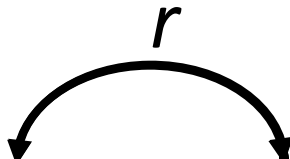


Multivariate association analysis

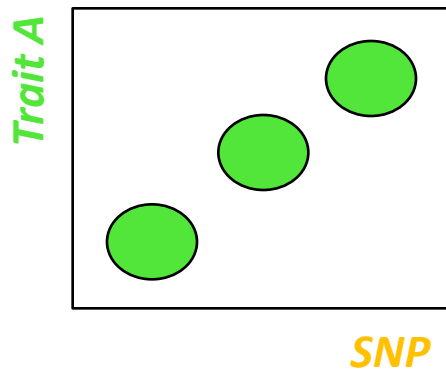
Manuel Ferreira & Shaun Purcell

Boulder, 2009

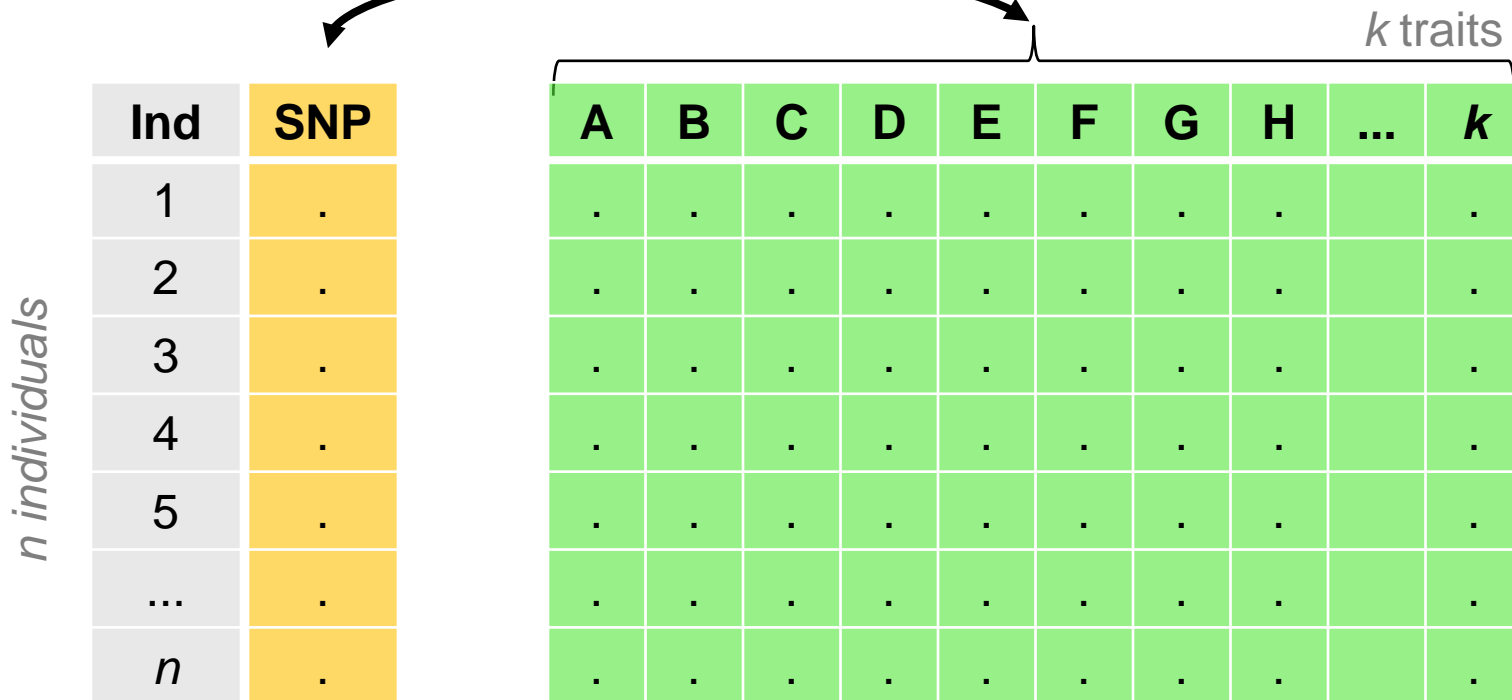
r



Ind	SNP	A	B	C	D	E	F	G	H	I	J
1
2
3
4
5
...
N



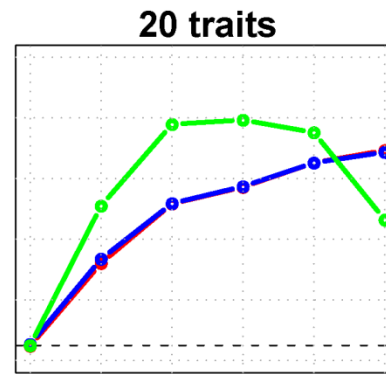
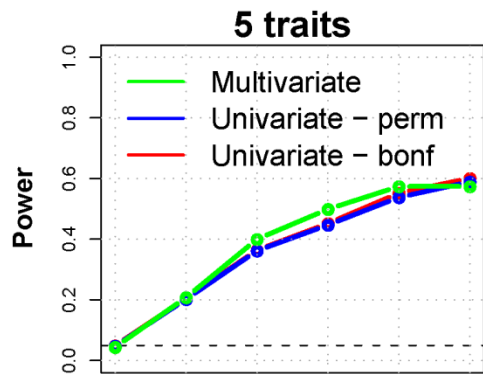
Canonical correlation



