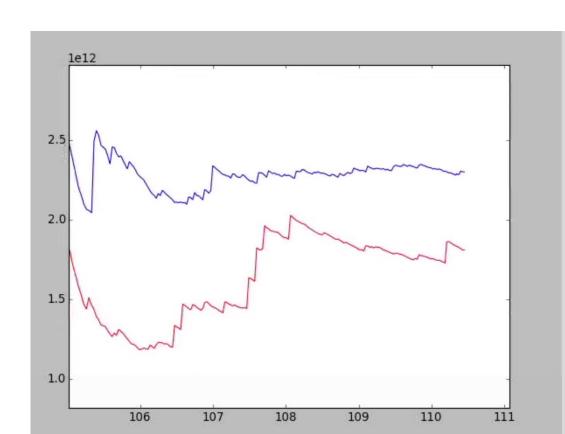
Simple binning no gmd





145

Simple binning with gmd

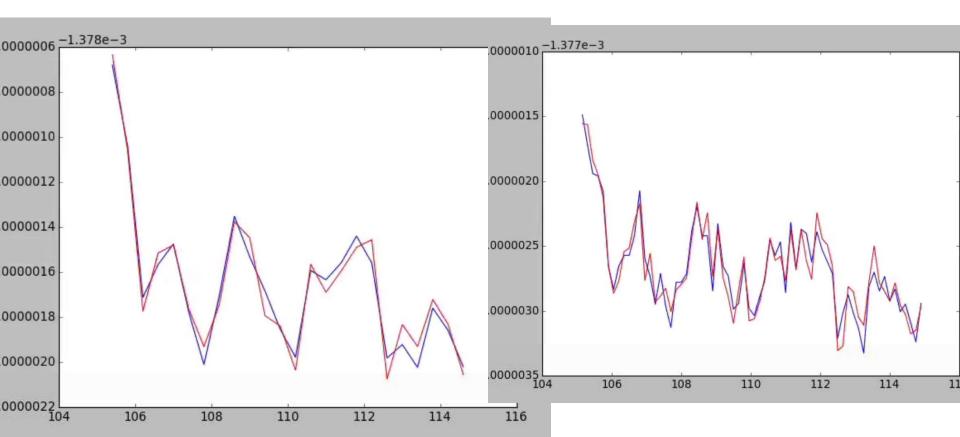


Run 149

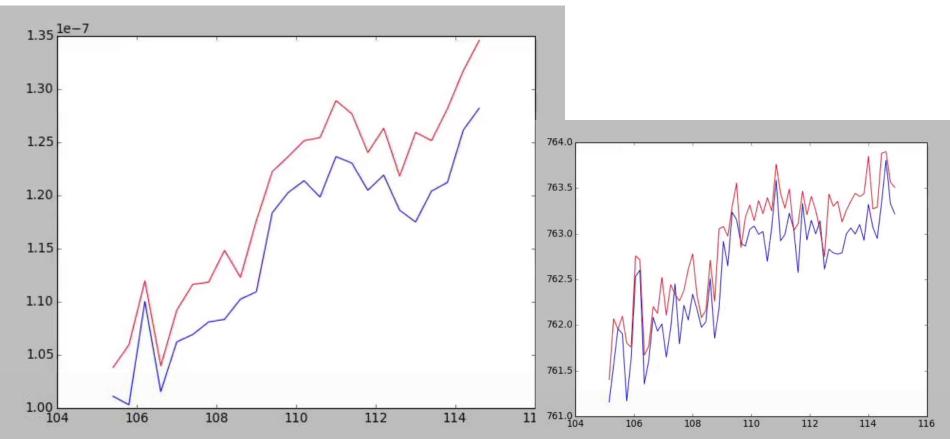
Before current program: (no gmd) current program 3.0 +2.73434427e8 .73434426e8 2.5 3.0 2.5 2.0 1.5 1.5 1.0 1.0 0.5 0.5 0.01 0.0 106 107 108 109 110 111 111 106 107 108 109 110 112

