

# **Computational Infrastructure for Systems Genetics Analysis**

**Brian Yandell, UW-Madison**

**high-throughput analysis of systems data  
enable biologists & analysts to share tools**

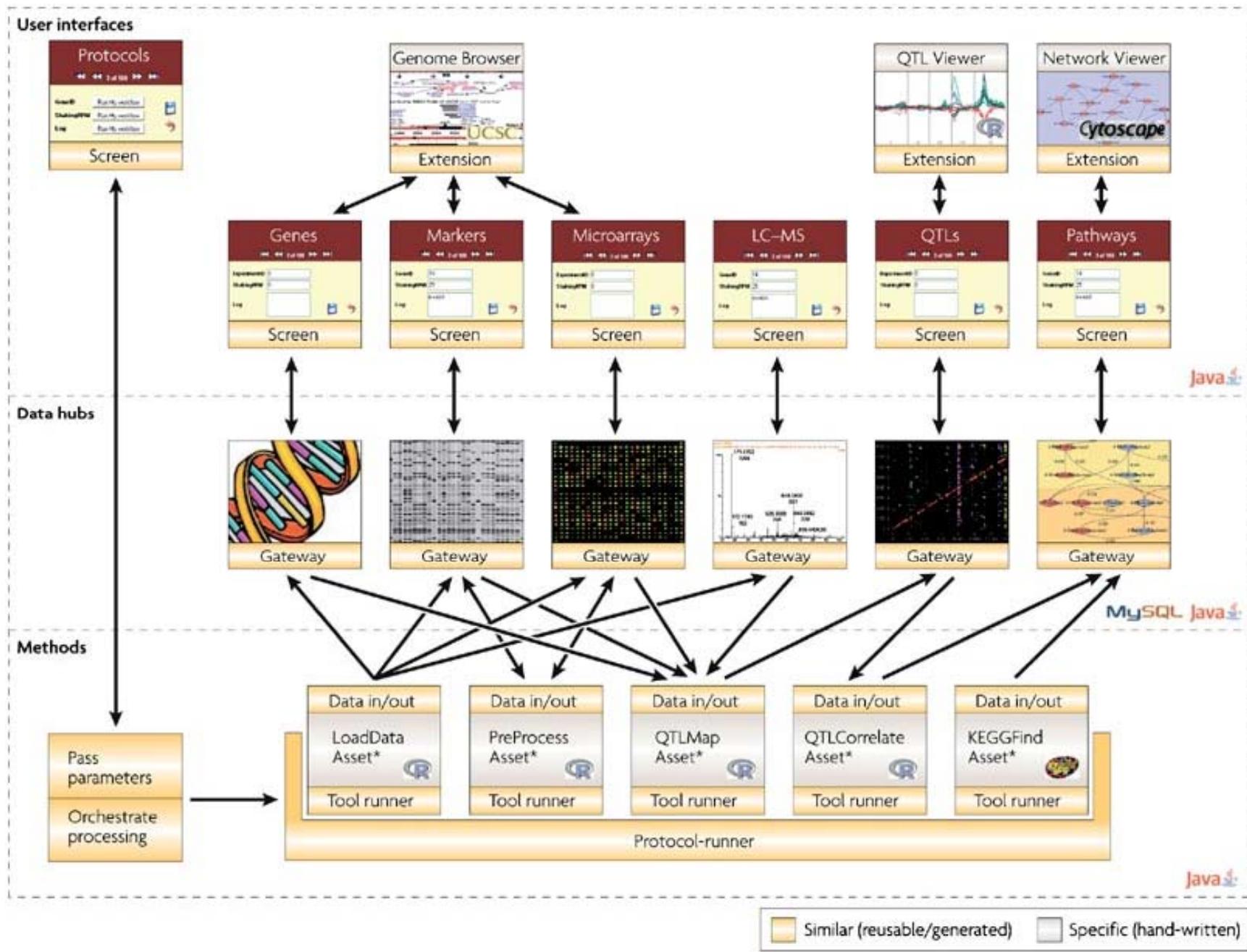
**UW-Madison:** Yandell, Attie, Broman, Kendzioriski