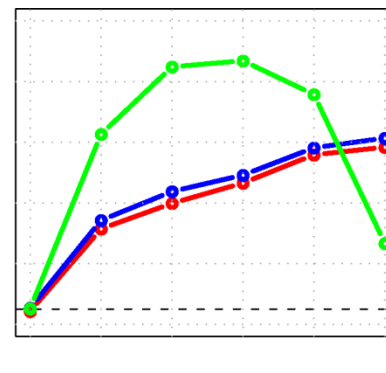
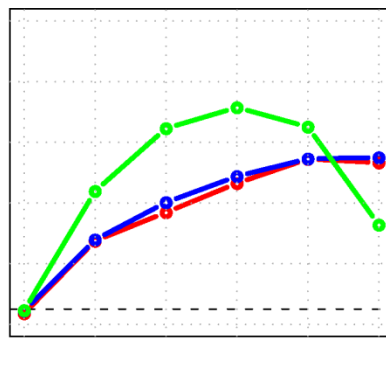
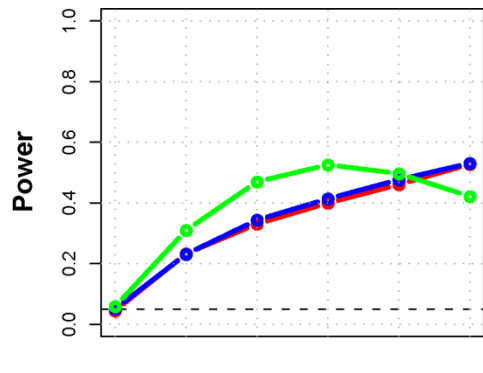
$\hat{\rho}$
SNP Score = $w_A * A + w_B * B + \dots + w_J * J$

$$F_{(k, n-k-1)} = \left[\frac{(1-\lambda)}{\lambda} \right] \cdot \left[\frac{(n-k-1)}{k} \right]$$

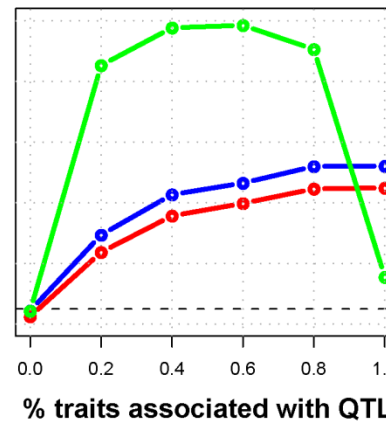
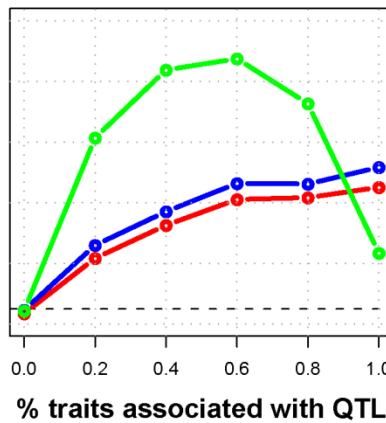
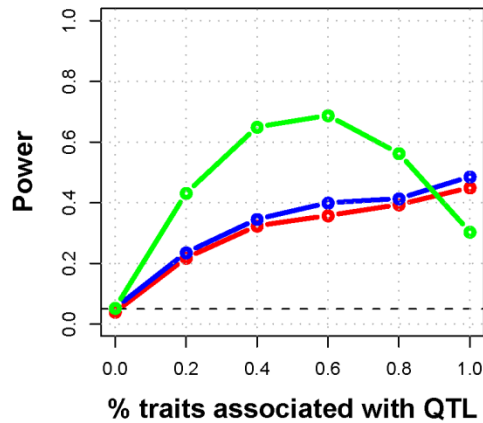
$$\lambda = 1 - \hat{\rho}^2$$