112

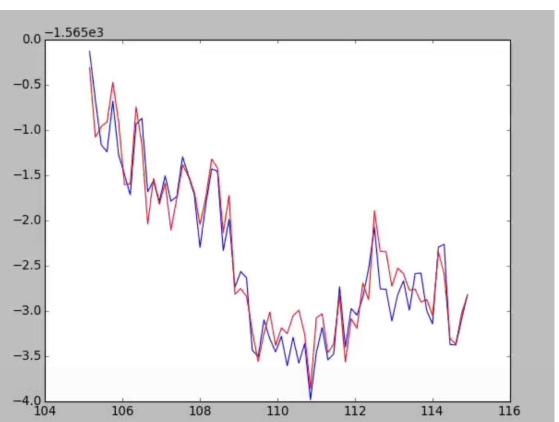
Batch system with laser



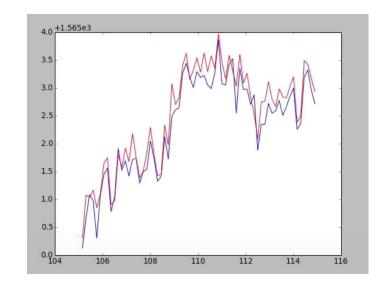
Using the old method gave different results...



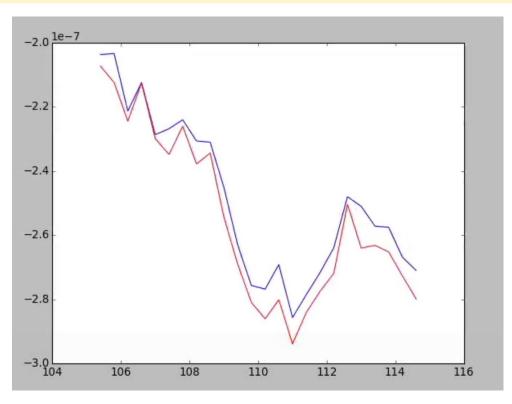
149 reformat. w/ new apd calc



It's about the same with gmd or without gmd. (The trench is just less extreme) flipped apd below



149(re)