**Jackson Labs:** Churchill

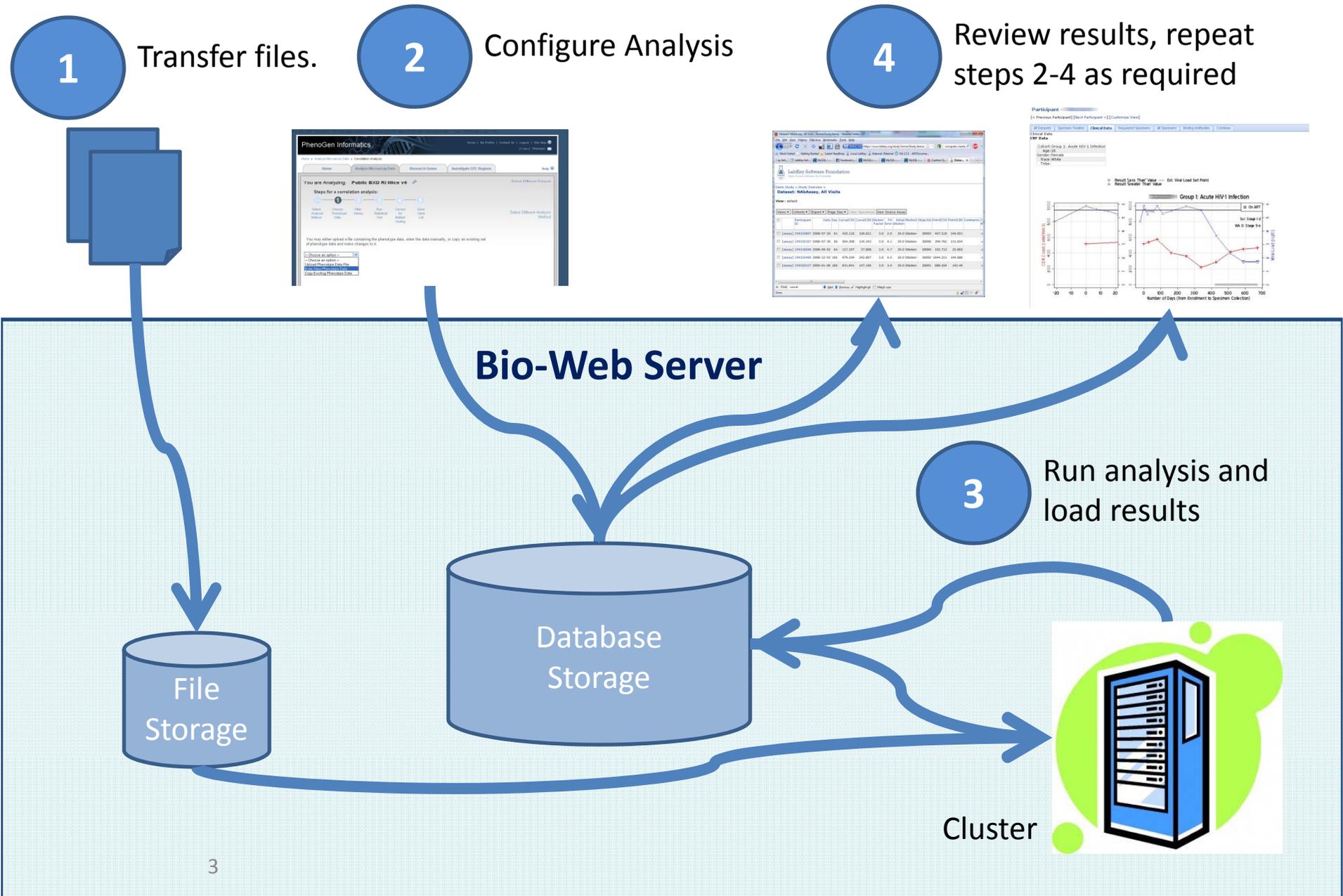
**U Groningen:** Jansen, Swertz

