On the difference in DA with and without multipole errors

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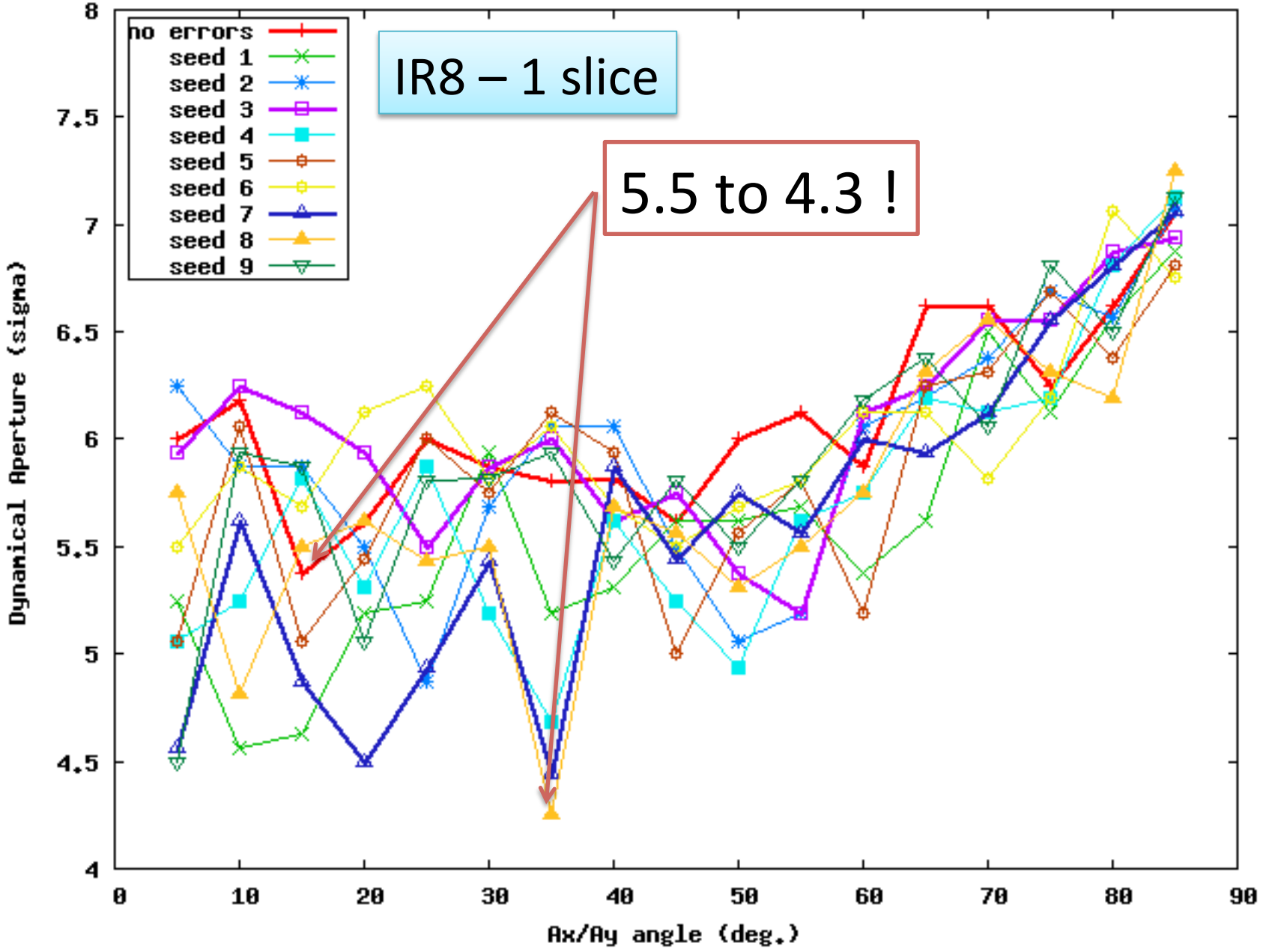
SLHCV3.1b (not HLLHC yet!)

