Exercises - QMSim

Summer Course – UNE – Armidale (Day1 – Feb 20, 2023)

1) Simulate a historical population with the following parameters:

Initial size	600
Initial number of SNPs	20,000
Initial number of QTLs	5,000
Initial allele frequency	Equal or fixed
Mutation rate for SNPs	2.5e-5 (recurrent)
Mutation rate for QTLs	2.5e-5
QTL h^2	0.2
Number of chromosomes	10
Replicate	1

- Determine how many generations are required to reach mutation-drift equilibrium when the initial allele frequency is equal or non-segregating.
- Plot allele frequency distribution in the last generation for both equal and non-segregation scenario.
- Use "`select_seg_loci`" command to select SNP with MAF of larger than 0.5%.
- Modify the necessary parameters to get at least 10K segregating SNP and 5K segregating QTL (MAF > 0.5%) in the last historical generation.

2) Select 10 sires and 500 dams from the last historical population in 1). Set parameters for the recent population in such a way to create long range LD observed in livestock. Name this population "LLD".

3) Simulate two populations by selecting 25 males and 250 females as founders from generation 10 of LLD population. The founders should not overlap between the two populations. Carry out divergent selection for true breeding values for 15 discrete generations. Cross the two populations and compare homozygosity and inbreeding of the cross with the parent lines. And finally save the genotypes of crosses in SNP genotype code format.

4) Use HP in 1) and simulate a population in which selection is based on EBV computed by an external solver. The external solver name is "`MySolver`"

Solutions:

1)

```
/*******************************
 **     Global parameters     **
 *******************************/
title = "Exercise 1 - 20k SNP panel";
h2    = 0.2;                  //Heritability
qtlh2 = 0.2;                  //QTL heritability
phvar = 1.0;                  //Phenotypic variance
nrep  = 1;                    //Number of replicates
//nthread = 1;

/*******************************
 **   Historical population   **
 *******************************/
begin_hp;
   hg_size = 600 [0]          //Size of the historical generations
             600 [10000];
   nmlhg   = 50;              //Number of males in the last generation
end_hp;

/*******************************
 **        Populations        **
 *******************************/

begin_pop = "LLD";
   begin_founder;
      male   [n =  50, pop = "hp"];
      female [n = 550, pop = "hp"];
   end_founder;
   ls  = 1;                   //Litter size
   ng  = 0;                   //Number of generations
   begin_popoutput;
        ld /maft 0.01;
   end_popoutput;
end_pop;

/*******************************
 **          Genome           **
 *******************************/
begin_genome;
   begin_chr = 10;
      chrlen = 100;           //Chromosome length
      nmloci = 2000;          //Number of markers
      mpos   = rnd;           //Marker positions
      nma    = all 2;         //Number of marker alleles
      maf    = all 0 1;       //Marker allele frequencies
      nqloci = 500;           //Number of QTL
      qpos   = rnd;           //QTL positions
      nqa    = all 2;         //Number of QTL alleles
      qaf    = all 0 1;       //QTL allele frequencies
      qae    = rndg 0.4;      //QTL allele effects
   end_chr;
   mmutr     = 2.5e-5 /recurrent; //Marker mutation rate
```

```
   qmutr     = 2.5e-5;            //QTL mutation rate
   interference = 25;
   select_seg_loci /maft .005;
end_genome;

/******************************
 **       Output options      **
 ******************************/
begin_output;
   monitor_hp_homo /freq 100;
   linkage_map;
   allele_effect;
end_output;
```

