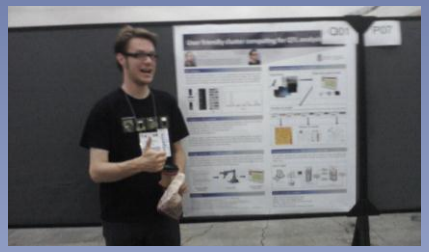
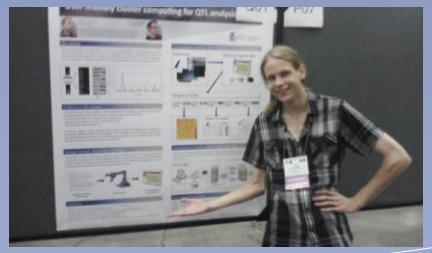
Quantitative trait likelihood analysis

Developing clever tools to mine large volumes of biotech data





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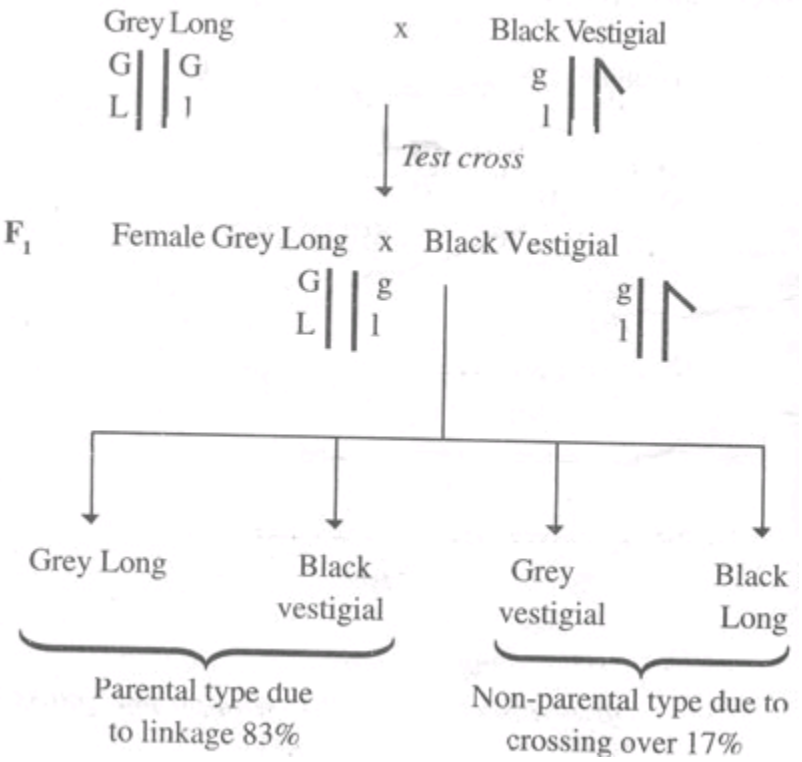
Overview

* Quantitative Trait
* History
  * 1917 Thomas Morgan and the map
  * 1989 E. S. Lander and D. Botstein
* Likelihood
* Huge data challenge
* Our sollution

