

pyAMPP vs GX/IDL Full Stage Assessment

Date: 2026-02-13

Scope: Stage-by-stage H5 vs SAV comparison for both HMI and SFQ branches.

Compared Model Series

- HMI SAV series: /Users/gelu/Library/CloudStorage/Dropbox/@Projects/sim4fasr/gx_models/2025-11-26/*W28S13CR.CEA.{NONE,POT,BND,NAS,NAS.GEN,NAS.CHR}.sav
- SFQ SAV series: /Users/gelu/Library/CloudStorage/Dropbox/@Projects/sim4fasr/gx_models_sfq/2025-11-26/*W28S13CR.CEA.{NONE,POT,BND,NAS,NAS.GEN,NAS.CHR}.sav
- Rebuilt HMI H5 series: /tmp/pyampp_models_rebuild_hmi_from_sav/2025-11-26/*W28S13CR.CEA.*.h5
- Rebuilt SFQ H5 series: /tmp/pyampp_models_rebuild_sfq_from_sav/2025-11-26/*W28S13CR.CEA.*.h5

Primary machine-readable report: - reports/parity_review/data/stage_compare_rebuild_vs_sav_full.json

Method

- Compare corresponding H5/SAV models stage-by-stage.
- Compute metrics for:
 - ▶ base/bx,by,bz (2D)
 - ▶ corona/bx,by,bz full cubes (3D)
 - ▶ corona z=0 maps (bx,by,bz)
- Metrics: MAE, RMSE, max-abs, correlation, bounded relative MAE.

Controlled Experiment: Strict Entry Resume (SAV NONE -> Forward)

- Entry models: SAV NONE (W28S13) for HMI and SFQ.
- Resume mode (no rebuild): --entry-box <NONE.sav> --jump2bounds and run forward to end.
- Also generated explicit NONE clones via --clone-only for identity validation.
- Report file:
 - ▶ reports/parity_review/data/stage_compare_resume_none_vs_sav_full.json

Key controlled results (MAE):

- HMI:
 - ▶ NONE: base/z0/cube all exactly 0.
 - ▶ BND: base/z0/cube all exactly 0.
 - ▶ NAS/NAS.GEN/NAS.CHR: base/z0 exactly 0; cube MAE Bx/By/Bz = 1.724/1.732/1.030 G.
- SFQ:
 - ▶ NONE: base/z0/cube all exactly 0.
 - ▶ BND: base/z0/cube all exactly 0.
 - ▶ NAS/NAS.GEN/NAS.CHR: base/z0 exactly 0; cube MAE Bx/By/Bz = 1.319/1.314/0.888 G.

Additional machine-readable detail report (GEN + CHR fields): - [reports/parity_review/data/gen_chromo_compare_resume_none_vs_sav.json](#)

HMI Summary Table

Stage	Base MAE (Bx/By/Bz) [G]	Corona (Bx/By/Bz) [G]	z=0 MAE (Bx/By/Bz) [G]
NONE	28.178/24.117/18.967	1.158/1.048/1.680	89.496/81.886/124.197
POT	28.178/24.117/18.967	1.078/0.531/1.254	12.670/13.266/18.967
BND	28.178/24.117/18.967	1.182/0.603/1.254	28.178/24.117/18.967
NAS	28.178/24.117/18.967	2.121/1.817/1.765	28.178/24.117/18.967
NAS.GEN	28.178/24.117/18.967	2.121/1.817/1.765	28.178/24.117/18.967
NAS.CHR	28.178/24.117/18.967	2.121/1.817/1.765	28.178/24.117/18.967

SFQ Summary Table

Stage	Base MAE (Bx/By/Bz) [G]	Corona (Bx/By/Bz) [G]	z=0 MAE (Bx/By/Bz) [G]
NONE	28.670/24.493/16.963	1.193/1.078/1.661	90.394/80.688/125.600
POT	28.670/24.493/16.963	0.609/0.324/0.758	11.915/12.825/16.963
BND	28.670/24.493/16.963	0.721/0.402/0.758	28.670/24.493/16.963
NAS	28.670/24.493/16.963	2.387/2.064/1.749	28.670/24.493/16.963
NAS.GEN	28.670/24.493/16.963	2.387/2.064/1.749	28.670/24.493/16.963
NAS.CHR	28.670/24.493/16.963	2.387/2.064/1.749	28.670/24.493/16.963