β^*=15cm, 590 μrad, Np=2.2E11

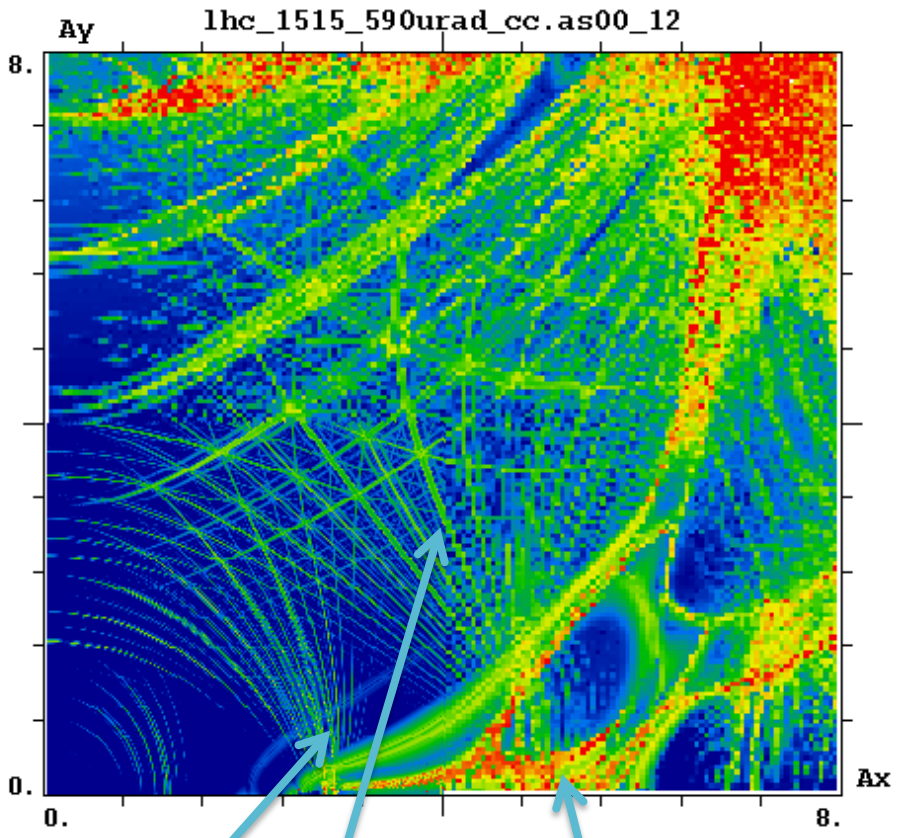
full crab at IP1,5, collision at IR8

Not baseline! – worst case scenario

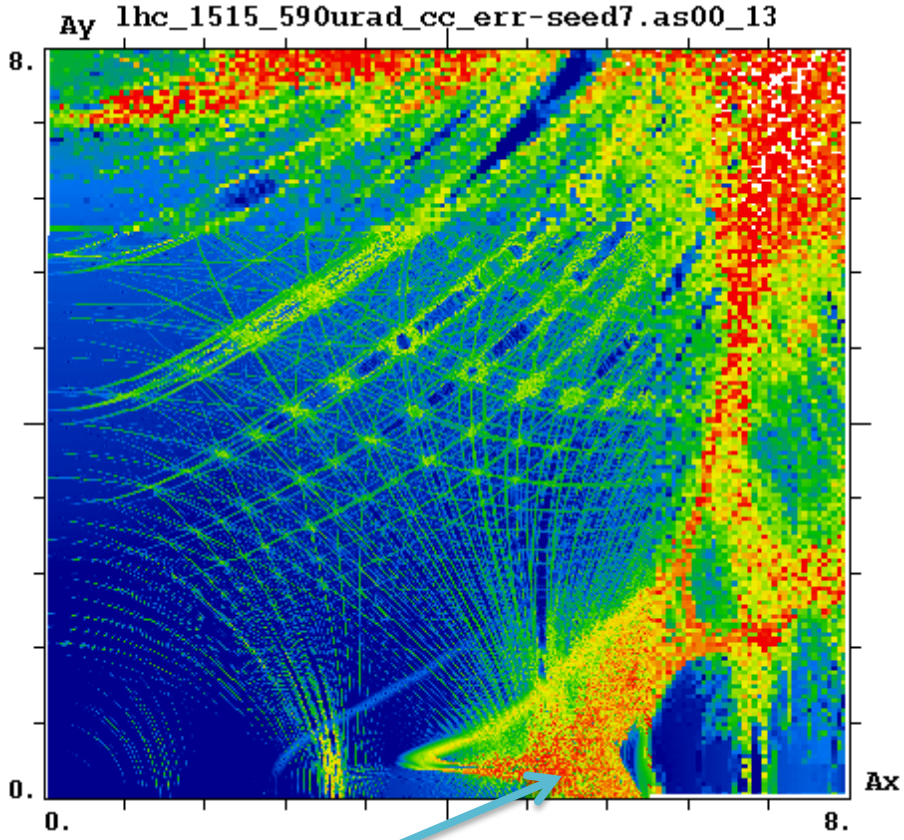

IR8 – 1 slice
5.5 to 4.3 !
no errors
seed 1
seed 2
seed 3
seed 4
seed 5
seed 6
seed 7
seed 8
seed 9
Dynamical Aperture (sigma)
Ax/Ay angle (deg.)
8
7.5
7
6.5
6
5.5
5
4.5
4
0
10
20
30
40
50
60
70
80
90

