

# Networks

RUG

## Networks

Danny Arends

GBIC, RUG

Prof. Dr R. Jansen GBIC, RUG

Ir. JCP. Prins

WUR, Wageningen

Karl W. Broman

University of Wisconsin

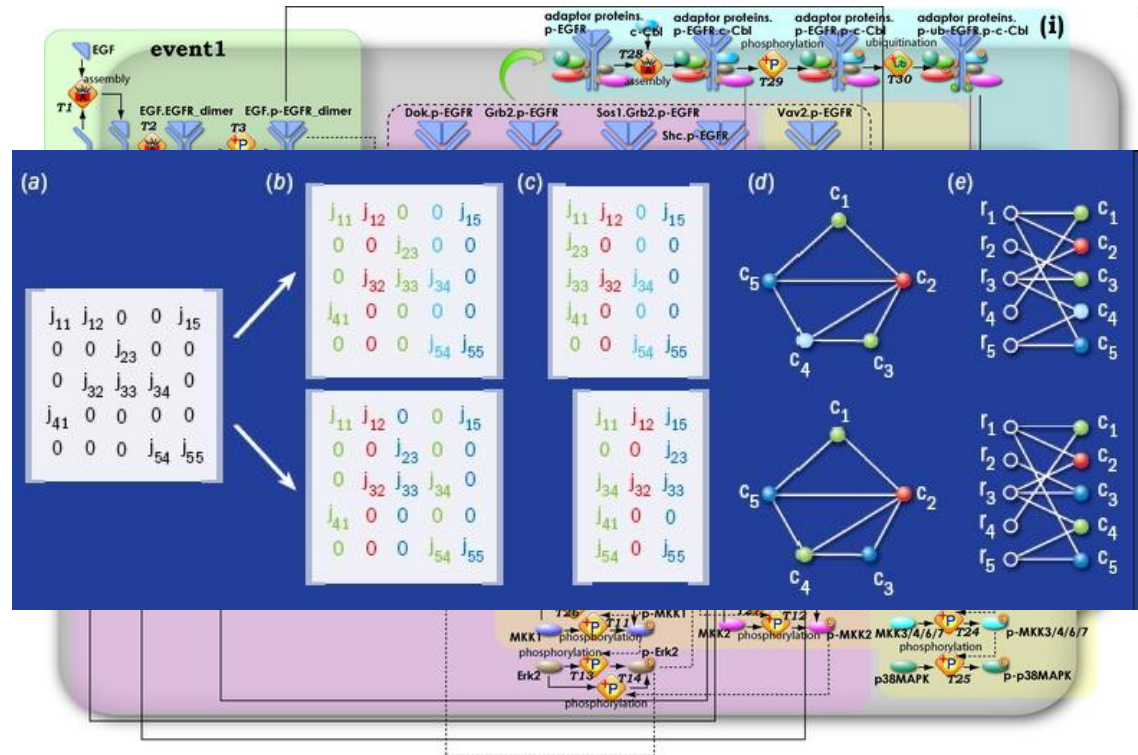
# Overview

RuG

- Networks
  - Causality / Regulatory
  - Interaction
- QTL mapping
- Peak detection
- Causal inference

# Network

- Is a Model
- Consists of:
  - Nodes
  - Edges



# Causal biological networks

RuG

- Nodes: Genes, Protein, Metabolites
- Edges: Causality
- Problems:
  - What is causality ?
  - What does causality tell us ?
  - Depending on environment ?
- Detectable using basic Genetical Genomics

# Biological interaction networks

RuG

- Pathway / Switchboards
- What happens in time to the system
- More elaborate because we need to embed our model into an environment
  