Interpretation

- In strict entry-resume mode, NONE and BND are exactly matched (as expected for shared starting payload + boundary replacement).
- POT stage: expected non-zero z=0 mismatch for Bx/By (true potential field at bottom, no boundary replacement).
- BND stage: z=0 mismatch levels become stable and are preserved through NAS, NAS.GEN, NAS.CHR.
- NAS.GEN and NAS.CHR do not alter corona vectors; their vector metrics match NAS (as expected).
- Full-cube H5-vs-SAV MAE remains low (order of ~0.3–2.4 G depending on branch/stage).

GEN/CHR Detailed Comparison (Strict Resume)

Source: - [reports/parity_review/data/gen_chromo_compare_resume_none_vs_sav.json](#)

GEN Line-Parameter Comparability

The number of active line voxels is not identical between H5 and SAV, so strict one-by-one line-property parity is not fully expected.

HMI line counts: - nonzero STARTIDX: SAV 1,686,514 vs H5 1,680,223 - nonzero ENDIDX: SAV 1,686,513 vs H5 1,680,223 - nonzero STATUS/voxel_status: SAV 1,687,500 vs H5 1,687,500

SFQ line counts: - nonzero STARTIDX: SAV 1,686,197 vs H5 1,679,724 - nonzero ENDIDX: SAV 1,686,197 vs H5 1,679,724 - nonzero STATUS/voxel_status: SAV 1,687,500 vs H5 1,687,500

Representative GEN metrics: - AVFIELD: relative MAE ~0.494 (HMI), 0.474 (SFQ), correlation ~0.38 - PHYSLENGTH: large mismatch in current representation (relative MAE ~492, correlation ~0.50) - STATUS exact-match fraction: ~0.496 (HMI), 0.507 (SFQ)

CHR Field Parity

Core index/topology arrays are effectively identical: - CHROMO_IDX: exact-match 1.0 (both branches) - TR: exact-match 1.0 (both branches) - CHROMO_LAYERS: exact-match 1.0 (both branches)

Thermodynamic CHR arrays (CHROMO_N, CHROMO_T, N_P, N_HI, NHTOT, DZ, TR_H) show near-perfect correlation (~1.0) and very small relative errors for density/temperature vectors: - HMI relative MAE: - CHROMO_N: 1.6e-05 - CHROMO_T: 2.5e-05 - N_P: 2.9e-05 - N_HI: 4e-06 - NHTOT: 4e-06 - SFQ relative MAE: - CHROMO_N: 1.4e-05 - CHROMO_T: 2.1e-05 - N_P: 2.5e-05 - N_HI: 3e-06 - NHTOT: 3e-06

CHR magnetic cube component parity (CHROMO_BCUBE -> chromo/bx,by,bz): - HMI relative MAE: - bx: 0.0745 - by: 0.1000 - bz: 0.0415 - SFQ relative MAE: - bx: 0.0934 - by: 0.1153 - bz: 0.0533

Conclusions

1. The strict controlled test **does** show exact identity at NONE and BND.
2. The first meaningful divergence appears at NAS cube volume (while base and z=0 stay exact), indicating residual differences are in NLFFF volume optimization/path, not entry/base handling.
3. Stage mechanics are internally consistent in pyAMPP:
 - POT behaves as true potential,
 - BND enforces observed bottom boundary,
 - NAS -> GEN -> CHR preserve corona vectors as expected.
4. For tighter SAV/H5 parity beyond this point, focus should shift to NAS/NLFFF numerical parity (solver settings/tolerances/implementation details), then re-run this controlled chapter.