Errors change nonlinear coupling

As=0, no errors



As=0, with errors

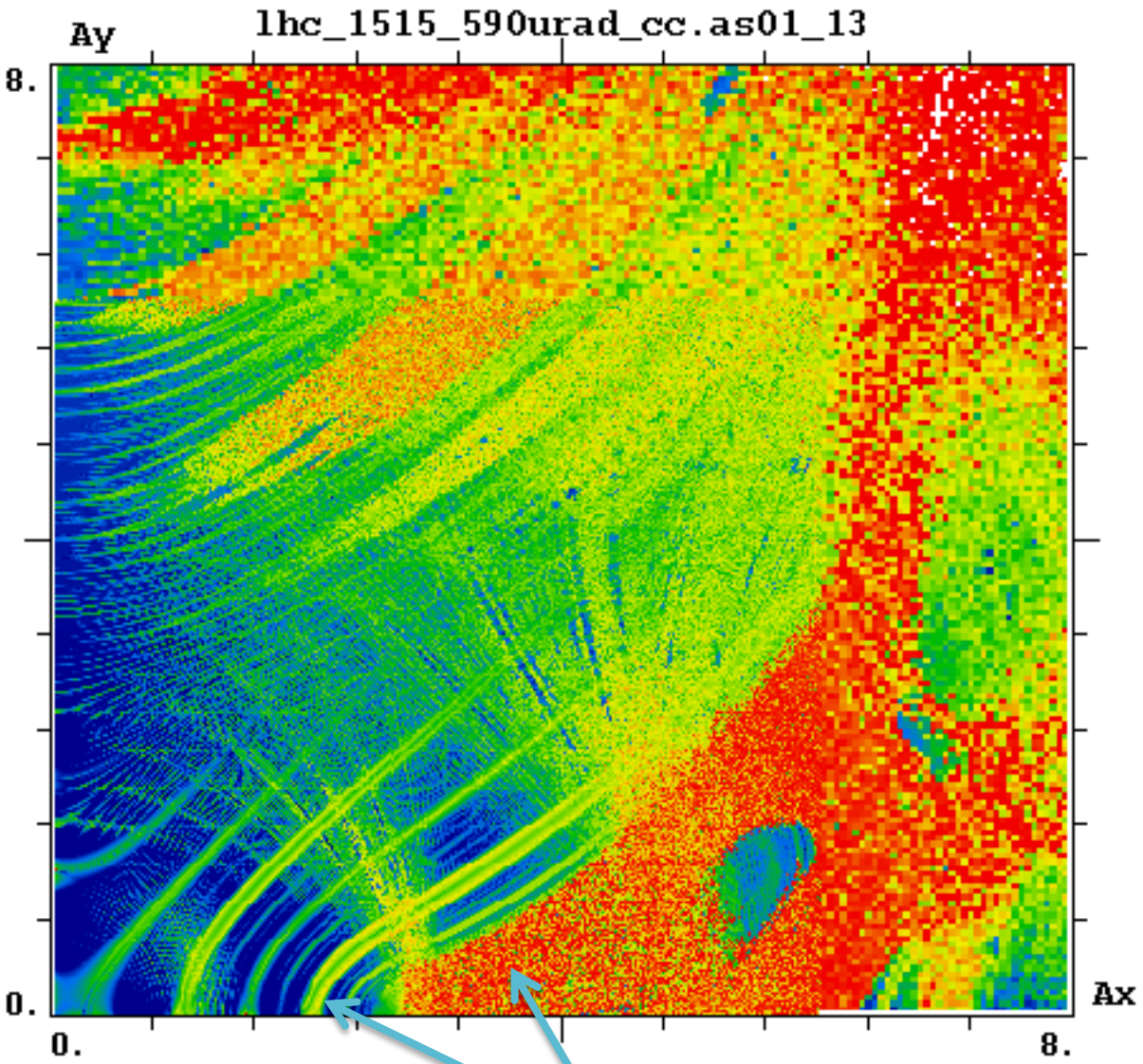


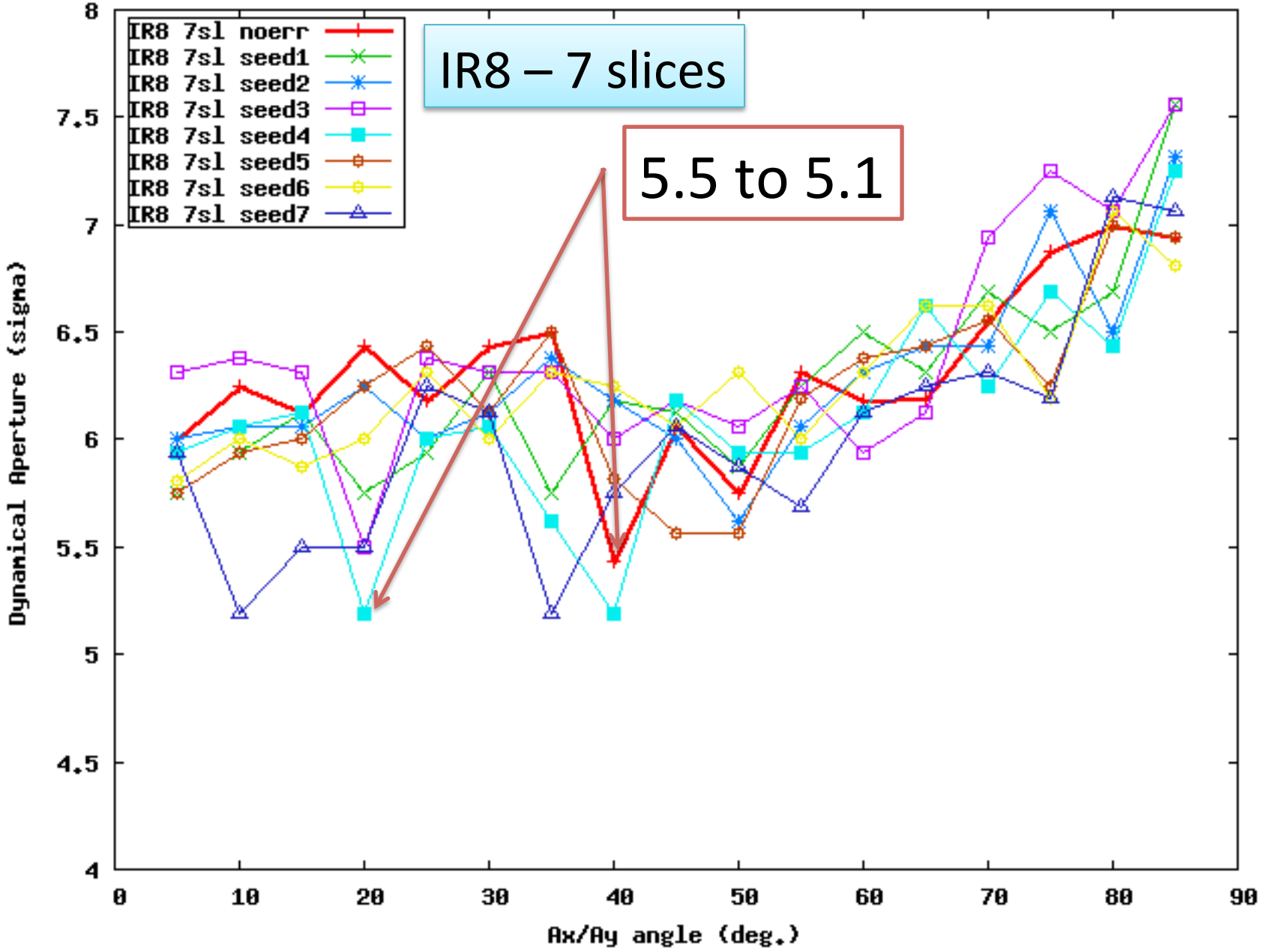
13th order

