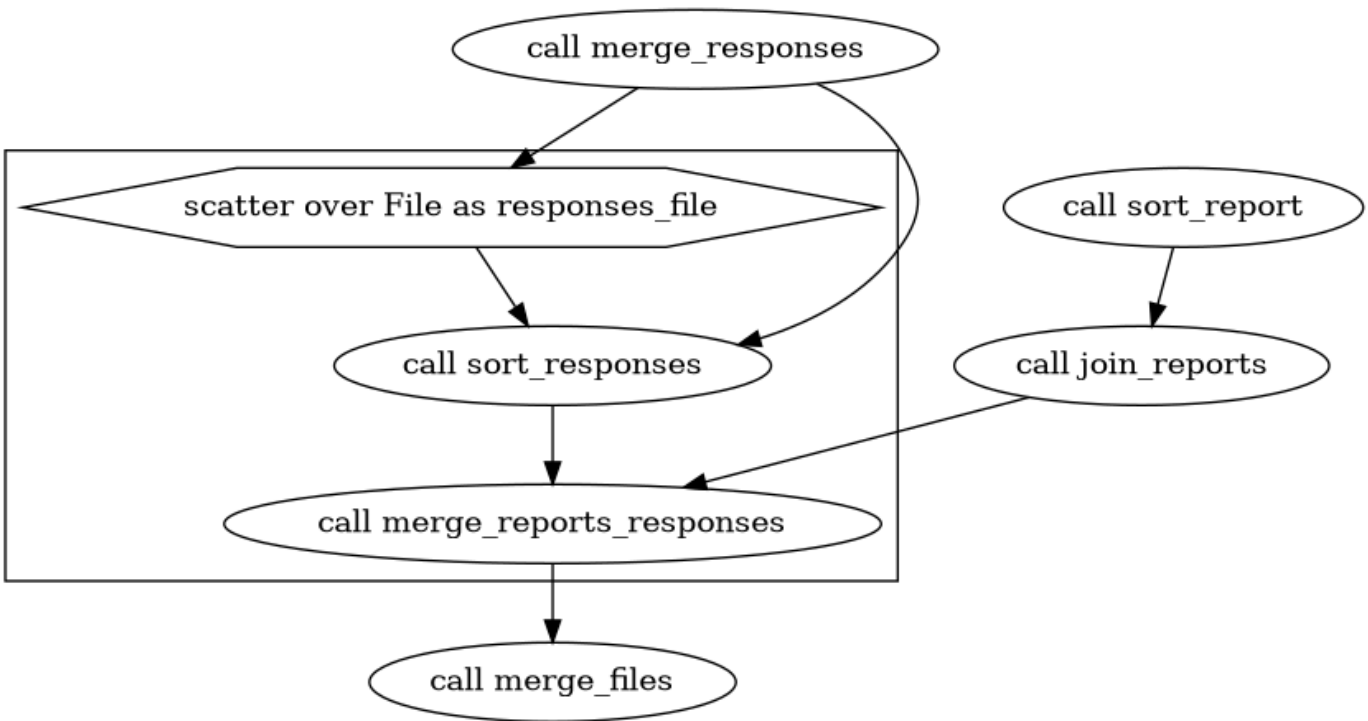


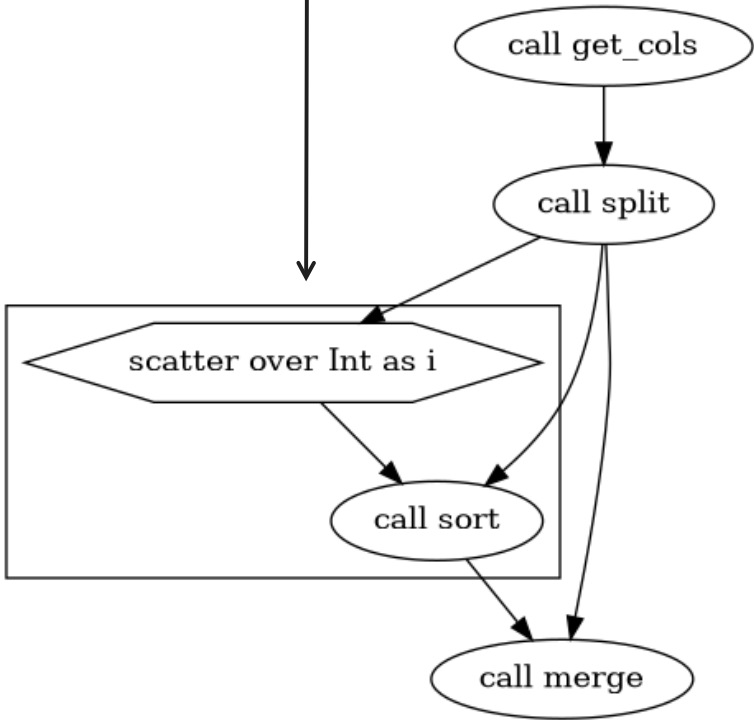
pre-munge.wdl

This steps sorts responses and reports based on the same key to merge them into a single file



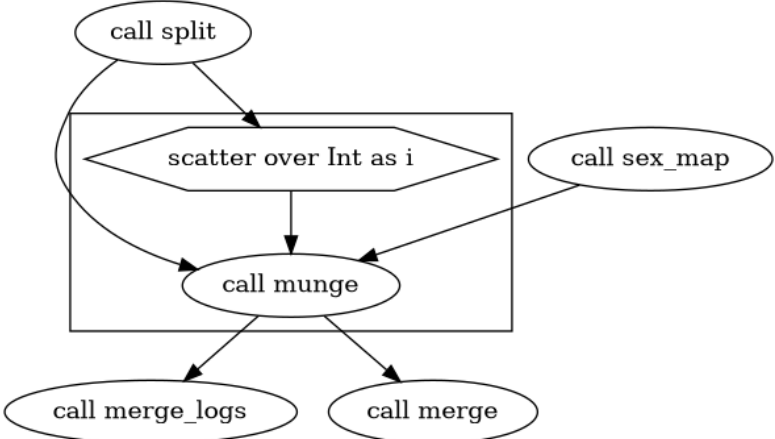
sort-dup.wdl

This step sorts the previous output by a set of keys that are used to intercept duplicate lines. ROW_IDs are also added



kanta_munge.wdl

This step munges the raw data,adds SEX info from the phenotype file and harmonizes via OMOP mappings. In the merge step post OMOP mapping duplicate lines are removed



kanta_core.wdl

This is the final step. The output of the post duplication removal step is further processed to extract new info, mostly from the MEASUREMENT_FREE_TEXT column. QC is done to prevent sensitive data to be shared. Release files are built both for core and metadata