Referenced Figures

Base HMI

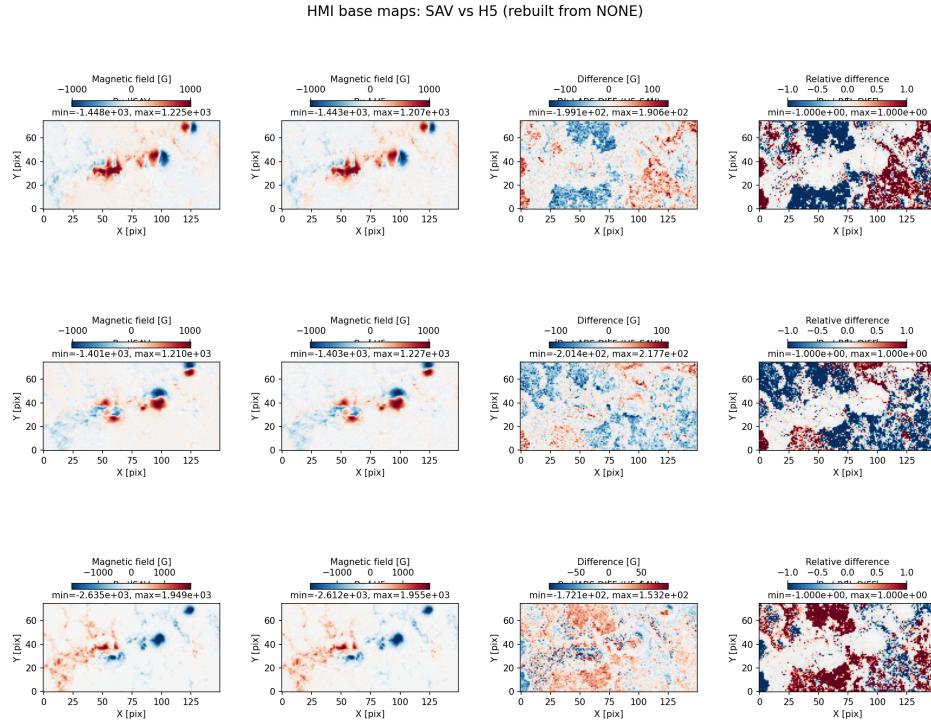


Figure 1: Base HMI

Base SFQ

SFQ base maps: SAV vs H5 (rebuilt from NONE)

