Annex 1 Matlab program for epistatic QTLs detected

step1: setup matlab

step2: copy test1.m-test7.m，test\_key.m to the current file of matlab

step3: apply the order of matlab import the data

test1.m

genotype variant named as da, structure is cell type;

Example as follow:

'A' 'A' 'A' 'A' 'A' 'A' 'A'

'A' 'A' 'A' 'A' 'A' 'A' 'A'

'A' 'A' 'A' 'A' 'A' 'A' 'A'

'A' 'A' 'A' 'A' 'A' 'A' 'A'

'A' 'A' 'A' 'A' 'A' 'A' 'A'

'A' 'A' 'A' 'A' 'A' 'A' 'A'

'A' 'A' 'A' 'A' 'A' 'A' 'A'

'A' 'A' 'A' 'A' 'B' 'B' 'A'

'A' 'A' 'A' 'A' 'A' 'A' 'A'

'A' 'A' 'A' 'A' 'B' 'B' 'A'

test2.m

phenotype data, structure is matrix;

Example as follow:

15.9116666666667

16.0182461809274

18.1425479452055

19.1326666666667

19.7677342313112

20.0025687665425

21.1253559801179

16.7471428571429

15.1148267622461

15.3042608695652

test3.m

in the background of suinong 14, check the effect of allele gene; method were two independent sample t test.

test4.m-test7.m

the produced effect information of group was import into the matrix all, the nomenclature follow the test6.m

**test1**

[m,n]=size(da);

d=1;

 for j=1:n

 for k=j+1:n

 for i=1:m

p{i,d}=strcat(da{i,j},da{i,k});

 end

 d=d+1;

 end

 end

**test2**

[m,n]=size(p);

for r=1:n

x(r).AA=0;

x(r).AB=0;

x(r).AC=0;

x(r).BA=0;

x(r).BB=0;

x(r).BC=0;

x(r).CA=0;

x(r).CB=0;

x(r).CC=0;

k1=1;

k2=1;

k3=1;

k4=1;

k5=1;

k6=1;

k7=1;

k8=1;

k9=1;

for i=1:m

 if sum(p{i,r}=='AA')==2

 x(r).AA(k1,1)=data(i);

 k1=k1+1;

 elseif sum(p{i,r}=='AB')==2

 x(r).AB(k2,1)=data(i);

 k2=k2+1;

 elseif sum(p{i,r}=='AC')==2

 x(r).AC(k3,1)=data(i);

 k3=k3+1;

 elseif sum(p{i,r}=='BA')==2

 x(r).BA(k4,1)=data(i);

 k4=k4+1;

 elseif sum(p{i,r}=='BB')==2

 x(r).BB(k5,1)=data(i);

 k5=k5+1;

 elseif sum(p{i,r}=='BC')==2

 x(r).BC(k6,1)=data(i);

 k6=k6+1;

 elseif sum(p{i,r}=='CA')==2

 x(r).CA(k7,1)=data(i);

 k7=k7+1;

 elseif sum(p{i,r}=='CB')==2

 x(r).CB(k8,1)=data(i);

 k8=k8+1;

 elseif sum(p{i,r}=='CC')==2

 x(r).CC(k9,1)=data(i);

 k9=k9+1;

 end

end

end

**test3**

% test the difference of phenotype with each allele gene group

[m,n]=size(p);

for r=1:n

y(r).AA=10;

y(r).AB=10;

y(r).AC=10;

y(r).BA=10;

y(r).BB=10;

y(r).BC=10;

y(r).CA=10;

y(r).CB=10;

y(r).CC=10;

 if sum(x(r).AB~=0)~=0

 [h,p1,ci,stats1]=ttest2(x(r).AB,x(r).AA);

 y(r).AB(1)=p1;

 y(r).AB(2)=stats1.tstat;

 end

 if sum(x(r).AC~=0)~=0

 [h,p2,ci,stats2]=ttest2(x(r).AC,x(r).AA);

 y(r).AC(1)=p2;

 y(r).AC(2)=stats2.tstat;

 end

 if sum(x(r).BA~=0)~=0

 [h,p3,ci,stats3]=ttest2(x(r).BA,x(r).AA);

 y(r).BA(1)=p3;

 y(r).BA(2)=stats3.tstat;

 end

 if sum(x(r).BB~=0)~=0

 [h,p4,ci,stats4]=ttest2(x(r).BB,x(r).AA);

 y(r).BB(1)=p4;

 y(r).BB(2)=stats4.tstat;

 end

 if sum(x(r).BC~=0)~=0

 [h,p5,ci,stats5]=ttest2(x(r).BC,x(r).AA);