- Not detectable using basic Genetical Genomics
- Timecourse information needed

# Visualization

RuG

- Using external tools
  - Cytoscape
  - Igraph package
  - Java2d
  
- Tools / Simulation in models
  - Petri nets
  - Metabolic models

# DOGMA

RuG

DNA -> Storing information

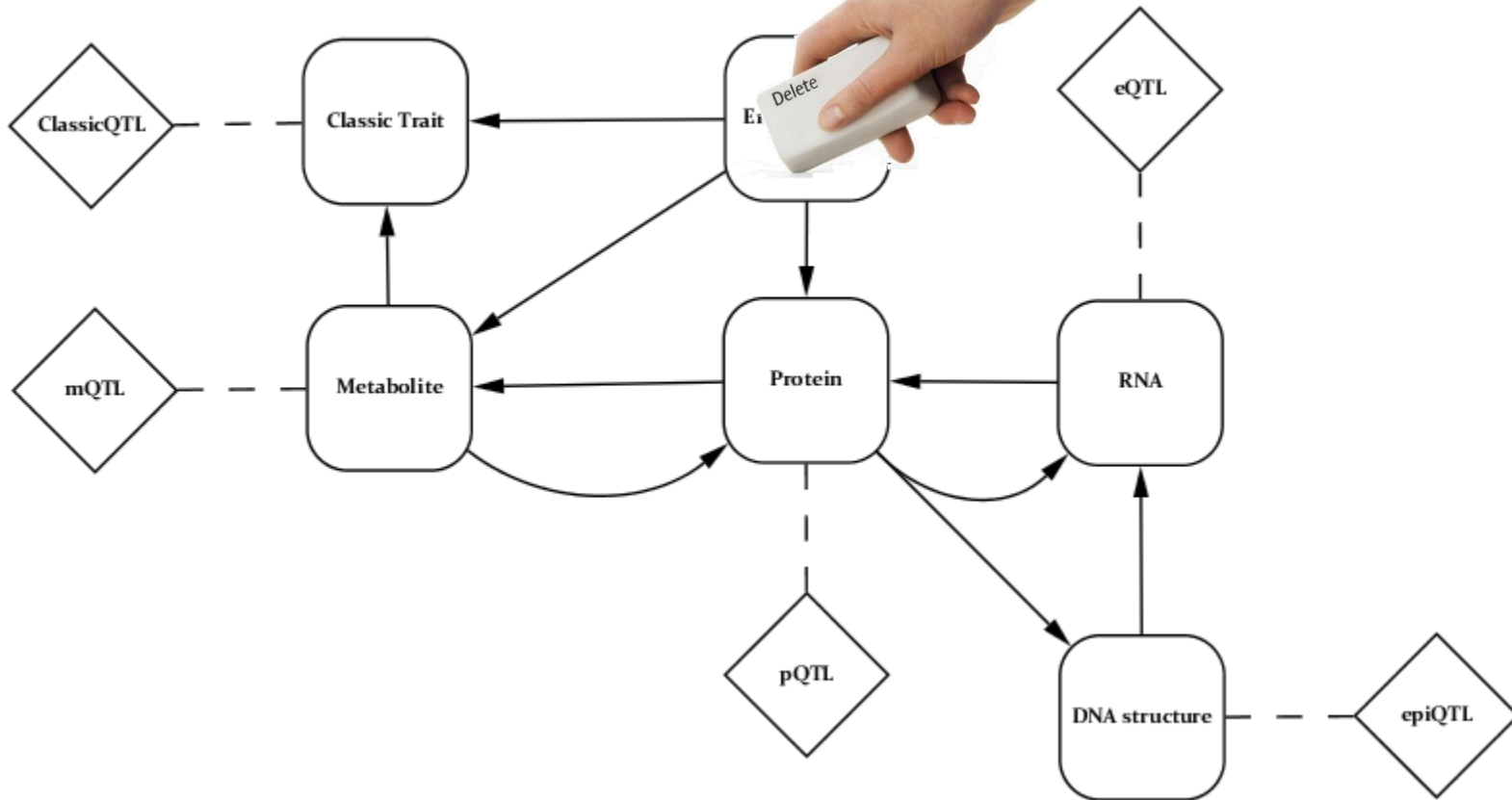
RNA -> Transporting information

PROTEIN -> Effector molecules