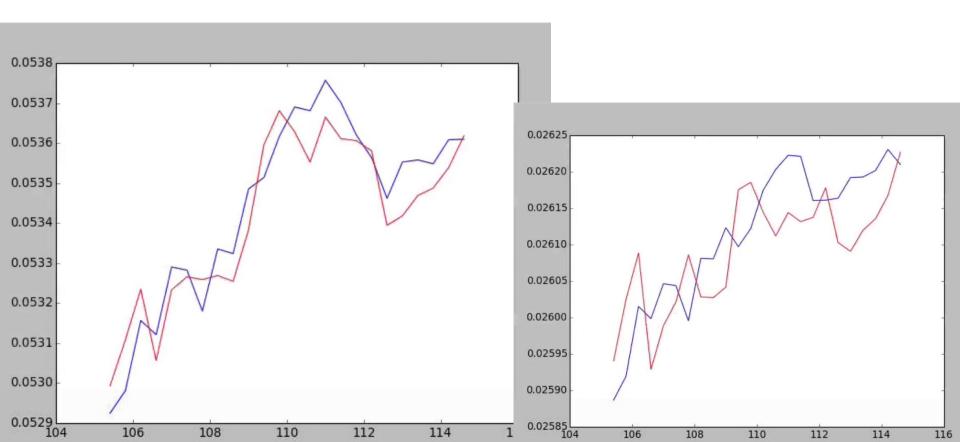


E9292.I-0.0 2.8 2.6 2.4 2.2 2.0 104 106 108 110 112 114 116

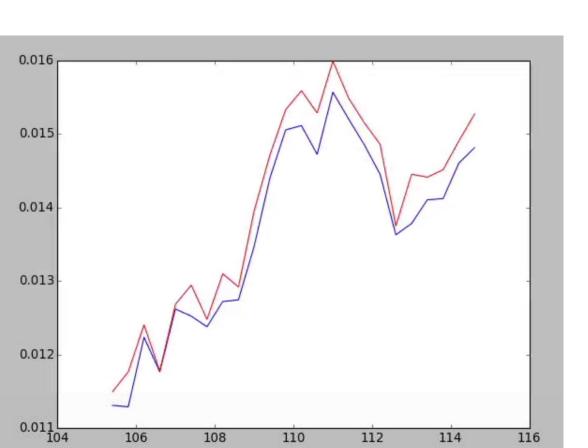
2.5-

^ .4 angle per bin

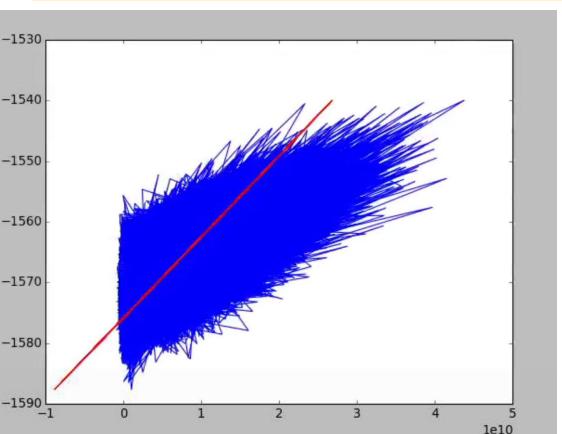
flipped



149 inteD



149 apd-gmd noise correlation



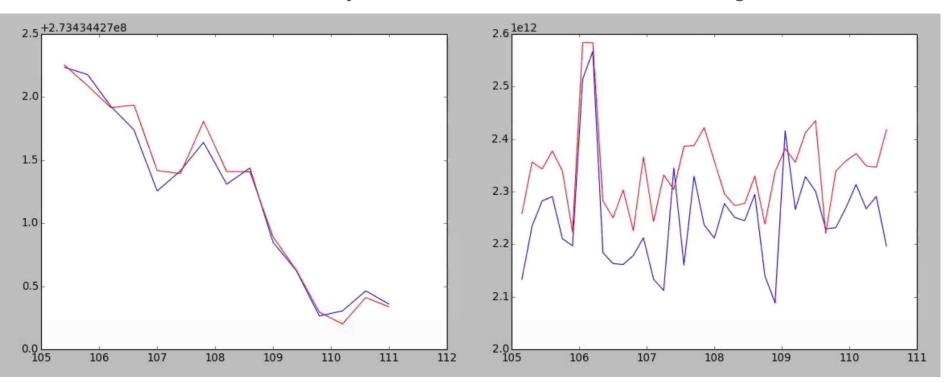
This is the correlation with all GMD points.

The correlation does not look good

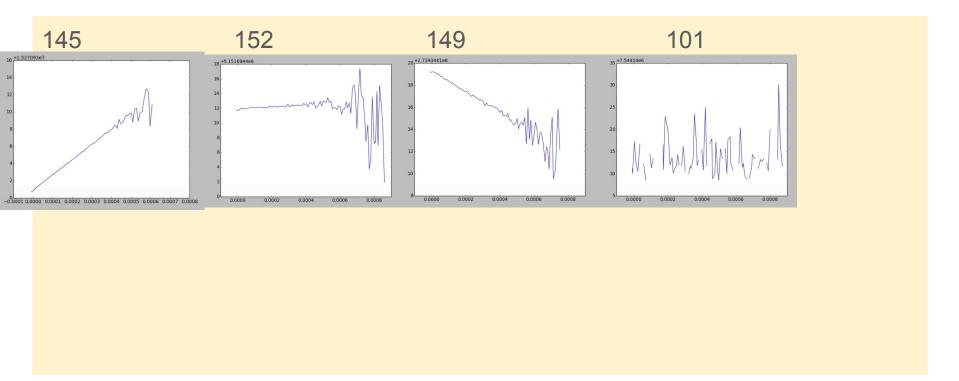
- -too many weights around 0 most likely taking it down
- filter beam drops out (slices below 0)? However this is on an e10 scale so 0's may already be gone.

149 relative gmd and large bins

It is the same as before. I've just increased the bin size. Gmd is right side



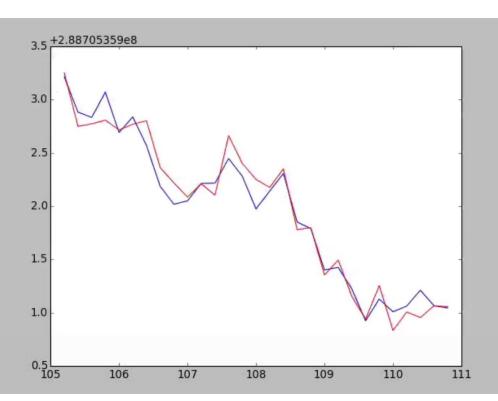
Something strange: gmd and apd correlation

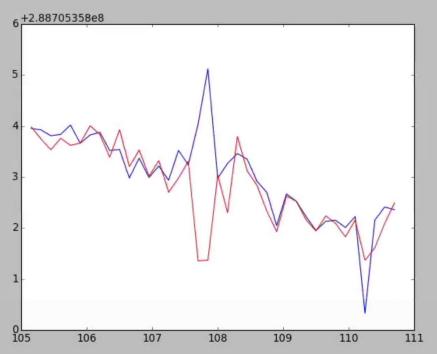


149 plus 145 (?)