$r = 0.2$



$r = 0.4$

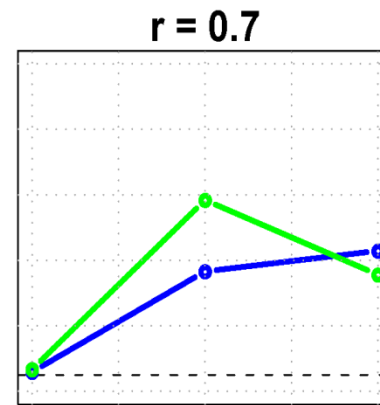
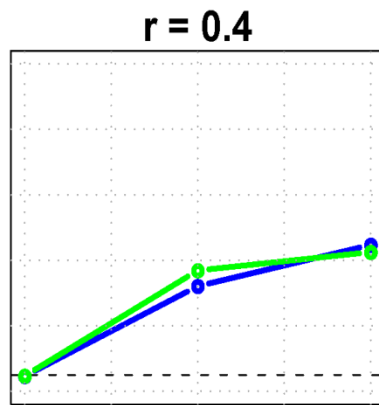
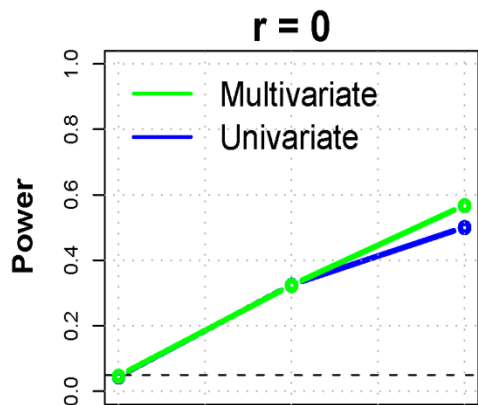


$r = 0.6$

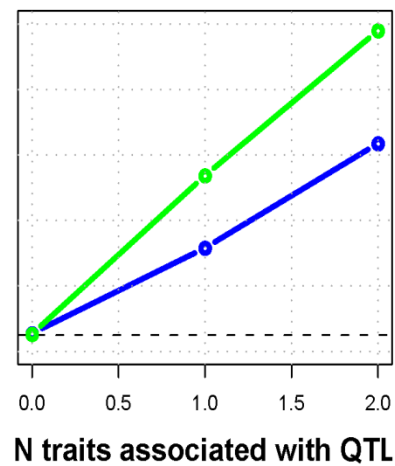
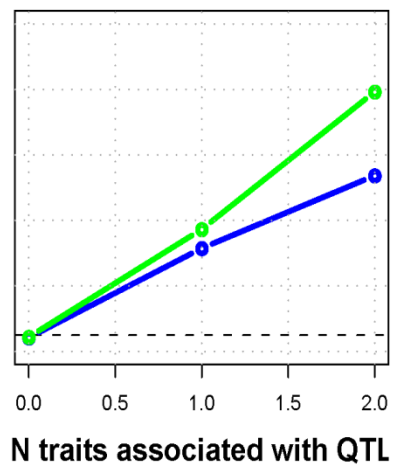
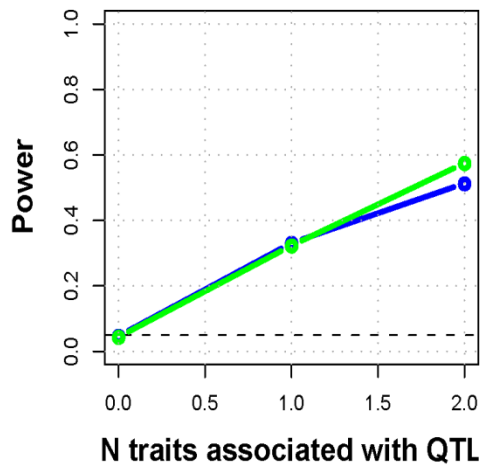
% traits associated with QTL

% traits associated with QTL

% traits associated with QTL



Same



Opposite

plink.multivariate

<http://genepi.qimr.edu.au/staff/manuelF/>

FILES:

[contents of modell.ped]

```
1 1 0 0 1 1 A A
2 1 0 0 1 1 A B
3 1 0 0 1 1 A A
4 1 0 0 1 1 A A
5 1 0 0 1 1 A A
6 1 0 0 1 1 A B
```

[contents of modell.phen]

```
1 1 1.050 -0.127 -0.327 0.899
2 1 0.255 -2.765 -0.15 -1.426
3 1 0.033 1.664 0.355 0.394
4 1 0.501 -0.657 -0.58 -0.012
5 1 0.025 1.242 1.012 1.132
6 1 0.786 0.495 -0.667 1.662
```

USAGE:

```
./plink.multivariate --file modell --covar modell.phen --mqfam
```

OUTPUT:

CHR	SNP	BP	NFAM	NIND	F	P	WEIGHTS
1	test	0	500	500	5.329	1.75e-07	-0.4264,-0.4766,-0.5416,-0.353

MODEL1

SNP	Beta	Univariate P
-----	------	----------------

1	3.01	0.002746
2	3.372	0.0008032
3	3.845	0.0001363
4	2.485	0.01329
5	0.622	0.5339
6	1.105	0.2697
7	-0.364	0.7159
8	-0.686	0.493
9	0.896	0.3704
10	-0.158	0.8738

Multivariate P 1.75e-07

MODEL2

SNP	Beta	Univariate P
-----	------	----------------

1	4.528	7.444e-06
2	2.362	0.01854
3	-2.802	0.005278
4	-2.607	0.00941
5	-0.366	0.7144
6	0.0938	0.9253
7	-0.086	0.931
8	0.1062	0.9154
9	0.6103	0.542
10	-0.122	0.9024

Multivariate P 1.404e-06