Genomic BLUP

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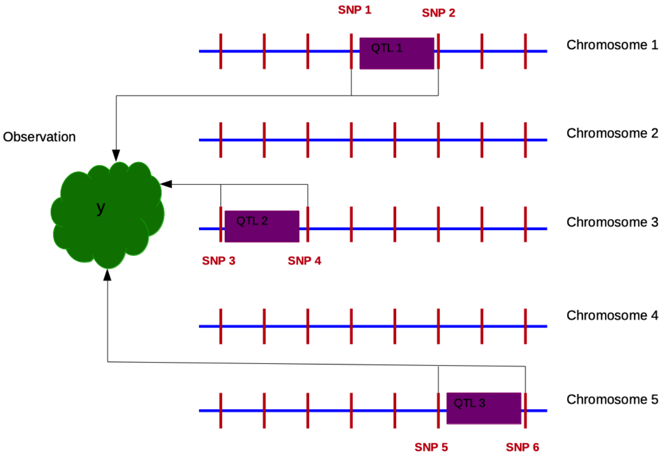
So Far

- Estimate effect of few SNP loci linked to QTL
- Use parameter estimates to predict genomic breeding values
- **New**: Many SNP, find the important ones

Situation



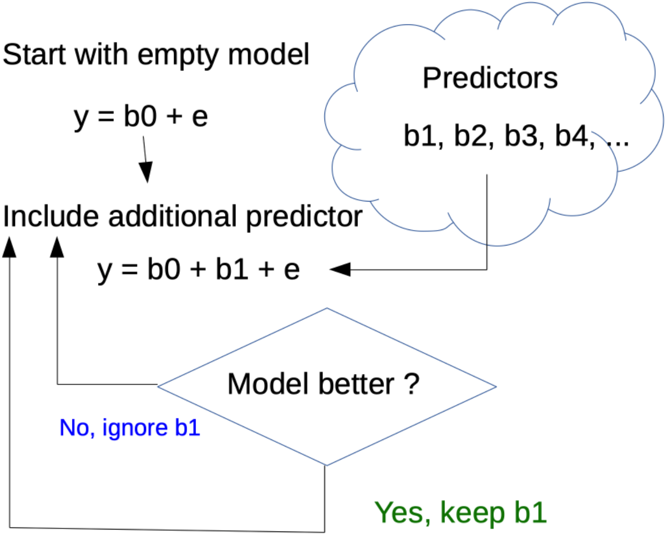
Goal: Find SNP 1 – SNP 6 out of the many SNPs

Approaches in Fixed Linear Model Framework

Two Approaches

1. Forward selection: Start with empty model, include predictors that improve model
2. Backward elimination: Start with full model, remove predictors as long as model does not get worse

Forward Selection



Start with empty model

y = b0 + e

Include additional predictor

Predictors

b1, b2, b3, b4, ...

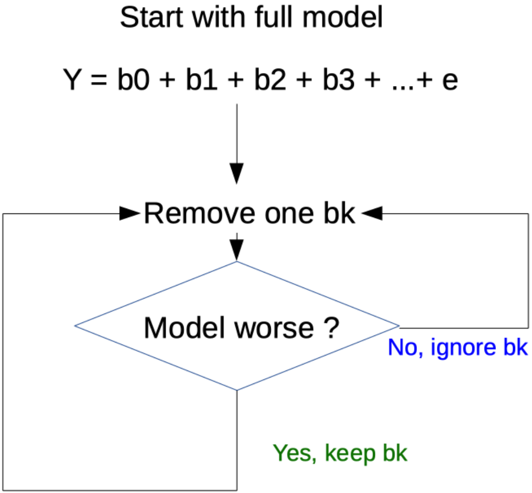
y = b0 + b1 + e

Model better ?

No, ignore b1

Yes, keep b1

Backward Elimination



Start with full model

Y = b0 + b1 + b2 + b3 + ...+ e

Remove one bk

Model worse ?

No, ignore bk

Yes, keep bk

Model Selection With Genomic Data

- Only backward elimination really works in practical problems
- Large number of predictors $(1.5 * 10^5)$
- How to determine sequence of predictors to eliminate
- Fitting the full model is problematic

Mixed Linear Effect Model

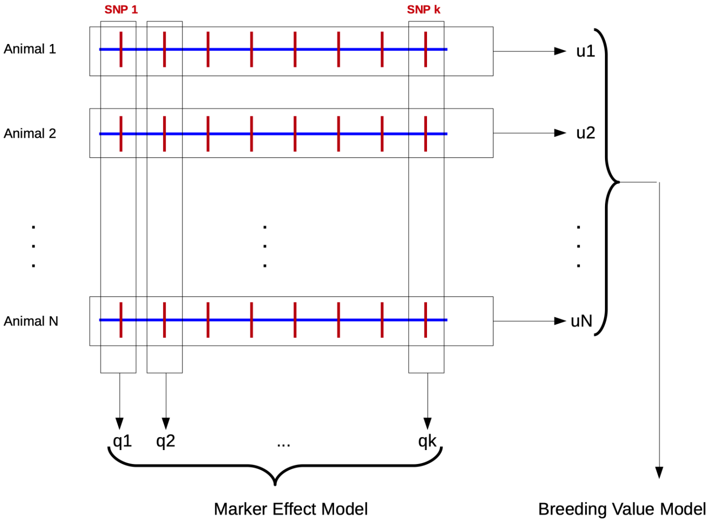
- One solution: replace fixed linear effect model by **mixed** linear effect model (mle)
- MLE: additional random effect besides error term
- Random effects are specified by expected value and variance
- In livestock breeding MLE have a good reputation from BLUP animal model

MLE In Genomics

- Two different parametrizations

1. Marker Effect Model (MEM)
2. Breeding Value Model (BVM)

Overview


SNP 1
SNP k
Animal 1
Animal 2
Animal N
u1
u2
uN
q1
q2
...
qk
Marker Effect Model
Breeding Value Model

Marker Effect Model

In MEM random effects of markers are directly included in the model. For an idealized data set we can write

$$y = 1_n\mu + Wq + e$$

where

y	vector of length n with observations
μ	general mean denoting fixed effects
1_n	vector of length n of all ones
q	vector of length m of random SNP effects
W	design matrix relating SNP-genotypes to observations
e	vector of length n of random error terms

Breeding Value Model

$$y = Xb + Zg + e$$

where

y	vector of length n with observations
b	vector of length r with fixed effects
X	incidence matrix linking elements in b to observations
g	vector of length t with random genomic breeding values
Z	incidence matrix linking elements in g to observations
e	vector of length n of random error terms