 y(r).BC(1)=p5;

 y(r).BC(2)=stats5.tstat;

 end

 if sum(x(r).CA~=0)~=0

 [h,p6,ci,stats6]=ttest2(x(r).CA,x(r).AA);

 y(r).CA(1)=p6;

 y(r).CA(2)=stats6.tstat;

 end

 if sum(x(r).CB~=0)~=0

 [h,p7,ci,stats7]=ttest2(x(r).CB,x(r).AA);

 y(r).CB(1)=p7;

 y(r).CB(2)=stats7.tstat;

 end

 if sum(x(r).CC~=0)~=0

 [h,p8,ci,stats8]=ttest2(x(r).CC,x(r).AA);

 y(r).CC(1)=p8;

 y(r).CC(2)=stats8.tstat;

 end

end

**test4**

% generate zuhe list

[m,n]=size(da)

d=1;

 for j=1:n

 for k=j+1:n

 id{d}(1,1)=j;

 id{d}(1,2)=k;

 d=d+1;

 id1=id';

 end

 end

**test5**

%combine the final table

%id1and y combine，generate a new structure

[m,n]=size(p);

for r=1:n

 z(r).id=id1{r};

 z(r).AA\_mean=mean(x(r).AA);

 z(r).AA\_num=length(x(r).AA);

 z(r).AB\_AA=y(r).AB;

 z(r).AB\_mean=mean(x(r).AB);

 z(r).AB\_num=length(x(r).AB);

 z(r).AC\_AA=y(r).AC;

 z(r).AC\_mean=mean(x(r).AC);

 z(r).AC\_num=length(x(r).AC);

 z(r).BA\_AA=y(r).BA;

 z(r).BA\_mean=mean(x(r).BA);

 z(r).BA\_num=length(x(r).BA);

 z(r).BB\_AA=y(r).BB;

 z(r).BB\_mean=mean(x(r).BB);

 z(r).BB\_num=length(x(r).BB);

 z(r).BC\_AA=y(r).BC;

 z(r).BC\_mean=mean(x(r).BC);

 z(r).BC\_num=length(x(r).BC);

 z(r).CA\_AA=y(r).CA;

 z(r).CA\_mean=mean(x(r).CA);

 z(r).CA\_num=length(x(r).CA);

 z(r).CB\_AA=y(r).CB;

 z(r).CB\_mean=mean(x(r).CB);

 z(r).CB\_num=length(x(r).CB);

 z(r).CC\_AA=y(r).CC;

 z(r).CC\_mean=mean(x(r).CC);

 z(r).CC\_num=length(x(r).CC);

end

**test6**

%control for z

s=length(z);

for i=1:s

 all(i,1)=z(i).id(1);

 all(i,2)=z(i).id(2);

 all(i,3)=z(i).AA\_mean;

 all(i,4)=z(i).AA\_num;

 all(i,5)=z(i).AB\_AA(1);

 all(i,6)=z(i).AB\_mean;

 all(i,7)=z(i).AB\_num;

 all(i,8)=z(i).AC\_AA(1);

 all(i,9)=z(i).AC\_mean;

 all(i,10)=z(i).AC\_num;

 all(i,11)=z(i).BA\_AA(1);

 all(i,12)=z(i).BA\_mean;

 all(i,13)=z(i).BA\_num;

 all(i,14)=z(i).BB\_AA(1);

 all(i,15)=z(i).BB\_mean;

 all(i,16)=z(i).BB\_num;

 all(i,17)=z(i).BC\_AA(1);

 all(i,18)=z(i).BC\_mean;

 all(i,19)=z(i).BC\_num;

 all(i,20)=z(i).CA\_AA(1);

 all(i,21)=z(i).CA\_mean;

 all(i,22)=z(i).CA\_num;

 all(i,23)=z(i).CB\_AA(1);

 all(i,24)=z(i).CB\_mean;

 all(i,25)=z(i).CB\_num;

 all(i,26)=z(i).CC\_AA(1);

 all(i,27)=z(i).CC\_mean;

 all(i,28)=z(i).CC\_num;

end

**test7**

k=1;

u0=41.34;

for i=1:7260

 if all(i,14)<0.01

 u=(z(i).AB\_mean+z(i).BA\_mean);

 [h,p\_value(k,1)]=ttest(x(i).BB+u0,u);

 all\_BB\_BA\_AB\_back(k,1)=all(i,1);

 all\_BB\_BA\_AB\_back(k,2)=all(i,2);

 all\_BB\_BA\_AB\_back(k,3)=p\_value(k,1)

 k=k+1;

 end

end