METABOLITE -> Goal or function

# Dogma in Network

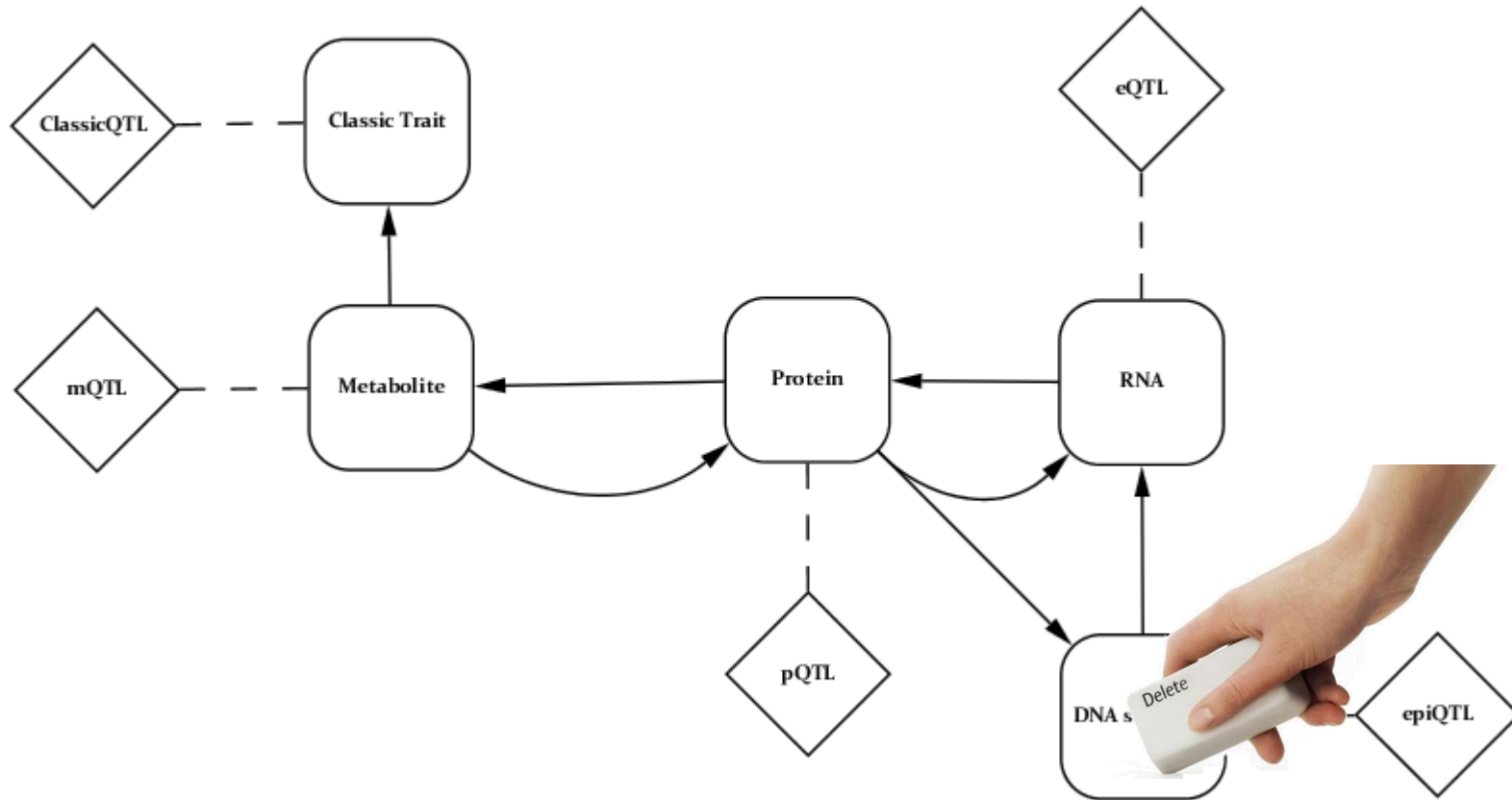
RUG





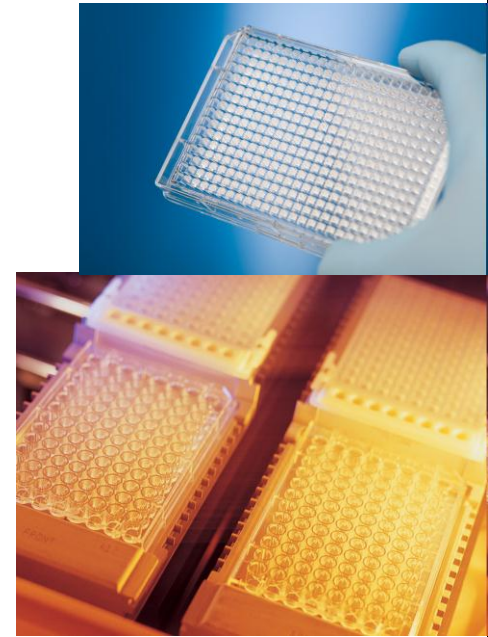
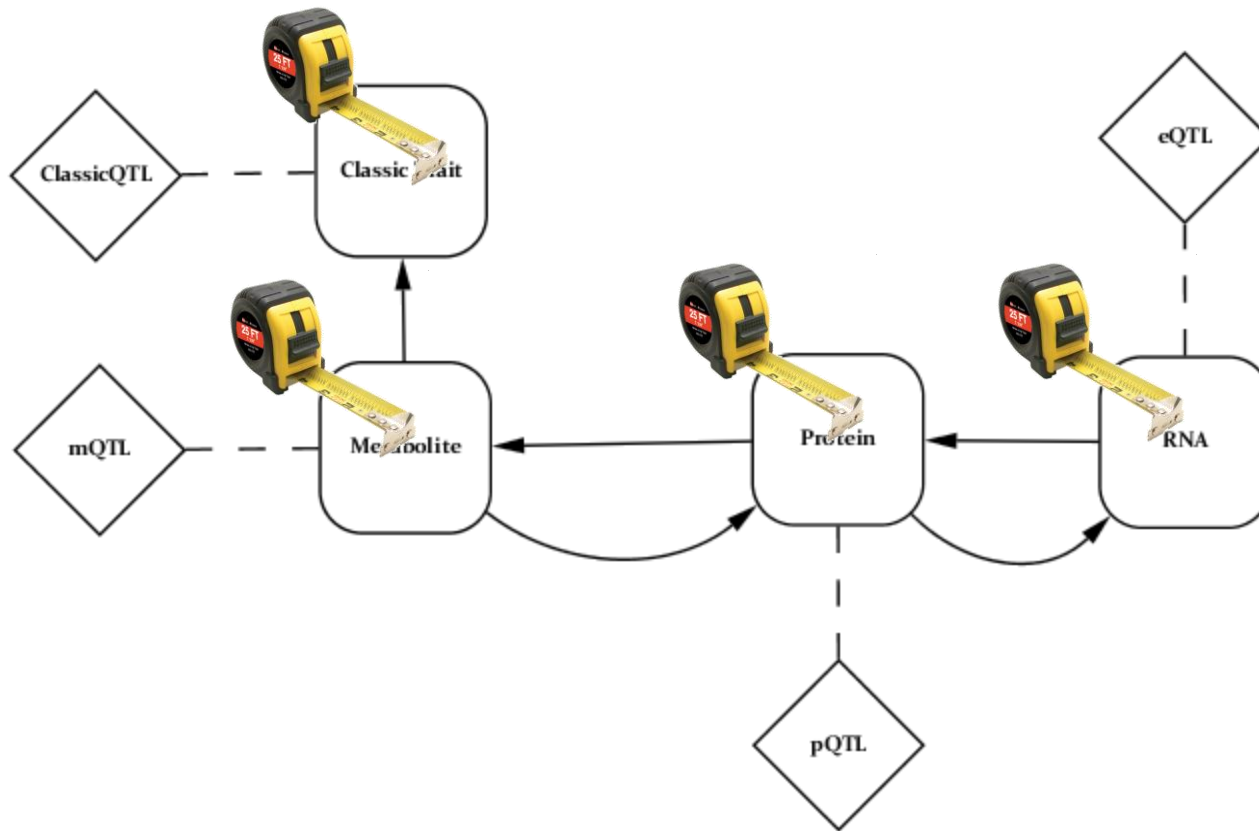
# Reducing the model