10th order

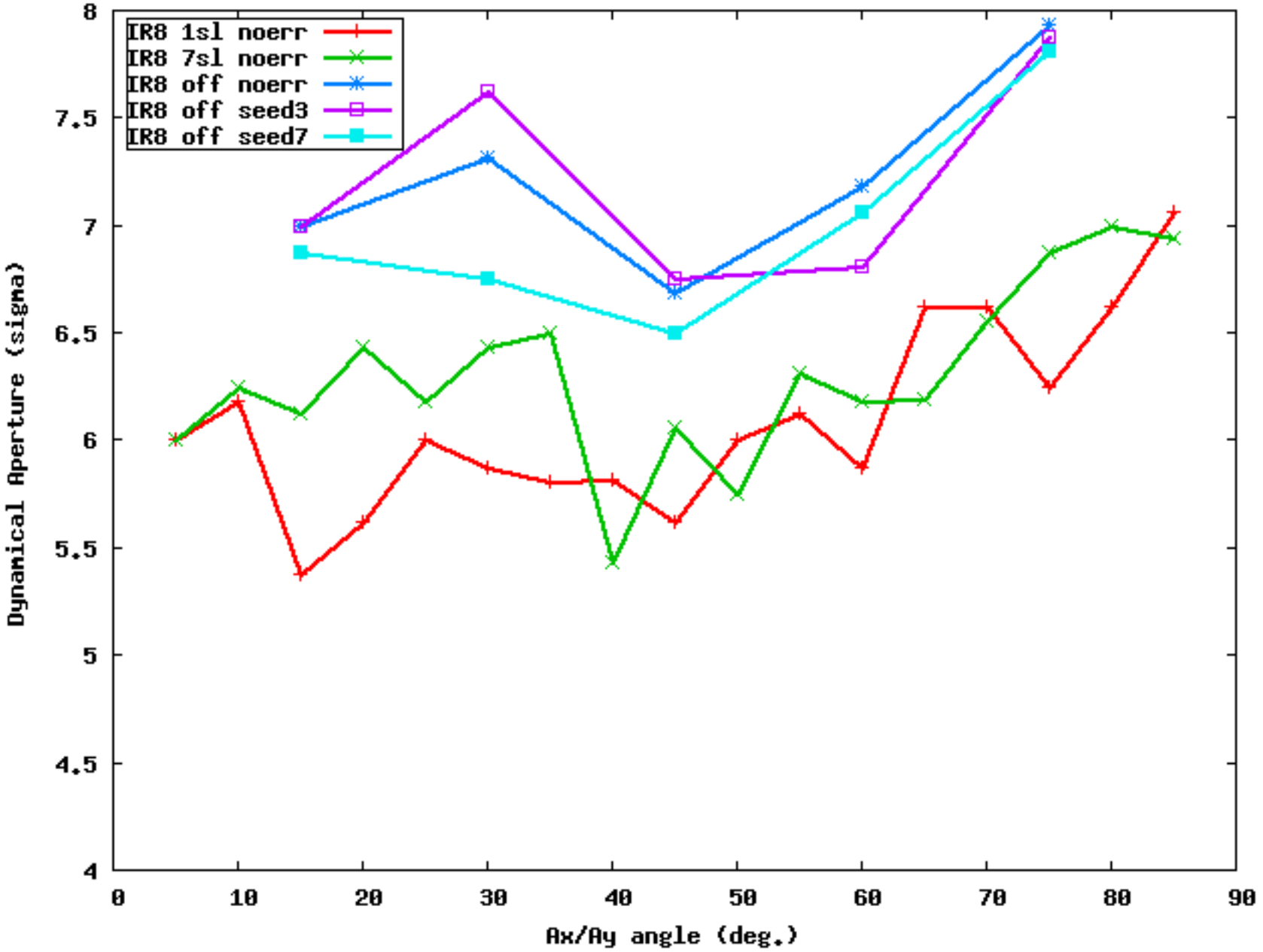
Coupling Qx-Qy=n

As=1, no errors




IR8 – 7 slices
5.5 to 5.1
IR8 7sl noerr
IR8 7sl seed1
IR8 7sl seed2
IR8 7sl seed3
IR8 7sl seed4
IR8 7sl seed5
IR8 7sl seed6
IR8 7sl seed7
Dynamical Aperture (sigma)
Ax/Ay angle (deg.)
8
7.5
7
6.5
6
5.5
5
4.5
4
0
10
20
30
40
50
60
70
80
90