Quantitative Trait

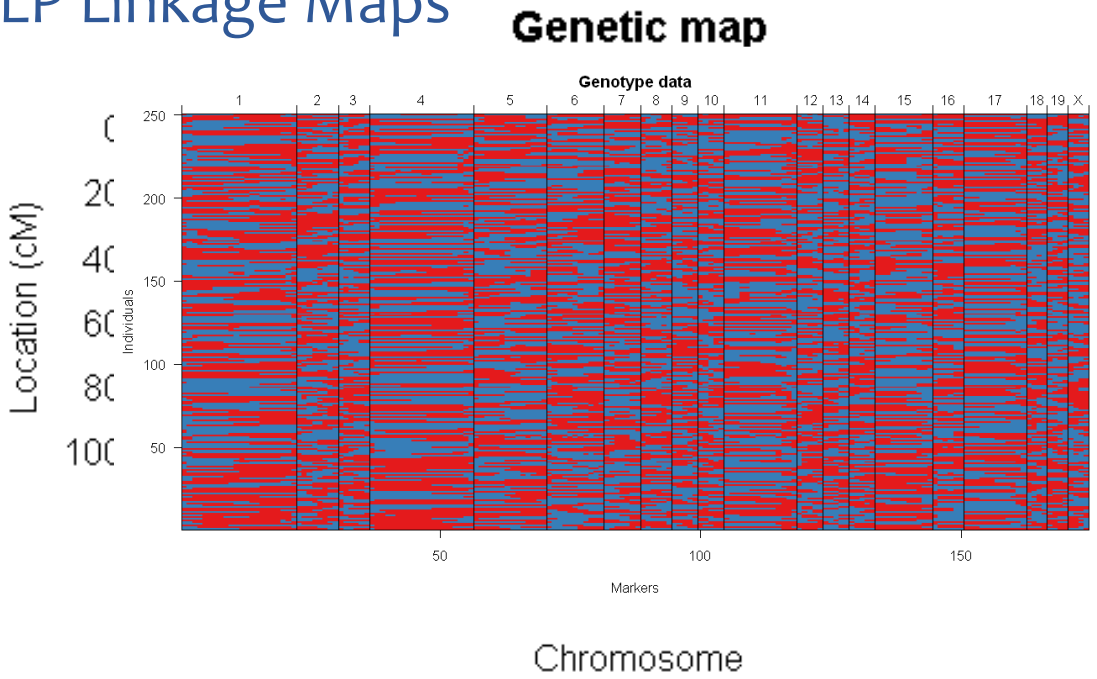
1917 Thomas Morgan and the map

* Linkage / Co-Inheritance
* Genetic map



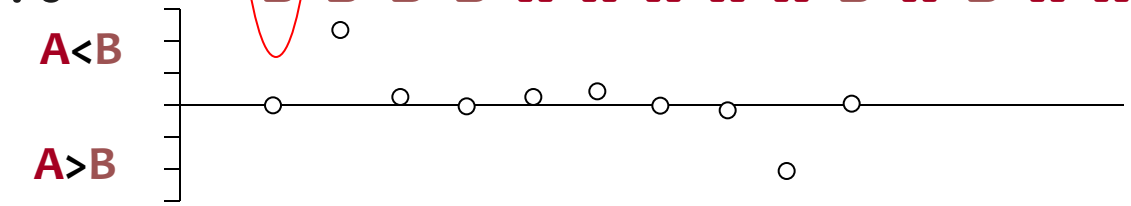
1989 E. S. Lander and D. Botstein

Mapping Mendelian Factors Underlying Quantitative Traits Using RFLP Linkage Maps



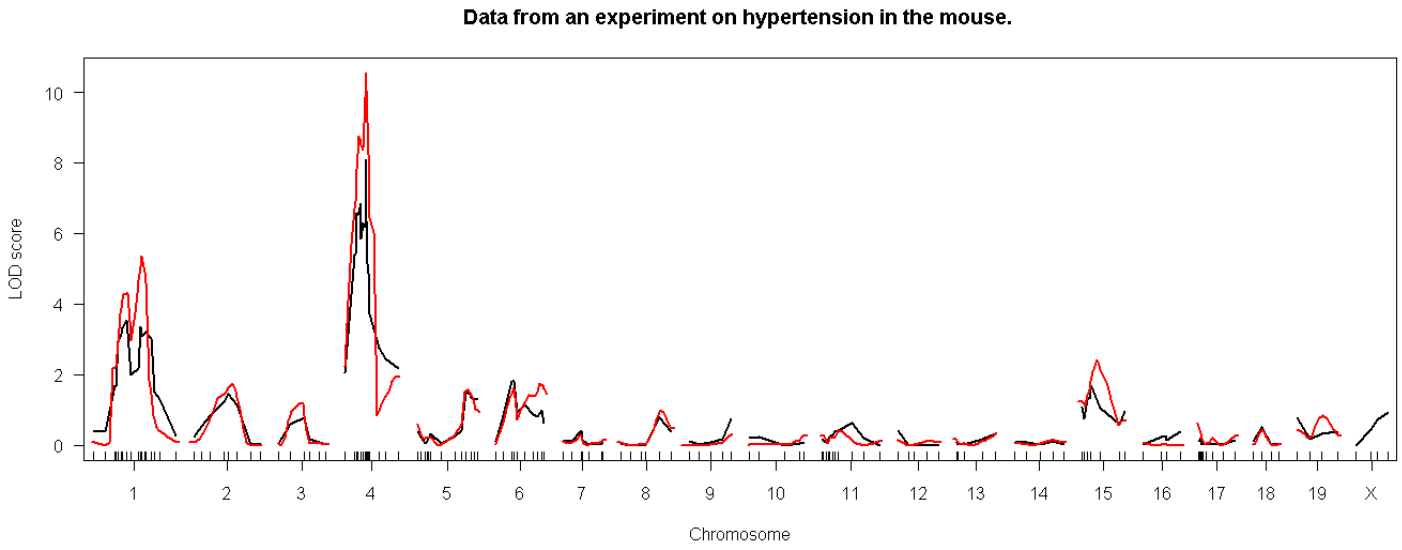
Quantitative Trait Likelihood analysis

Weight	Genotype
6.0	B A B B B A B A B A B A B B B A B A B A
6.5	A A B A B A B B B B B A B B B A B A B A
7.0	B A A B B B A A B B B A A B A A B B A A
7.1	A A A B A A B B B A A A A B A A B B A A
7.5	B A B A A A B B B A A B A A B A B A A B