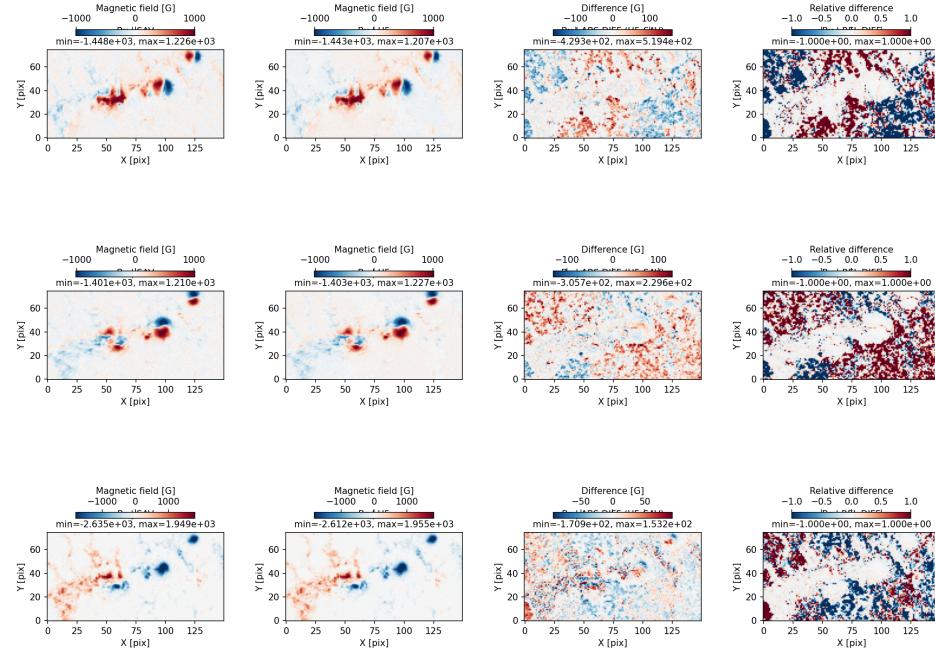


Figure 2: Base SFQ

z=0 HMI POT

HMI POT: corona z=0 SAV vs HS

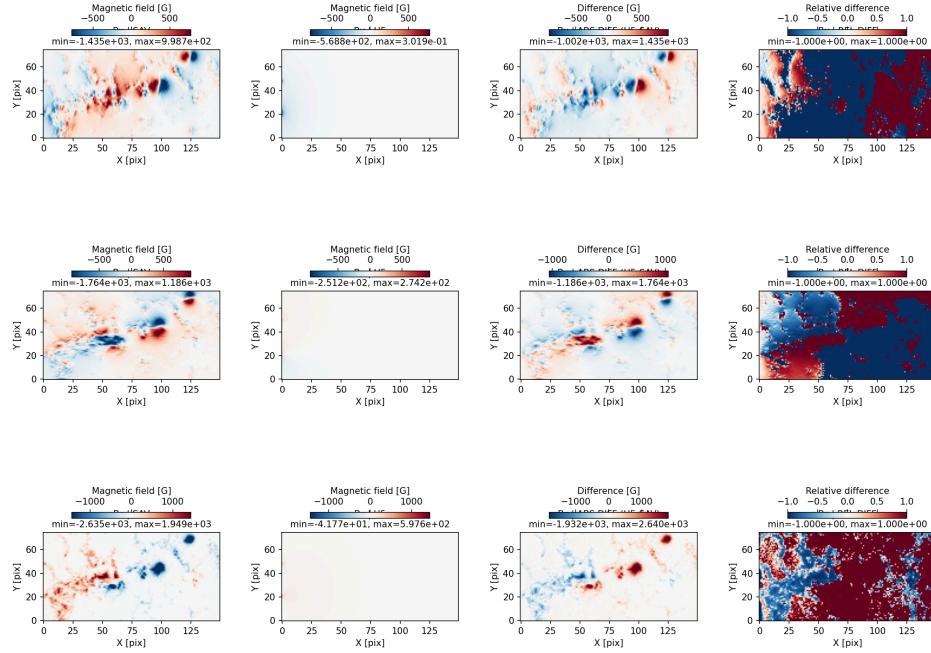


Figure 3: z=0 HMI POT

z=0 HMI BND

HMI BND: corona z=0 SAV vs H5

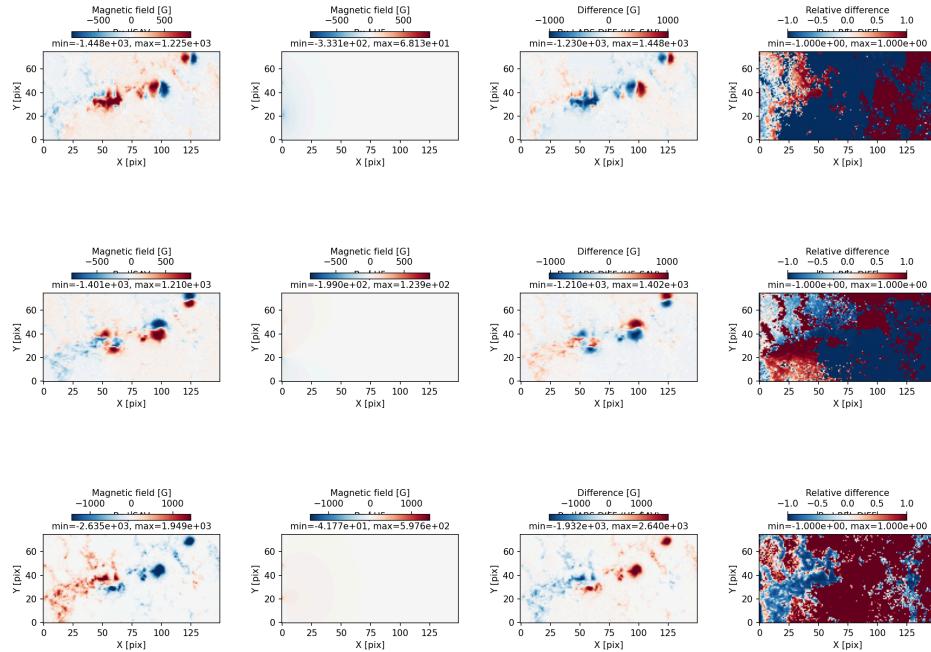