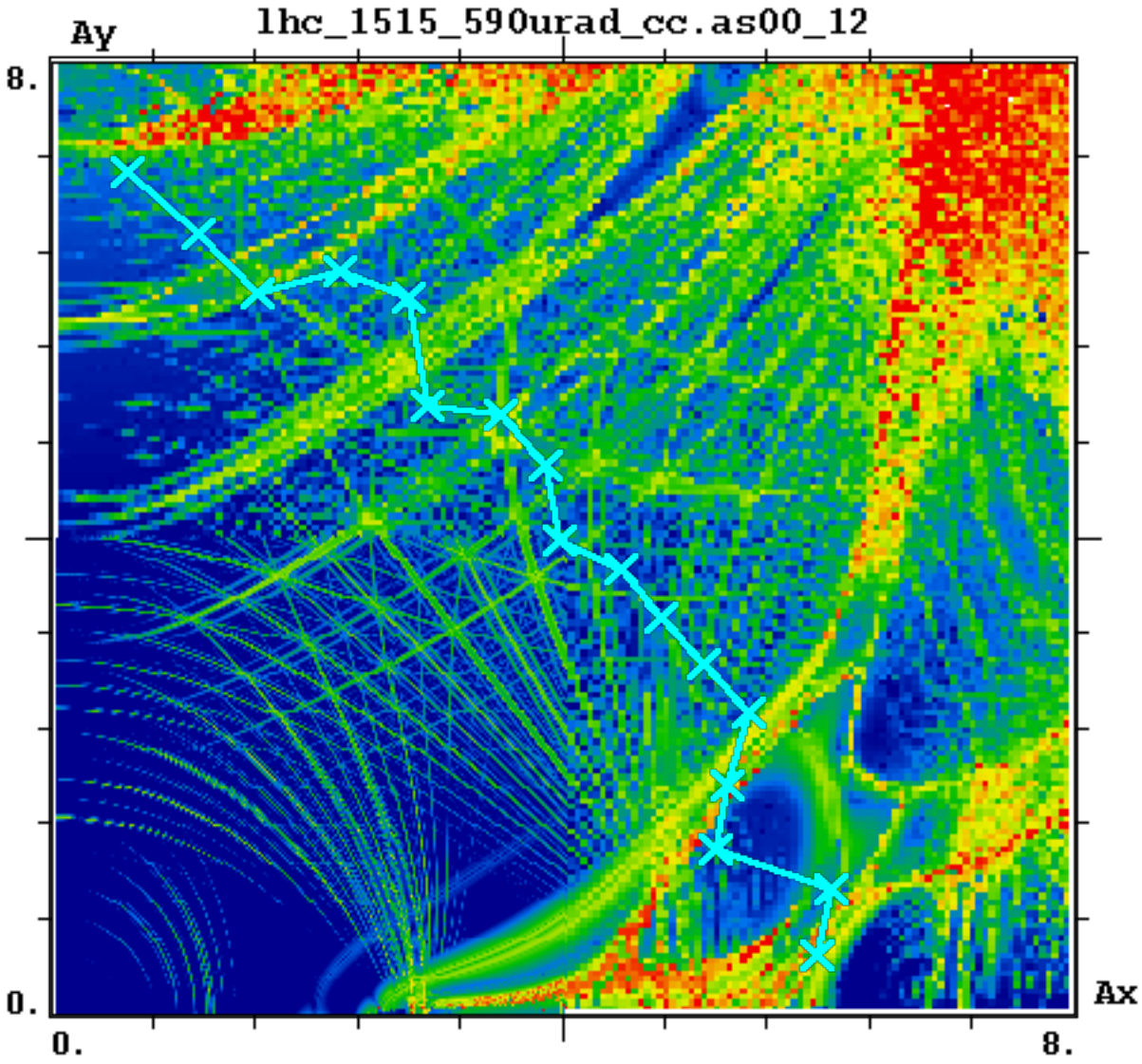
Effect of IR8

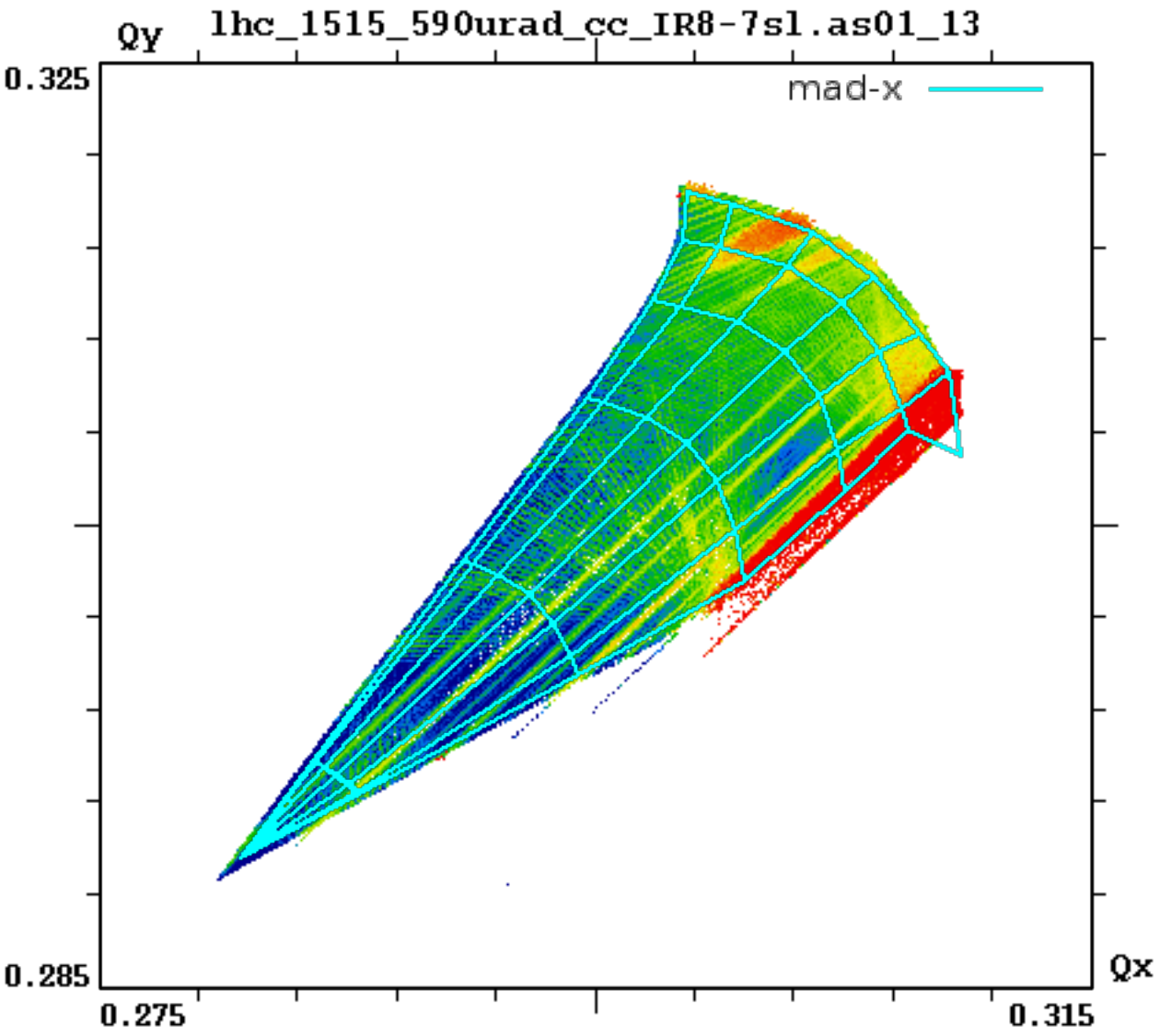
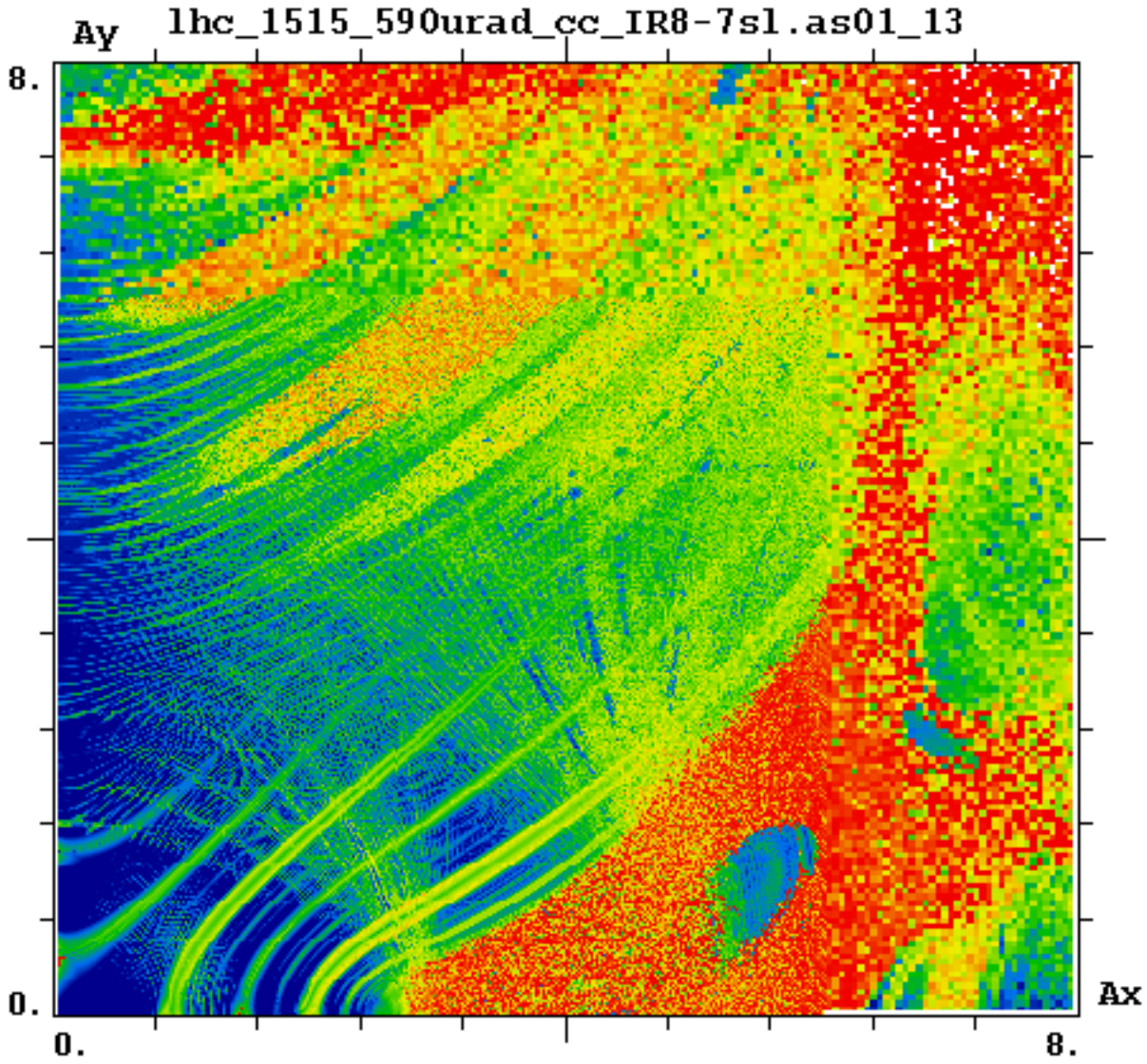


Conclusions

- It is important to use the number of slices in IR8 >1
  - Despite small σ_z/β^*
  - Crossing angle is significant
- The worst-worst-case scenario is marginally acceptable without/with errors with respect to DA
- However, overlapping resonances will enhance diffusion → bad emittance and luminosity lifetime
- To be confirmed for HLLHCv1

As=0, no errors




Qy
lhc_1515_590urad_cc_IR8-7sl.as01_13
mad-x
0.325
0.285
0.275
0.315
Qx

As=1, no errors, IR8 7 slices