RUG



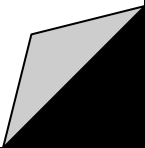
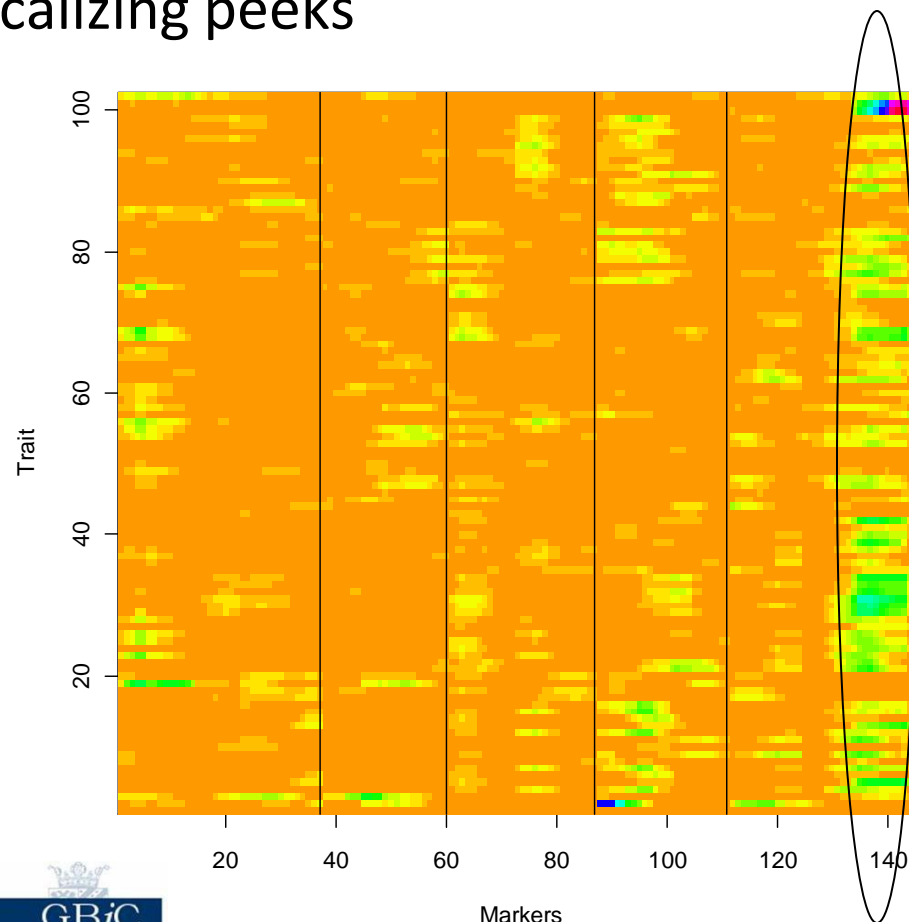
# Reduced Model

RUG



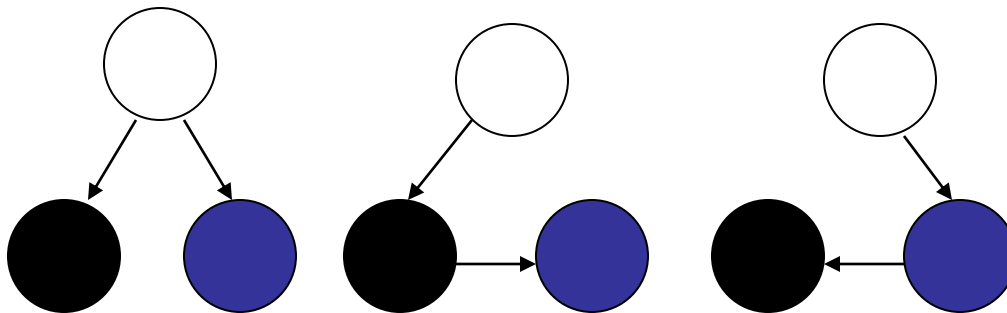
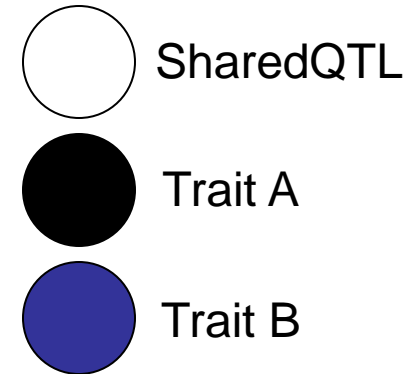
# QTL analysis

