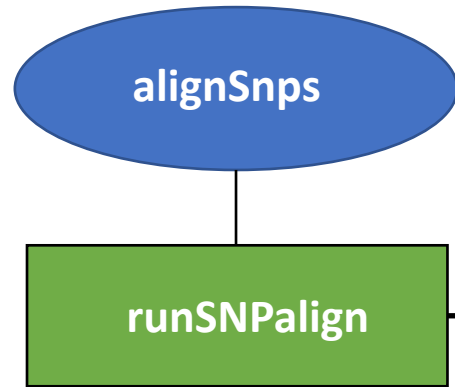
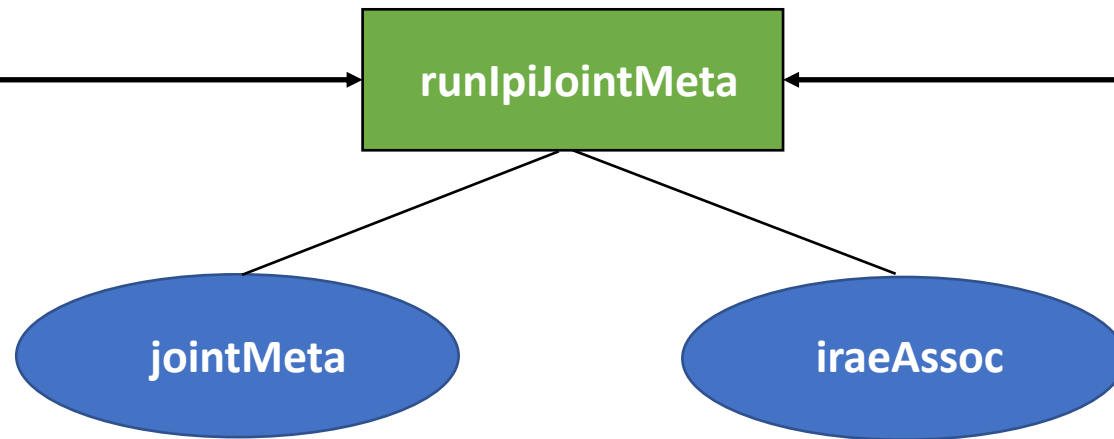


- Functions to align alleles and genotypes across  $n$  studies



- Reduce data to the set of SNPs common across all data sets
- Match alleles across studies
- Write output for repeat runs of runlpiJointMeta

- Using aligned SNPs, calculate associations and combine summary statistics in meta-analysis



- Function for joint meta analysis of  $n$  studies

- Functions for association of irAE and survival with genotype and covariates
- No prior and prior interaction models

- File containing the parameters of each study in meta analysis
- File names, covariates

