*Test\_Run\_One\_Year.R is the file contains scripts to run the simulation for 1-year per cycle scheme*

*Total number of breeding Cycles is set at 10*

*Number of simulation reps is set at 20*

runOneRep(): the function of running 1-year per cycle scheme for one time, it requires inputs:

"selection": what is the selection scheme at SP stage, it is either "rand" or "pheno", as defined by AlphaSimR syntax

"nPheno":the number of SP plots to be tested on farm, it is either 400 pr 1000

"nDH": the number of GPs survive through flow cetometry system, it is either 24 or 96

"varE": the error variance to get the estimated heritability of 0.2 or 0.5, it is either 4 or 1

"Ne":the effective population size, it is either 60 to 600

n\_gp: the number of GPs that would be generated from selected SPs, each GP is set to make 2 crosses

founderPop: founder population,

AlphaSimR syntax:

nInd: the number of individuals is 1000, nChr is set at 31, which is the number of chromosomes in Saccharina japonica

segSites: number of segregating sites per chromosome is set at 500

Ne: effective popuation size for founders

bp: base pair length of chromosome, set at default value of 1e+08

genLen: genetic length of chromosome in Morgans, set at 1

nQtlPerChr : Add trait QTL for the founder SPs, the trait has 100 QTLs per chromosome, with mean 0 and variance of 1.

nSnpPerChr: Add genotypic data for the SPs, where number of SNPs per Chromosome is 100.

pop: the founder population being created in each simulation rep.

meanG(): is the mean genetic value of the population by AlphaSimR

generation: the vector stores the generation from founders, to cycle 1,2…10 generations

*The breeding pipeline (Figure XXX) starts with founder popualtions (pop)*

GP0\_DH : Creating the double haploids of founders

GP0\_DH\_all : Get genetic information on all the GP0\_DH individuals. Please note, these syntax are for double haploid individuals that AlphaSimR could only generate

*Then going forward for each cycle (j)*

*For the first 2 years (j <2),*

females: randomly selecting female gametophytes from the stock of founders GPs

males: randomly selecting male gametophytes from the stock of founders GPs

GP\_F and GP\_M: genotype these female and male gametophytes

crossPlan: randomly mating the female GPs to male GPs, while each GP is being used for crossing twice

Spj: the SPs crossed from the aforementioned GPs

Spj is phenotyped

Sporo: the SP population from year 1 to jth years

Spj\_s: The 10% SPs being selected, based on “selection cheme”

SPselInt: Estimating empirical selection intensity based on difference of standardized mean of Spj population and the Spj\_s population

GP\_DHj: creating GPs from the SPj\_s population

GP\_DH: the list of GPs from year 1 to jth years

*Going forward starting year 3,*

TP\_j: is the population at jth year, Sporo, which is all historical years of SP data

GS\_j is the training population model at jth year

GEBV\_j: GEBVs for the GPs at one years ago (j-1), given a One-year per cycle scheme

Or two years ago (j-2), given a Two\_year per cycle scheme

GScor: GS correlation accuracy at the jth GPs stage

females: selecting female GPs based on their estimated GEBVs. The number of GPs being selected is nPheno/2

males: selecting male GPs based on their estimated GEBVs

GPselInt: Selection intensity on the GPs stage

crossPlan: the list of crosses to make using selected GPs baed on their GEBVs

Sporo\_j: crossing the GPs and set phenotypes

Sporo: is the list for 1 to jth year phenotyped Farm grown SPs

Sporo\_js<-selecting the 10% SPs from the jth year field SPs

Sporo\_s<-the list of 1 to ith year selected SPs

SPselInt: selection intensity for the SP stage at jth year, when j >2

GP\_DH\_j: the GPs generated from the jth selection SP population (Sporo\_s)

GP\_DH: the list of GPs being selected from 1 to jth year

mean\_g1: the mean genetic value for Farm tested SPs

sd\_g1: the total genetic variance for Farm tested SPs

mean\_g2: the mean genetic value for GPs

sd\_g2: the total genetic variance for GPs

Test\_Run\_Two\_Years.R

Follows the same workflow of the breeding pipeline, except that starting from year 3 (j=3), on the *jth* year, the genomic selection step to select GPs for making crosses is based on GPs from two years ago (GP\_DH[[j-2]] generation), due to that GPs takes extra time to grow and accumulate biomass.