- Find regulatory locations for traits
- Find co-localizing peaks

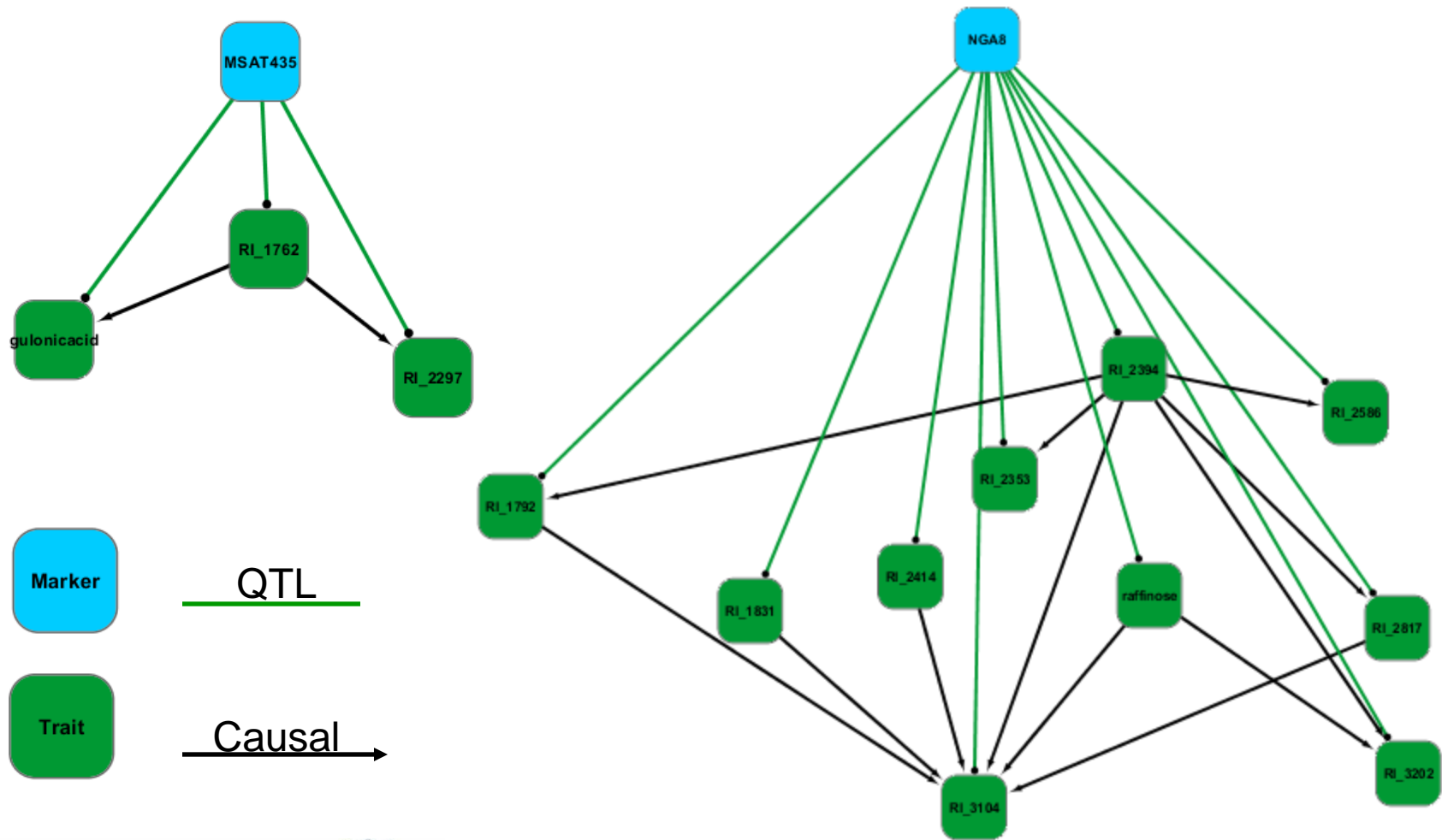


# Network inference

- Regression of traits that share a QTL
- Mapping the residuals
  - Causal
  - Independent
  - Undecided



# So how does this look like



# Questions

RuG