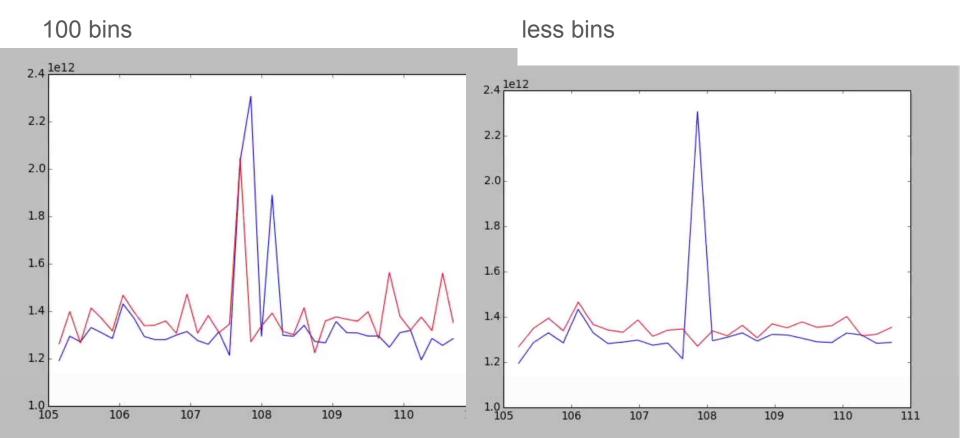
Less filtering

only match ups (both on/both off)

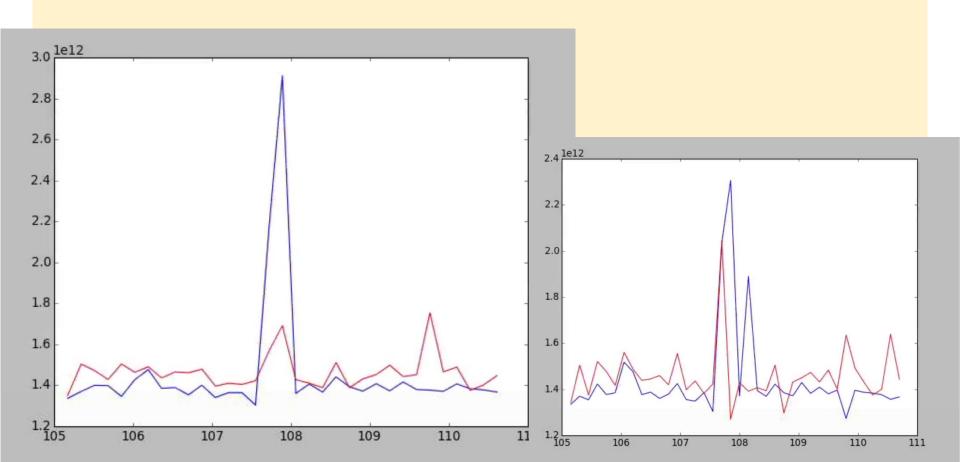




149 and 145 with gmd

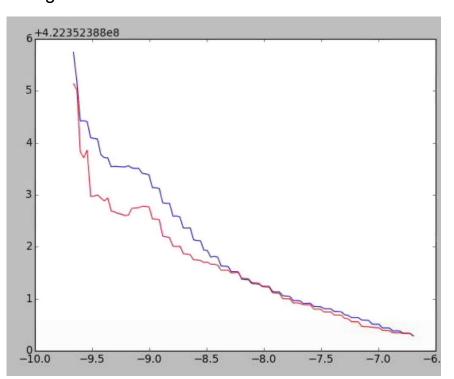


145 and 149 with more constraint and .17 binsize

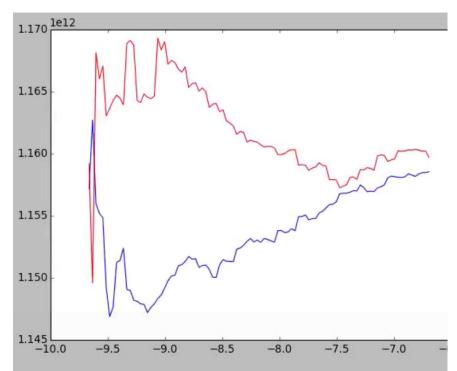


TIME TRIALS

151 No gmd



gmd



151 simple

