

Computational Infrastructure for Systems Genetics Analysis

Brian Yandell, UW-Madison

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

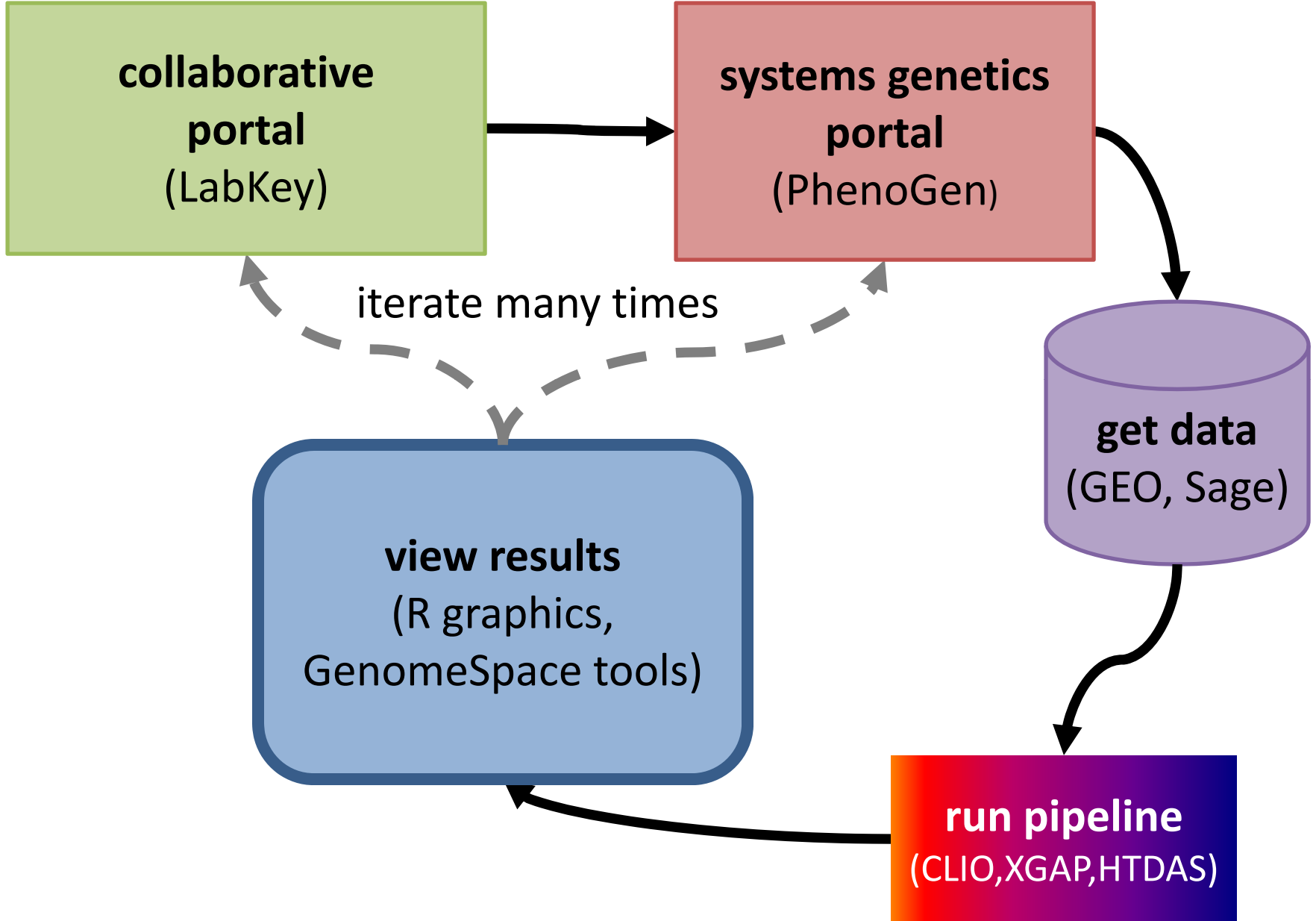
UW-Madison: Yandell, Attie, Broman, Kendzioriski