Figure 4: z=0 HMI BND

z=0 HMI NAS

HMI NAS: corona z=0 SAV vs H5

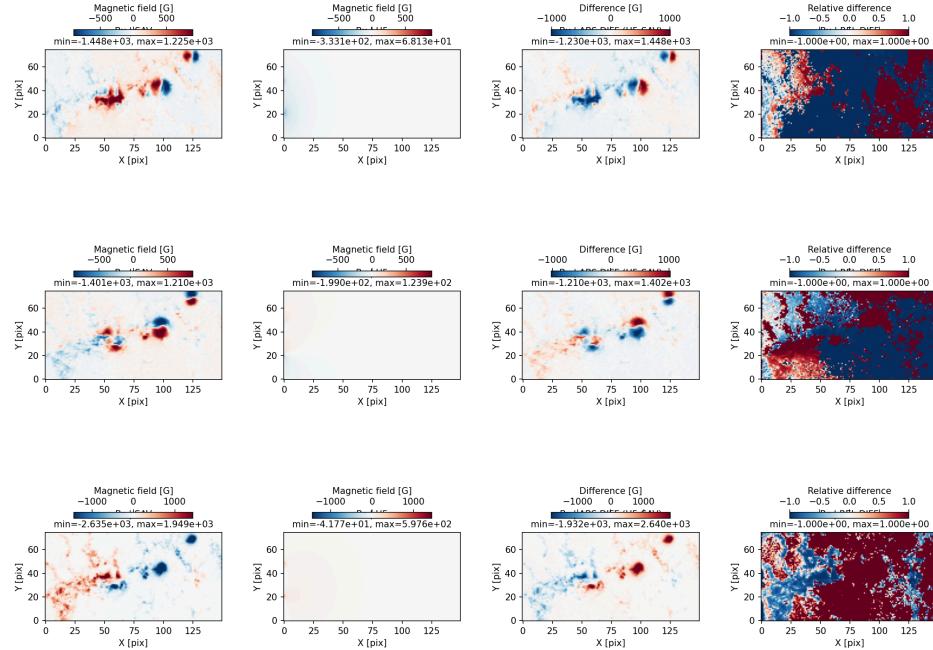


Figure 5: z=0 HMI NAS

z=0 SFQ POT

SFQ POT: corona z=0 SAV vs H5

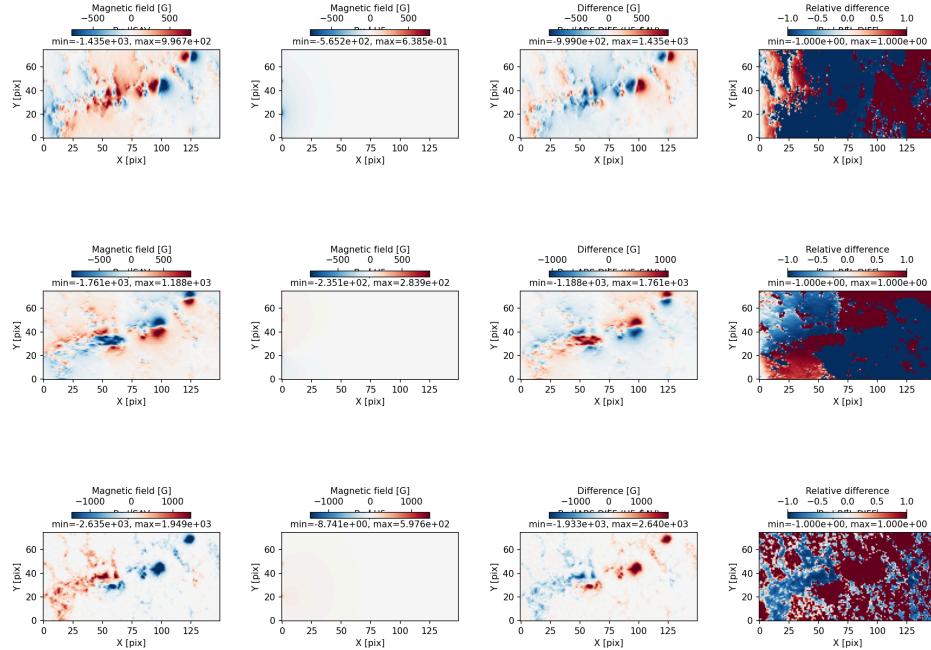