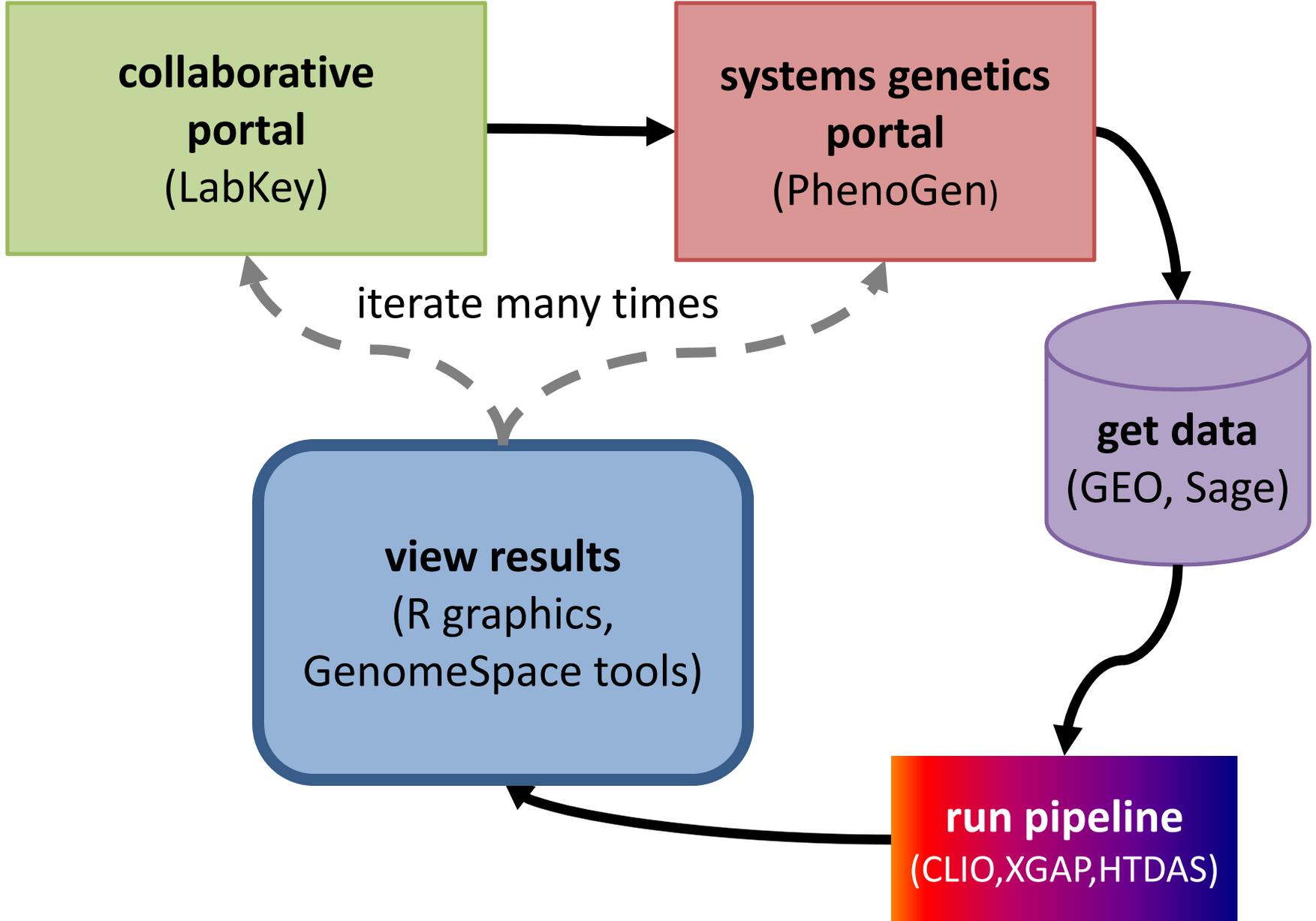
**UC-Denver:** Tabakoff

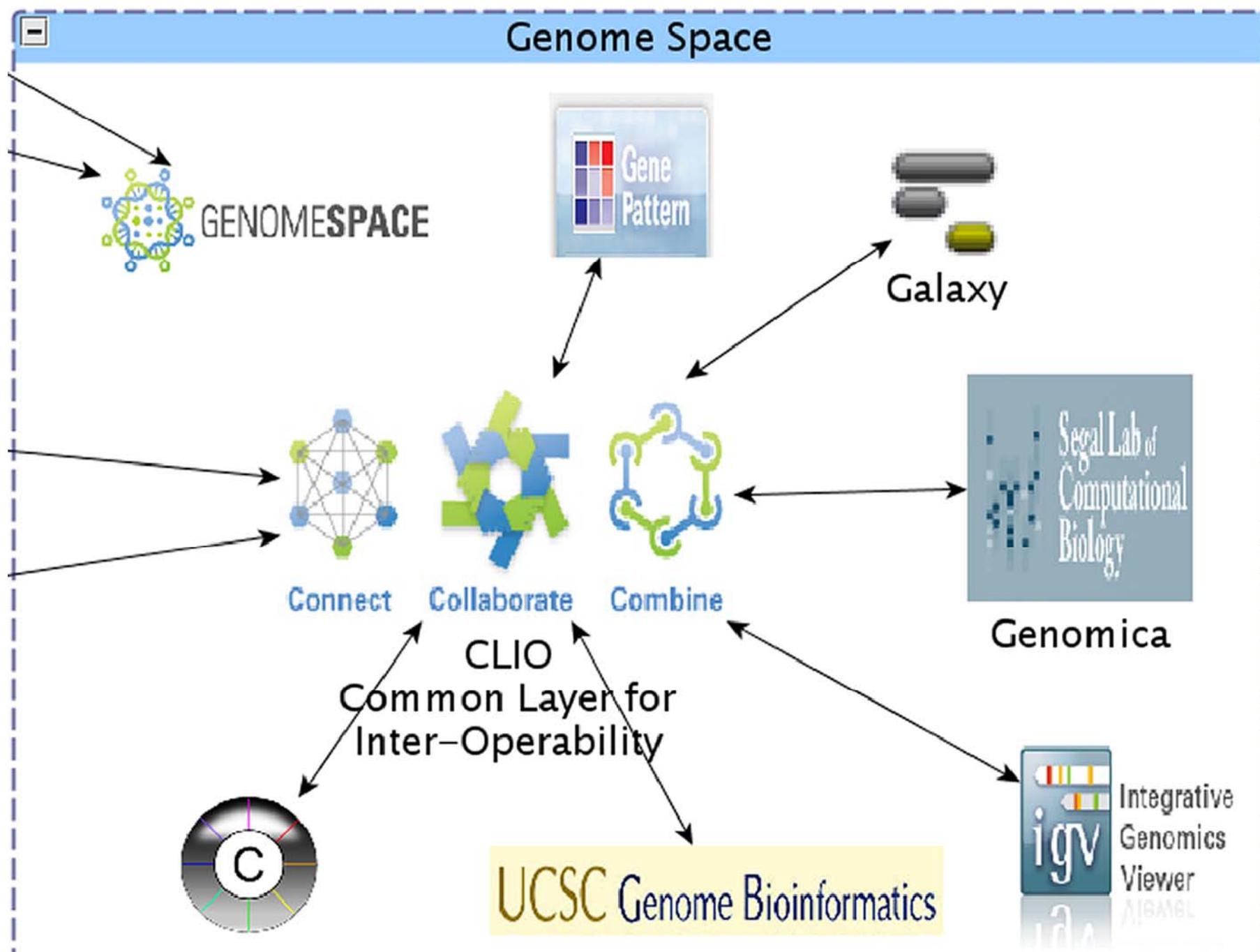