8.3	A B A A A A B A A A A B A A B A B A A B
8.6	A B B A A B A A A B A A A B B A B B A B
8.9	A B A B B B B B A A A B A A A A B A A B
9.1	B B A B A B A B A B A B A A A A B A A A
9.6	B B B B A A A A A B A B A A A A B A A A



Example

* LOD = Log (ODD)

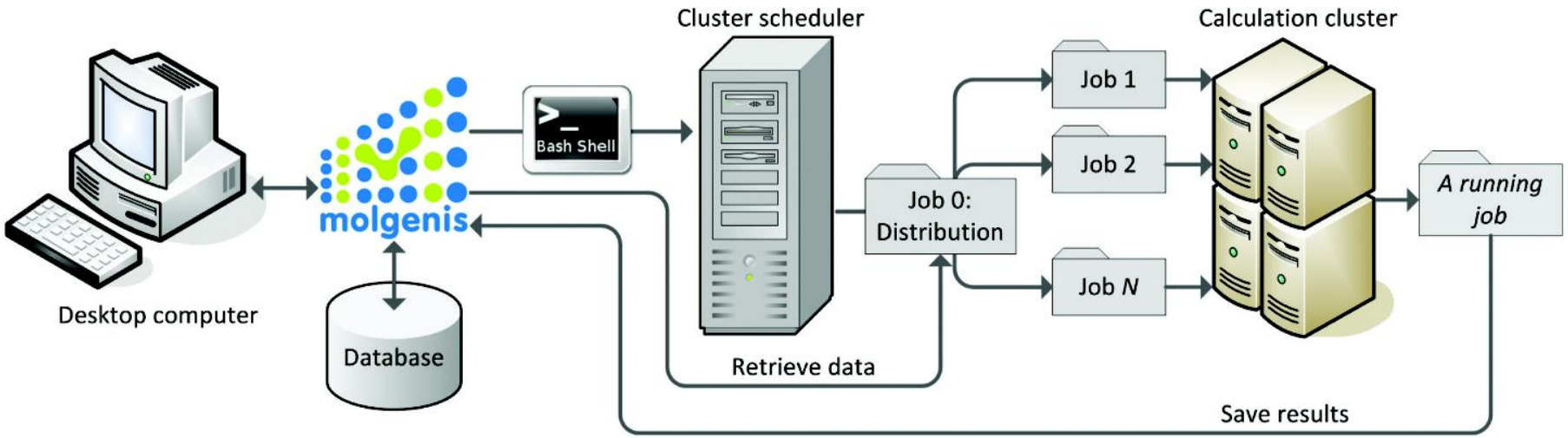


Huge data challenge
Traits

* SNP/CNV genetic markers
* RNA abundance
* Protein abunance
* Metabolite abunance
* Metabolite flux

? What to use ?

Our sollution



Conclusions

* Traits, History, QTL
* Huge data challenge
* OUR sollution

challenges ahead ?

* ??? NEW MAP ???

* Epigenetics
  * Inheritance
  * stability rules