

The published version of the MORB phase diagram section (Fig 3., Holland et al., JPet, 2013) vs raw output from Perple_X 6.8.5 (computed with the morb_hhph.dat input file, originally compiled by Bob Myhill).
 morb_hhph calculation: global_reach_increment = 1, x/y_nodes = [60 60], all other options default.

Computation time ~6 h.

A global_reach_increment of 1 was specified to reduce cosmetic flaws (phase boundary roughness). Without global_reach_increment computation time is reduced by > 2 orders of magnitude (< 20 min).

The reduced stability field for the NAI phase in the Perple_X calculation is the most notable discrepancy. Most likely, the NAI phase field discrepancy is due to a change, or transcription error, in the NAI phase data. The similarity of phase boundaries irrespective of the presence of the NAI phase suggests that the NAI phase has no significant influence on bulk properties in the original calculation.