**LabKey:** Igra



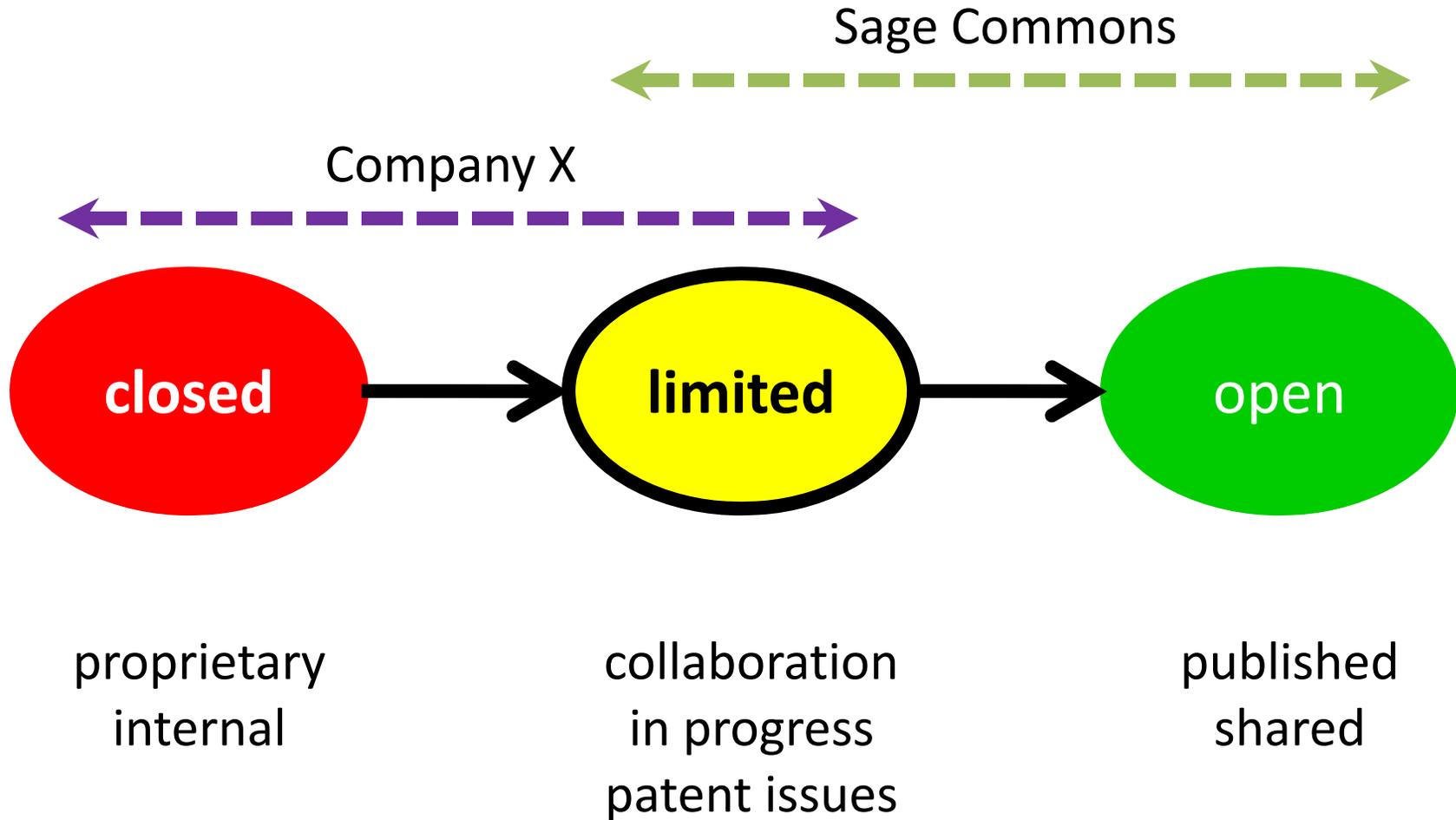
# typical workflow (from Mark Igra, LabKey)