2)

```
/******************************
 **     Global parameters     **
 ******************************/
title = "Exercise 2 - Long range LD";
h2    = 0.2;                  //Heritability
qtlh2 = 0.2;                  //QTL heritability
phvar = 1.0;                  //Phenotypic variance
nrep  = 1;                    //Number of replicates
//nthread = 1;

/******************************
 **   Historical population   **
 ******************************/
begin_hp;
   hg_size = 600 [0]          //Size of the historical generations
             600 [5000];
   nmlhg   = 50;              //Number of males in the last generation
end_hp;

/******************************
 **        Populations        **
 ******************************/

begin_pop = "LLD";
   begin_founder;
      male   [n =  10, pop = "hp"];
      female [n = 500, pop = "hp"];
   end_founder;
   ls  = 2;                   //Litter size
   pmp = 0.5 /fix;            //Proportion of male progeny
   ng  = 20;                  //Number of generations
   md  = rnd;                 //Mating design
   sr  = 0.5;                 //Replacement ratio for sires
   dr  = 0.3;                 //Replacement ratio for dams
   sd  = rnd;                 //Selection design
   cd  = age;                 //Culling design
   begin_popoutput;
        ld /maft 0.01 /gen 0 10 20;
   end_popoutput;
end_pop;
```

```
/*******************************
 **          Genome           **
 *******************************/
begin_genome;
   begin_chr = 10;
      chrlen = 100;           //Chromosome length
      nmloci = 10000;         //Number of markers
      mpos   = rnd;           //Marker positions
      nma    = all 2;         //Number of marker alleles
      maf    = all 0 1;       //Marker allele frequencies
      nqloci = 5000;          //Number of QTL
      qpos   = rnd;           //QTL positions
      nqa    = all 2;         //Number of QTL alleles
      qaf    = all 0 1;       //QTL allele frequencies
      qae    = rndg 0.4;      //QTL allele effects
   end_chr;
   mmutr     = 2.5e-5 /recurrent; //Marker mutation rate
   qmutr     = 2.5e-5;            //QTL mutation rate
   interference = 25;
   select_seg_loci /maft .005 /nmrk 20000 /nqtl 5000;
end_genome;

/*******************************
 **       Output options      **
 *******************************/
begin_output;
   monitor_hp_homo /freq 100;
   linkage_map;
   allele_effect;
end_output;
```

3)

```
/*******************************
 **     Global parameters     **
 *******************************/
title = "Exercise 3 - Multiple populations";
h2    = 0.2;                  //Heritability
qtlh2 = 0.2;                  //QTL heritability
phvar = 1.0;                  //Phenotypic variance
nrep  = 1;                    //Number of replicates
//nthread = 1;

/*******************************
 **   Historical population   **
 *******************************/
begin_hp;
   hg_size = 600 [0]          //Size of the historical generations
             600 [5000];
   nmlhg   = 50;              //Number of males in the last generation
end_hp;

/*******************************
 **        Populations        **
```

```
 *******************************/

begin_pop = "LLD";
   begin_founder;
      male   [n =  20, pop = "hp"];
      female [n = 500, pop = "hp"];
   end_founder;
   ls  = 2;                   //Litter size
   pmp = 0.5 /fix;            //Proportion of male progeny
   ng  = 20;                  //Number of generations
   md  = rnd;                 //Mating design
   sr  = 0.5;                 //Replacement ratio for sires
   dr  = 0.3;                 //Replacement ratio for dams
   sd  = rnd;                 //Selection design
   cd  = age;                 //Culling design
   begin_popoutput;
        ld /maft 0.01 /gen 0 10 20;
   end_popoutput;
end_pop;

begin_pop = "p1";
   begin_founder;
      male   [n =  25, pop = "LLD", gen = 20, select = rnd];
      female [n = 250, pop = "LLD", gen = 20, select = rnd];
   end_founder;
   ls  = 2;                   //Litter size
   pmp = 0.5 /fix;            //Proportion of male progeny
   ng  = 15;                  //Number of generations
   sr  = 1;                   //Replacement ratio for sires
   dr  = 1;                   //Replacement ratio for dams
   sd  = tbv /h;              //Selection design
   begin_popoutput;
        ld /maft 0.01 /gen 10;
        stat;
        data;
   end_popoutput;
end_pop;

begin_pop = "p2";
   begin_founder;
      male   [n =  25, pop = "LLD", gen = 20, select = rnd] /not_founder_yet;
      female [n = 250, pop = "LLD", gen = 20, select = rnd] /not_founder_yet;
   end_founder;
   ls  = 2;                   //Litter size
   pmp = 0.5 /fix;            //Proportion of male progeny
   ng  = 15;                  //Number of generations
   sr  = 1;                   //Replacement ratio for sires
   dr  = 1;                   //Replacement ratio for dams
   sd  = tbv /l;              //Selection design
   begin_popoutput;
        ld /maft 0.01 /gen 10;
        stat;
        data;
   end_popoutput;
end_pop;

begin_pop = "Cross";
```

```
   begin_founder;
      male   [n =  25, pop = "p1", gen = 15, select = tbv /h];
      female [n = 250, pop = "p2", gen = 15, select = tbv /l];
   end_founder;
   ls  = 2;                   //Litter size
   pmp = 0.5 /fix;            //Proportion of male progeny
   ng  = 1;                   //Number of generations
   sr  = 1;                   //Replacement ratio for sires
   dr  = 1;                   //Replacement ratio for dams
   begin_popoutput;
        ld /maft 0.01 /gen 0 1;
        stat;
        data;
        genotype /snp_code /gen 1;
   end_popoutput;
end_pop;


/*******************************
 **          Genome           **
 *******************************/
begin_genome;
   begin_chr = 10;
      chrlen = 100;           //Chromosome length
      nmloci = 10000;         //Number of markers
      mpos   = rnd;           //Marker positions
      nma    = all 2;         //Number of marker alleles
      maf    = all 0 1;       //Marker allele frequencies
      nqloci = 5000;          //Number of QTL
      qpos   = rnd;           //QTL positions
      nqa    = all 2;         //Number of QTL alleles
      qaf    = all 0 1;       //QTL allele frequencies
      qae    = rndg 0.4;      //QTL allele effects
   end_chr;
   mmutr     = 2.5e-5 /recurrent; //Marker mutation rate
   qmutr     = 2.5e-5;            //QTL mutation rate
   interference = 25;
   select_seg_loci /maft .005 /nmrk 20000 /nqtl 5000;
end_genome;

/*******************************
 **       Output options      **
 *******************************/
begin_output;
   monitor_hp_homo /freq 100;
   linkage_map;
   allele_effect;
end_output;
```

