**Power and sample size analysis for three-way admixture mapping**

The descriptions are based on the PAMAM R functions for the power and sample size in three-way admixture mapping studies. The source codes can be downloaded from the github page <https://github.com/MershaLab/PAMAM/blob/master/AMPower_3way.R>.

* Case-only study for discrete phenotype

PowerCase3way(null\_vector, risk\_freq, grr, alpha, sample\_case)

SampleCase3way(null\_vector, risk\_freq, grr, alpha, sample\_case)

* Case-control study for discrete phenotype

PowerCC3way(null\_prop, risk\_freq, grr, sample\_case, sample\_control, alpha)

SampleCC3way(null\_prop, risk\_freq, grr, alpha, beta)

The arguments in the functions are,

null\_vector = a vector of size 3 of global ancestry proportions

risk\_freq = a vector of size 3, each element represents the risk allele frequency in respective ancestral population, order of population should match to that in null\_vector

grr = genotype risk ratio under multiplicative mode

sample\_case = numbers of cases

sample\_control = numbers of controls

alpha = Type 1 error rate after the adjustment for multiple testing, such as after Bonferroni correction

beta = Type 2 error rate

* Quantitative Trait:

PowerQTrait3way(nullR2, alternateR2, anc, alpha, N, covariates)

SampleQTrait3way(nullR2, alternateR2, anc, alpha, power, covariates)

The arguments of the functions are,

nullR2 = Proportion of variance of phenotype/trait explained under null model

alternateR2 = Proportion of variance of phenotype/trait explained under alternate model

u = # of ancestral populations

N = Sample size

covariates = # of covariates in the model

alpha = Type 1 error rate after the adjustment for multiple testing, such as after Bonferroni correction

beta = Type 2 error rate