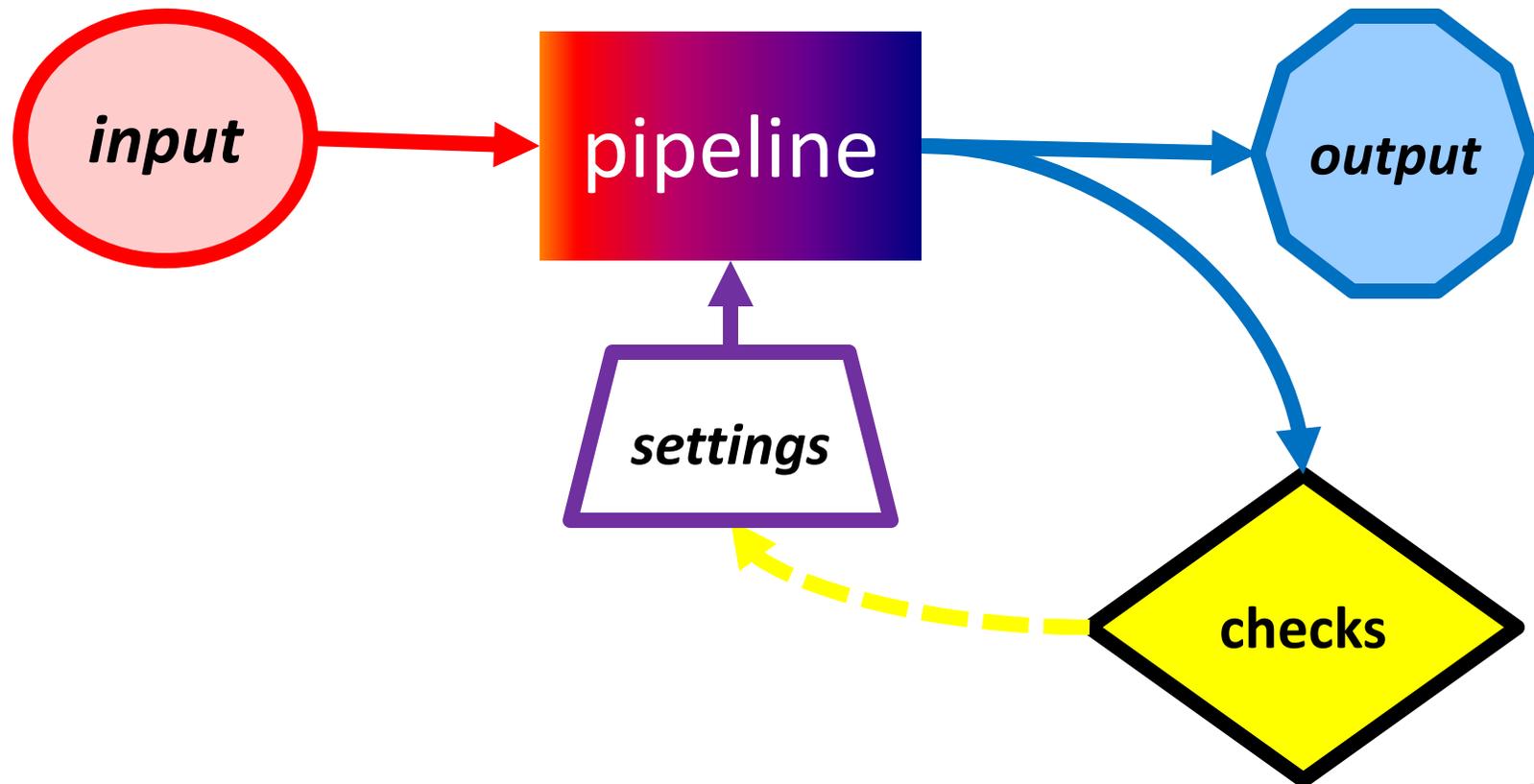




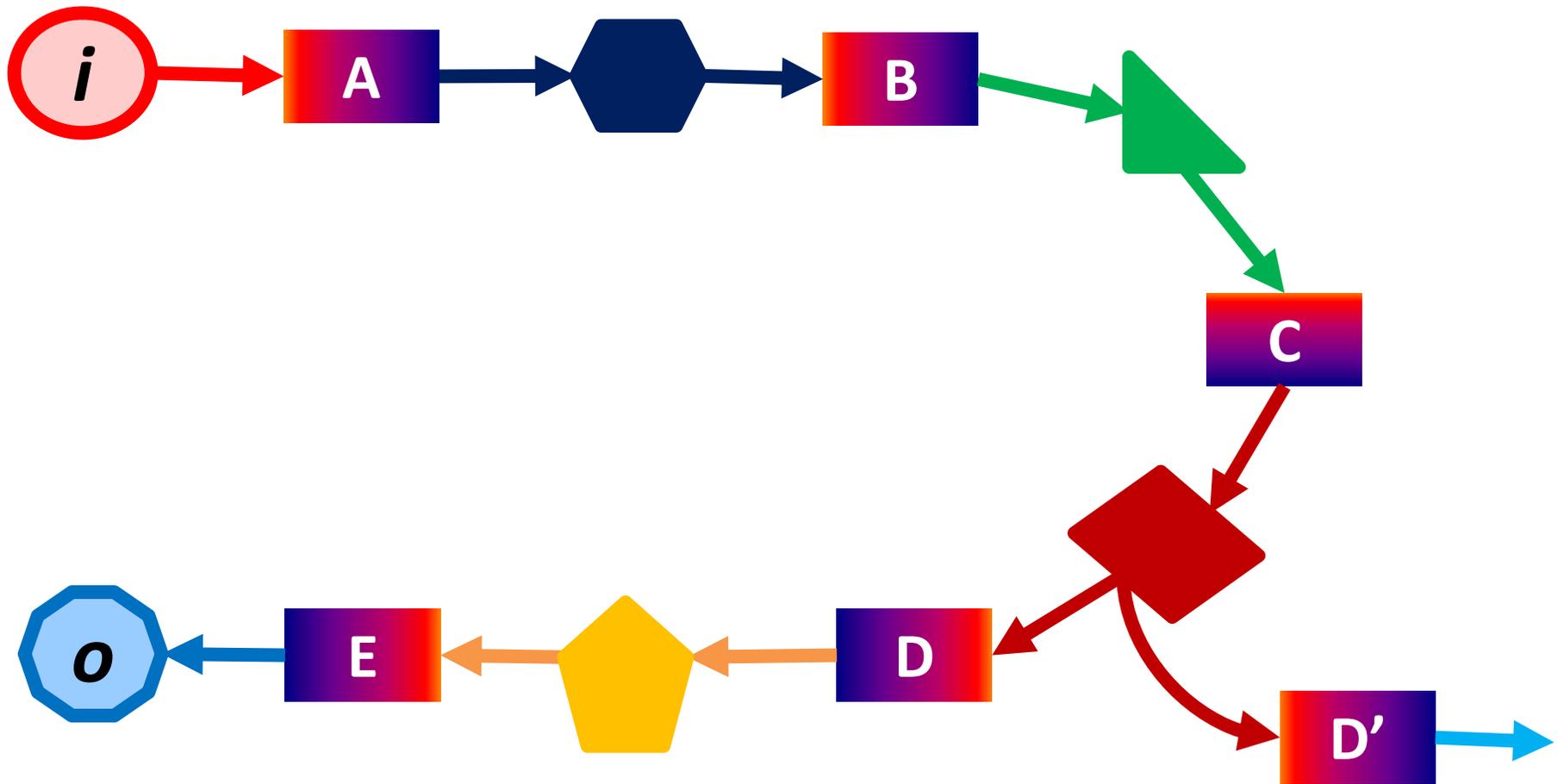
# data access model



analysis pipeline acts on objects  
(extends concept of GenePattern)