4)

```
/*******************************
 **     Global parameters     **
 *******************************/
title = "Exercise 4 - External EBV solver";
```

```
h2    = 0.2;                  //Heritability
qtlh2 = 0.2;                  //QTL heritability
phvar = 1.0;                  //Phenotypic variance
nrep  = 1;                    //Number of replicates
//nthread = 1;

/*******************************
 **   Historical population   **
 *******************************/
begin_hp;
   hg_size = 600 [0]          //Size of the historical generations
             600 [5000];
   nmlhg   = 50;              //Number of males in the last generation
end_hp;

/*******************************
 **        Populations        **
 *******************************/

begin_pop = "LLD";
   begin_founder;
      male   [n =  20, pop = "hp"];
      female [n = 500, pop = "hp"];
   end_founder;
   ls  = 2;                   //Litter size
   pmp = 0.5 /fix;            //Proportion of male progeny
   ng  = 20;                  //Number of generations
   md  = rnd;                 //Mating design
   sr  = 0.5;                 //Replacement ratio for sires
   dr  = 0.3;                 //Replacement ratio for dams
   sd  = rnd;                 //Selection design
   cd  = age;                 //Culling design
   ebv_est = external_bv "MySolver";
   begin_popoutput;
        ld /maft 0.01 /gen 0 10 20;
        data;
        genotype /snp_code /gen 17 18 19 20;
   end_popoutput;
end_pop;


/*******************************
 **          Genome           **
 *******************************/
begin_genome;
   begin_chr = 10;
      chrlen = 100;           //Chromosome length
      nmloci = 10000;         //Number of markers
      mpos   = rnd;           //Marker positions
      nma    = all 2;         //Number of marker alleles
      maf    = all 0 1;       //Marker allele frequencies
      nqloci = 5000;          //Number of QTL
      qpos   = rnd;           //QTL positions
      nqa    = all 2;         //Number of QTL alleles
      qaf    = all 0 1;       //QTL allele frequencies
      qae    = rndg 0.4;      //QTL allele effects
   end_chr;
```

```
   mmutr     = 2.5e-5 /recurrent; //Marker mutation rate
   qmutr     = 2.5e-5;            //QTL mutation rate
   interference = 25;
   select_seg_loci /maft .005 /nmrk 20000 /nqtl 5000;
end_genome;

/*******************************
 **       Output options      **
 *******************************/
begin_output;
   monitor_hp_homo /freq 100;
   linkage_map;
   allele_effect;
end_output;
```