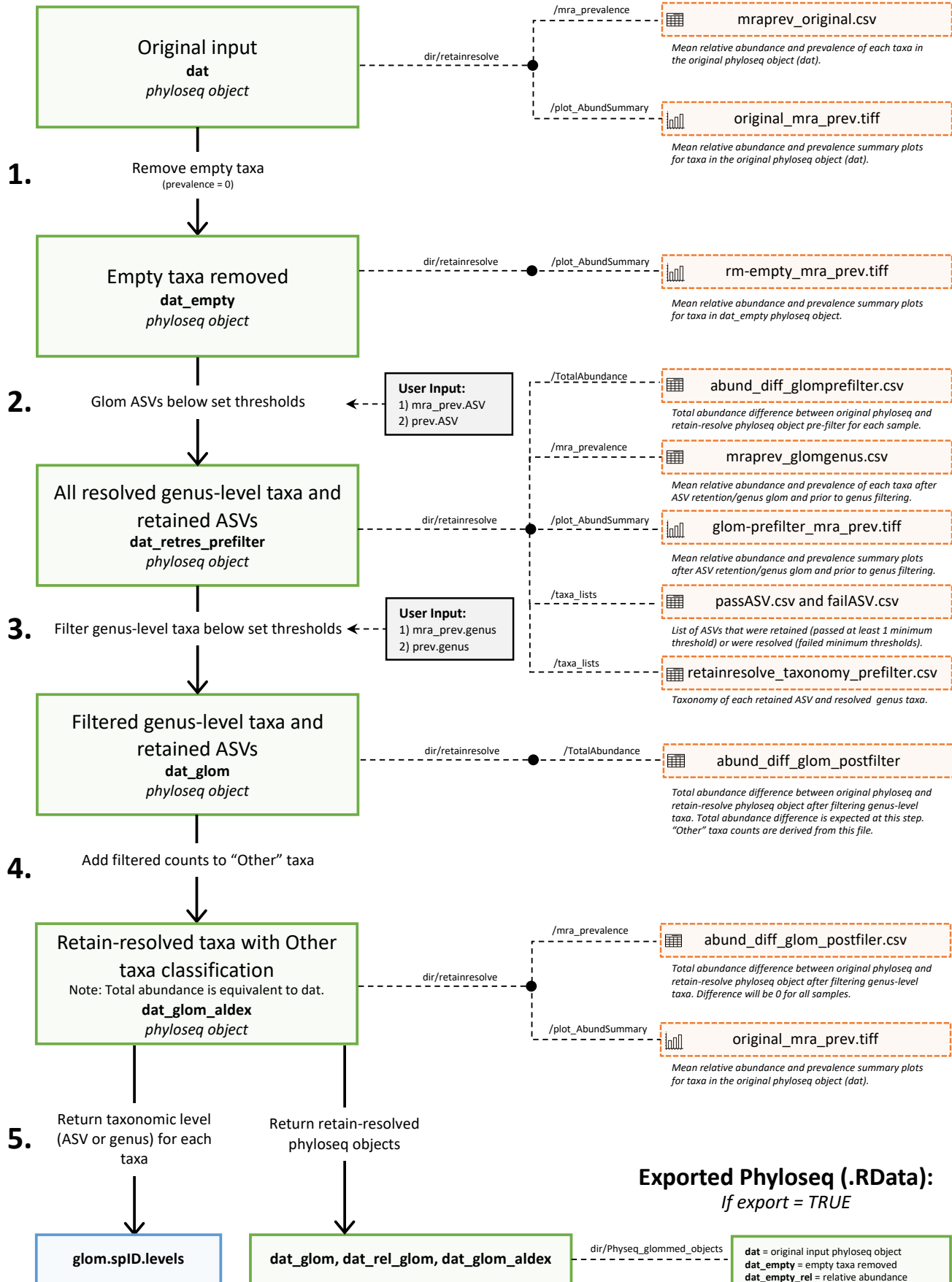


Retain-resolve Algorithm:

Exported QC Files:

If export = TRUE



Exported Phyloseq (.RData):

If export = TRUE

dat = original input phyloseq object
 dat_empty = empty taxa removed
 dat_empty_rel = relative abundance calculated from dat_empty
 dat_retres_prefilter = retained ASVs and resolved genus taxa before genus filter
 dat_glom = retained ASV-level and filtered genus-level taxa
 dat_glom_aldex = ASV-retained and post-filter genus-level phyloseq with Other taxa
 dat_rel_glom = relative abundance calculated from dat_glom_aldex. Other taxa removed.