pipeline is composed of many steps



# causal model selection choices in context of larger, unknown network



causal



reactive

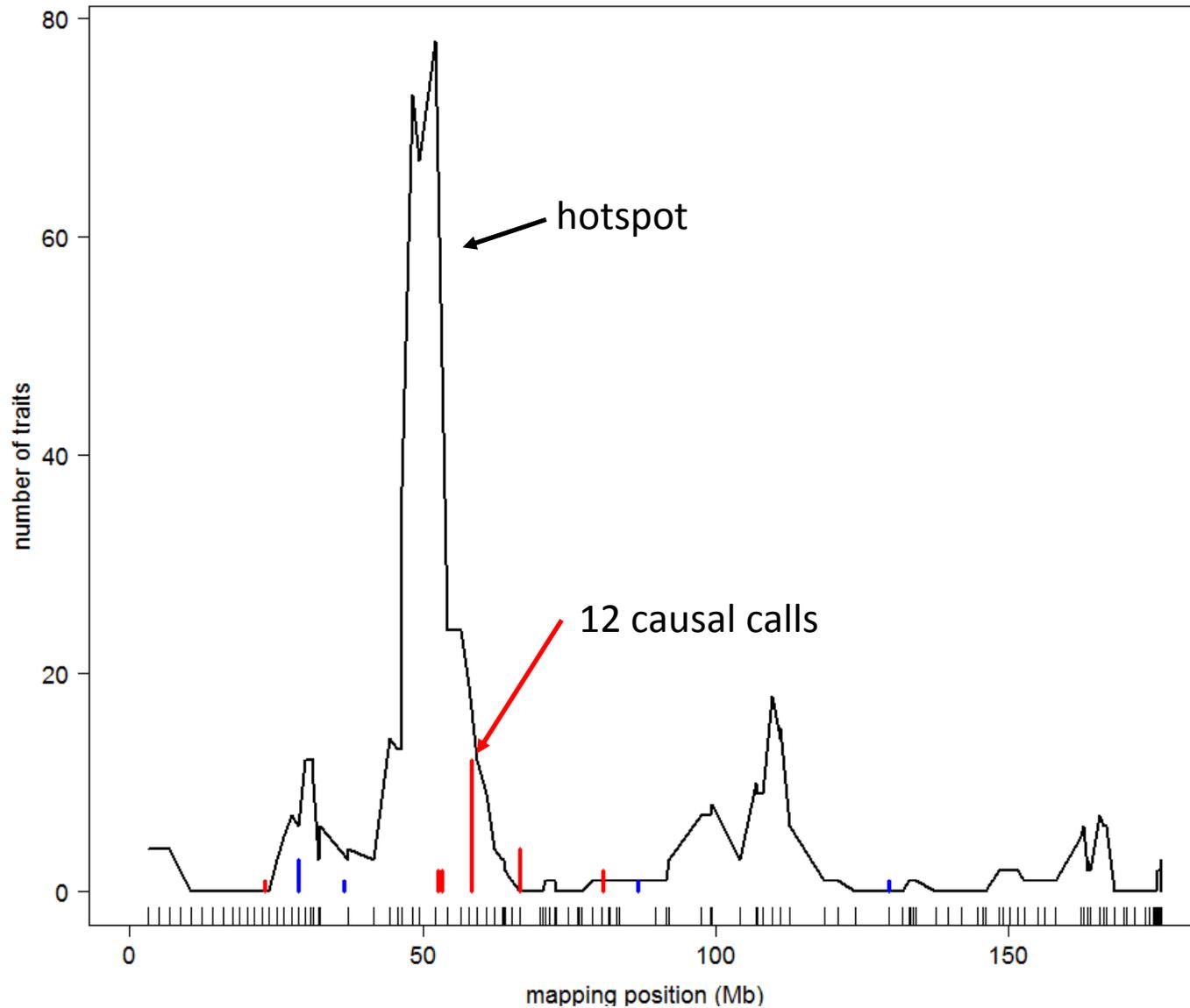


correlated

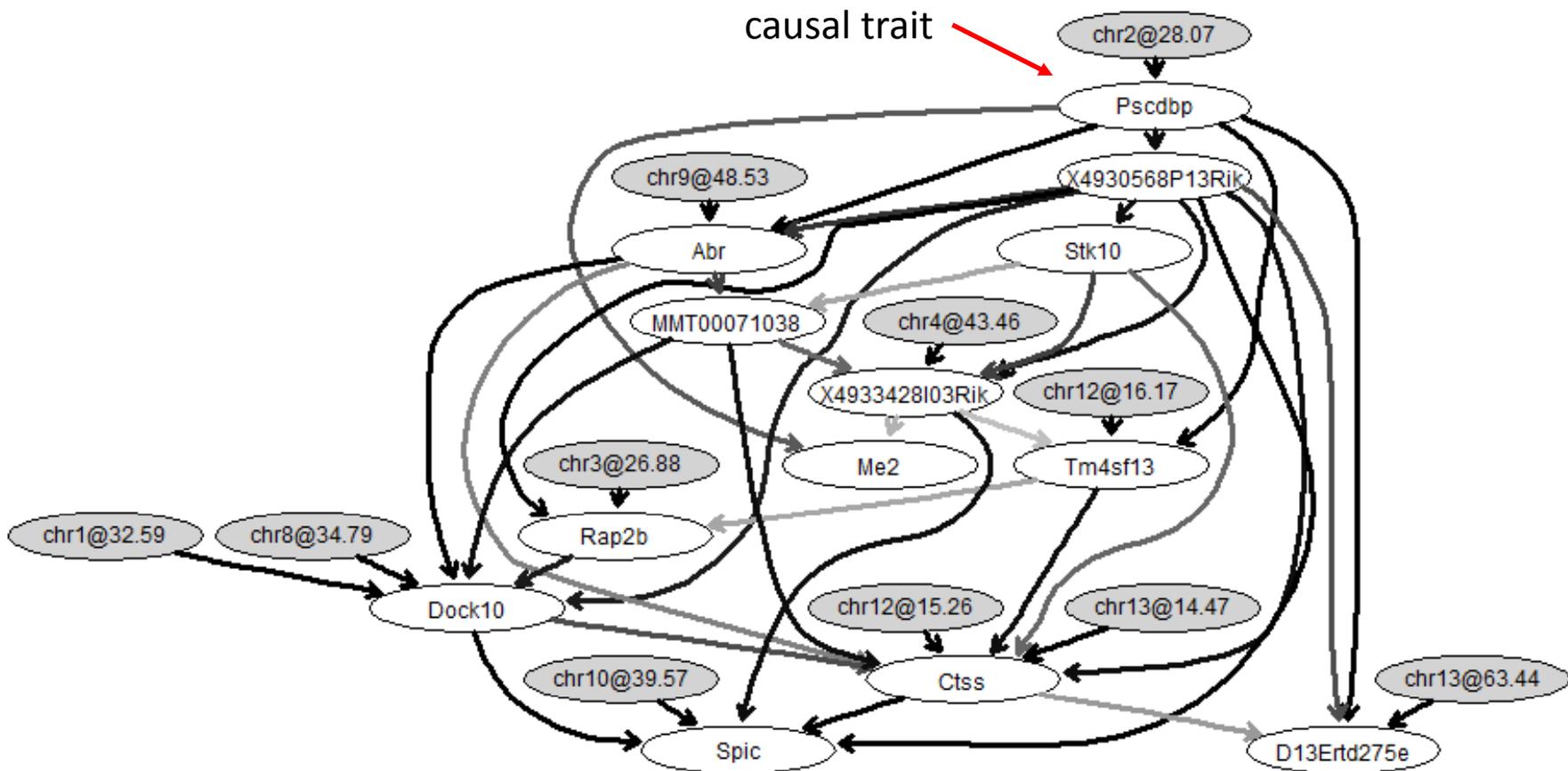


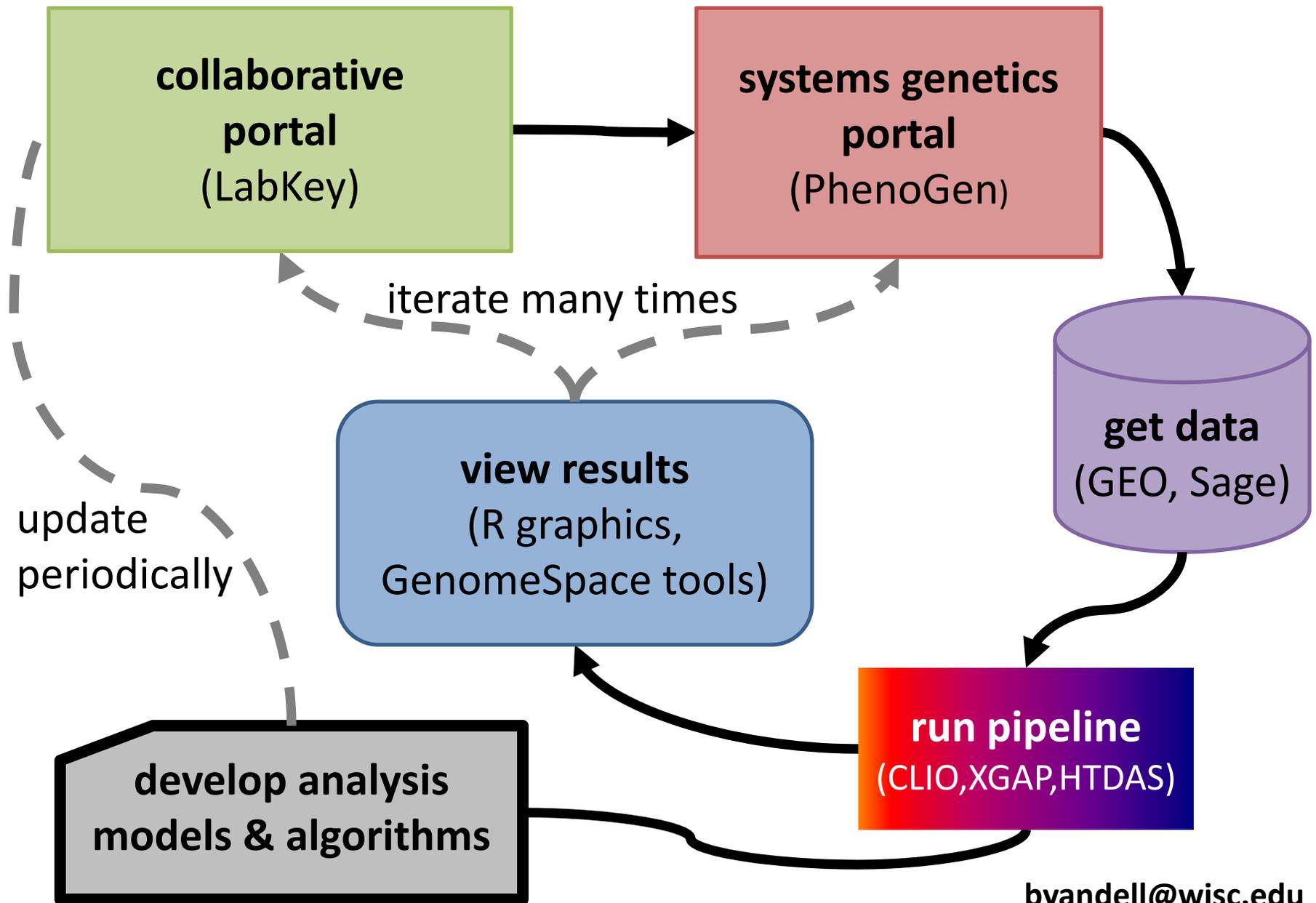
uncorrelated

# BxH ApoE-/- chr 2: causal architecture



# BxH ApoE-/- causal network for transcription factor Pscdbp

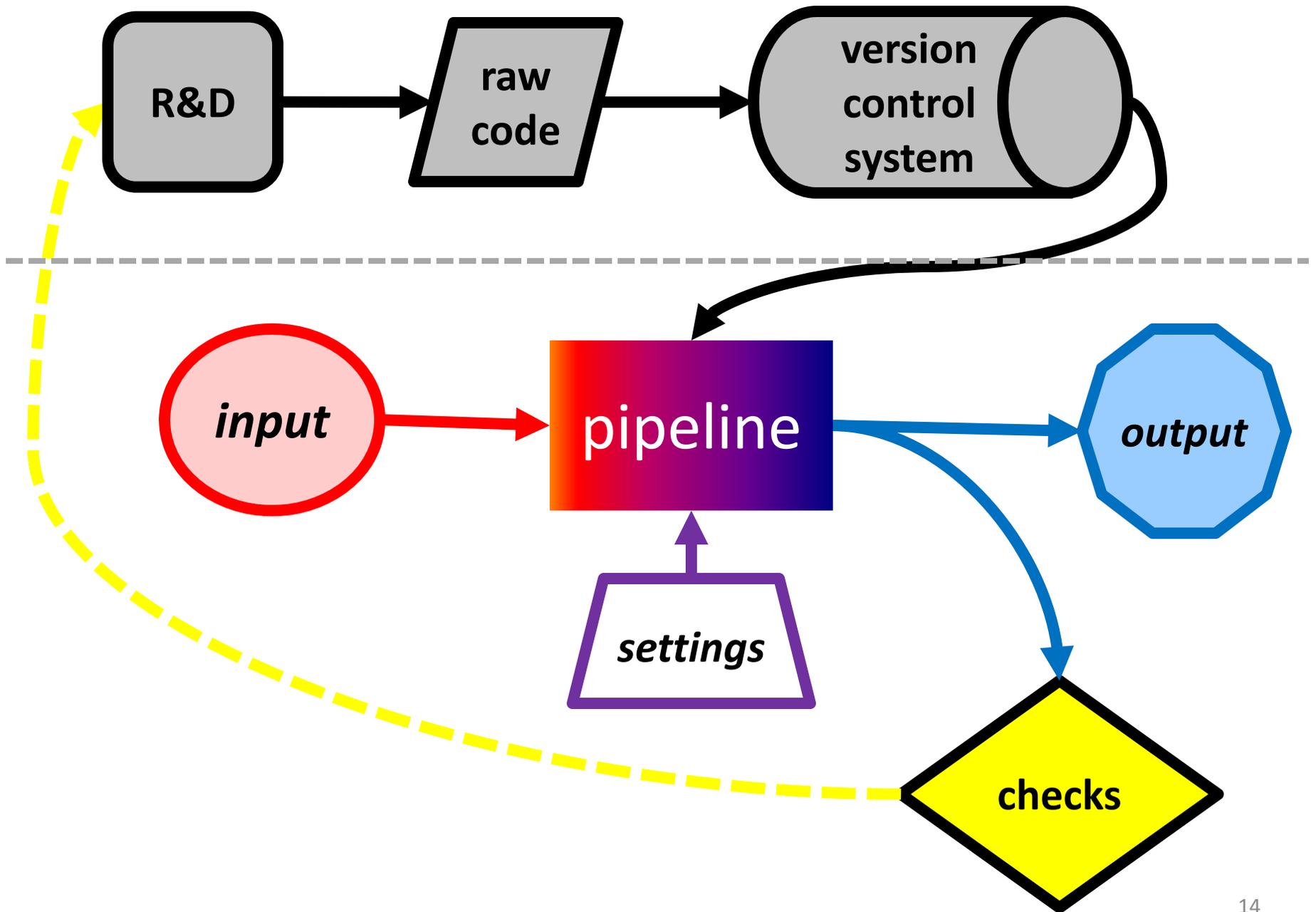




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# platform for biologists *and* analysts

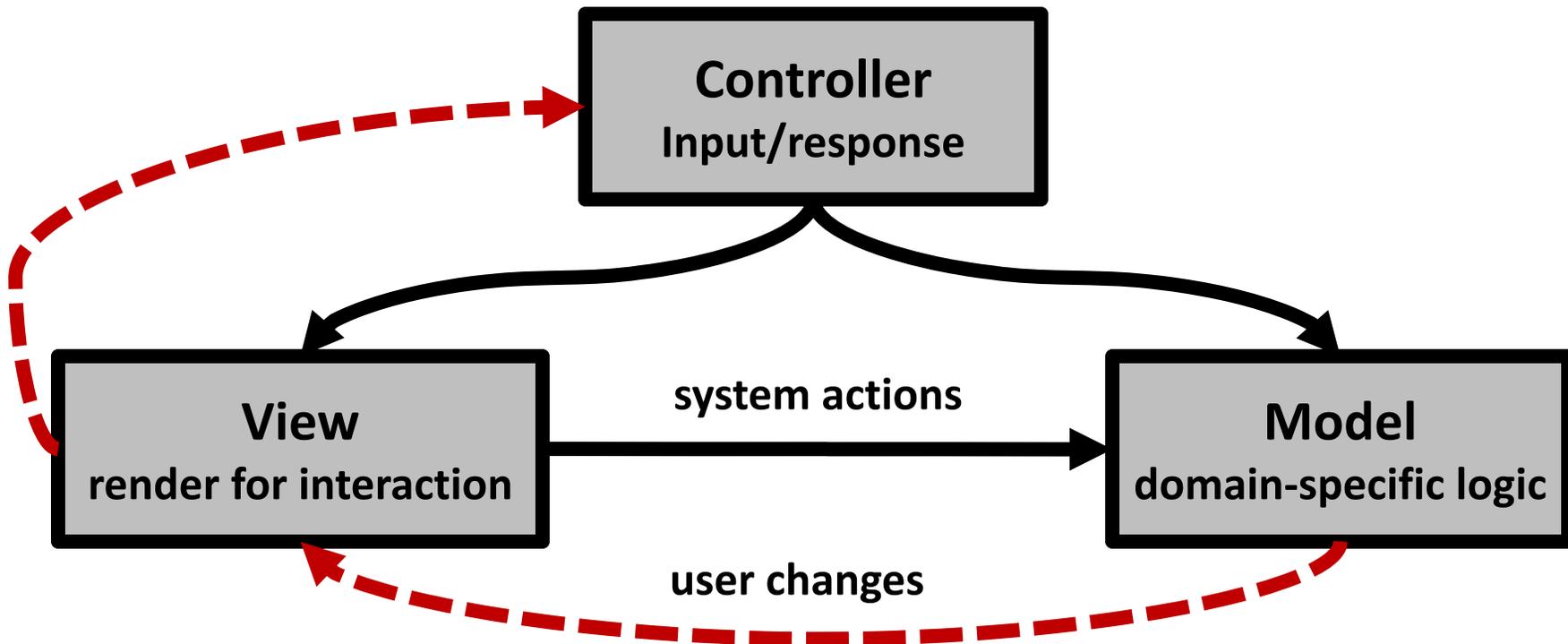
- create and extend pipeline steps
- share algorithms
  - public library
  - private authentication
- compare methods on one platform
- combine data from multiple studies