Figure 6: z=0 SFQ POT

z=0 SFQ BND

SFQ BND: corona z=0 SAV vs H5

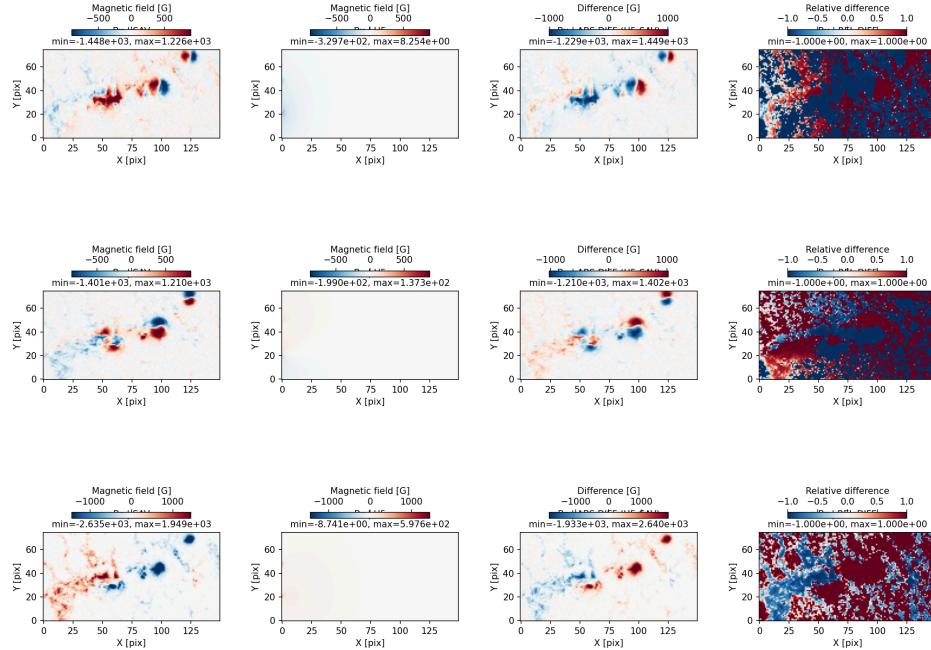


Figure 7: z=0 SFQ BND

z=0 SFQ NAS

SFQ NAS: corona z=0 SAV vs H5

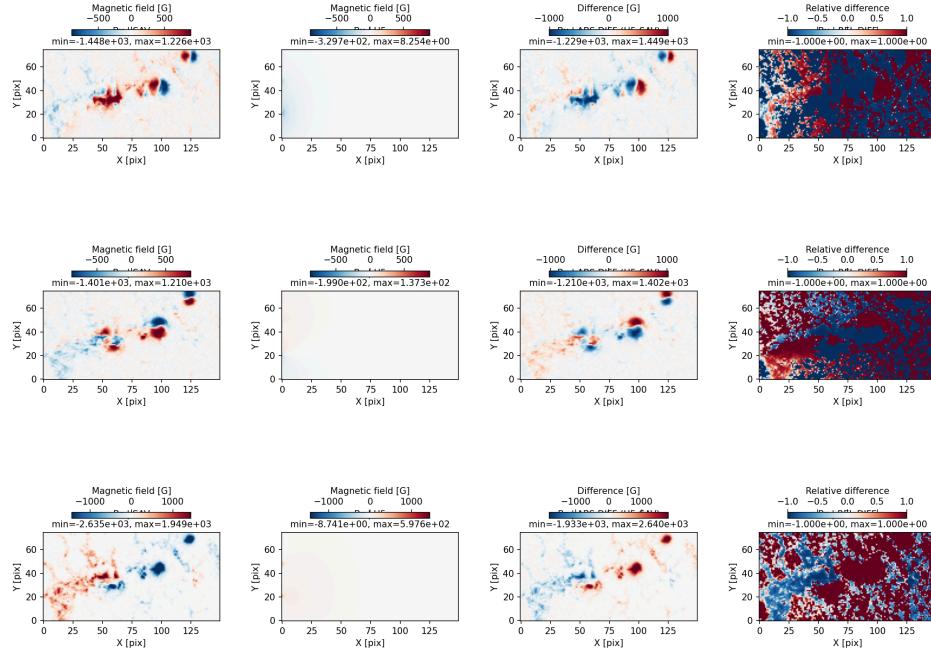


Figure 8: z=0 SFQ NAS