# Model/View/Controller (MVC)

## software architecture

- isolate domain logic from input and presentation
- permit independent development, testing, maintenance



# perspectives for building a community where disease data and models are shared

## **Benefits of wider access to datasets and models:**

- 1- catalyze new insights on disease & methods
- 2- enable deeper comparison of methods & results

## **Lessons Learned:**

- 1- need quick feedback between biologists & analysts
- 2- involve biologists early in development
- 3- repeated use of pipelines leads to  
documented learning from experience  
increased rigor in methods

## **Challenges Ahead:**

- 1- stitching together components as coherent system
- 2- ramping up to ever larger molecular datasets

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  - Elias Chaibub Neto
  - Jee Young Moon
  - John Dawson
  - Ping Wang
  - NIH Grants DK58037, DK66369, GM74244, GM69430 , EY18869
- Jackson Labs (HTDAS)
  - Gary Churchill
  - Ricardo Verdugo
  - Keith Sheppard
- UC-Denver (PhenoGen)
  - Boris Tabakoff
  - Cheryl Hornbaker
  - Laura Saba
  - Paula Hoffman
- Labkey Software
  - Mark Igra
- U Groningen (XGA)
  - Ritsert Jansen
  - Morris Swertz
  - Pjotr Pins
  - Danny Arends
- Broad Institute
  - Jill Mesirov
  - Michael Reich

# Systems Genetics Analysis Platform

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Jackson Labs: Churchill

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UC-Denver: Tabakoff

LabKey: Igra