Jackson Labs: Churchill

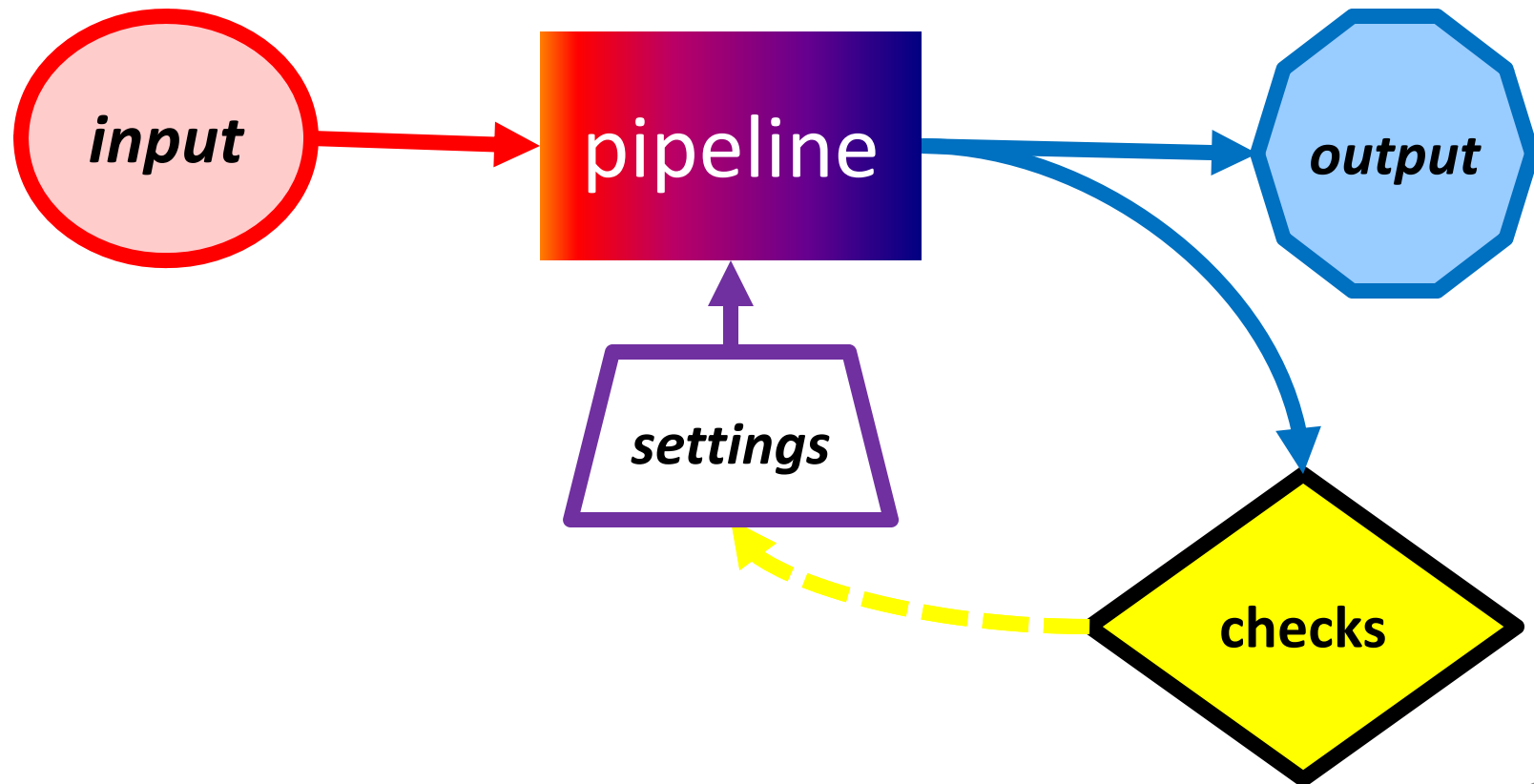
U Groningen: Jansen, Swertz

UC-Denver: Tabakoff

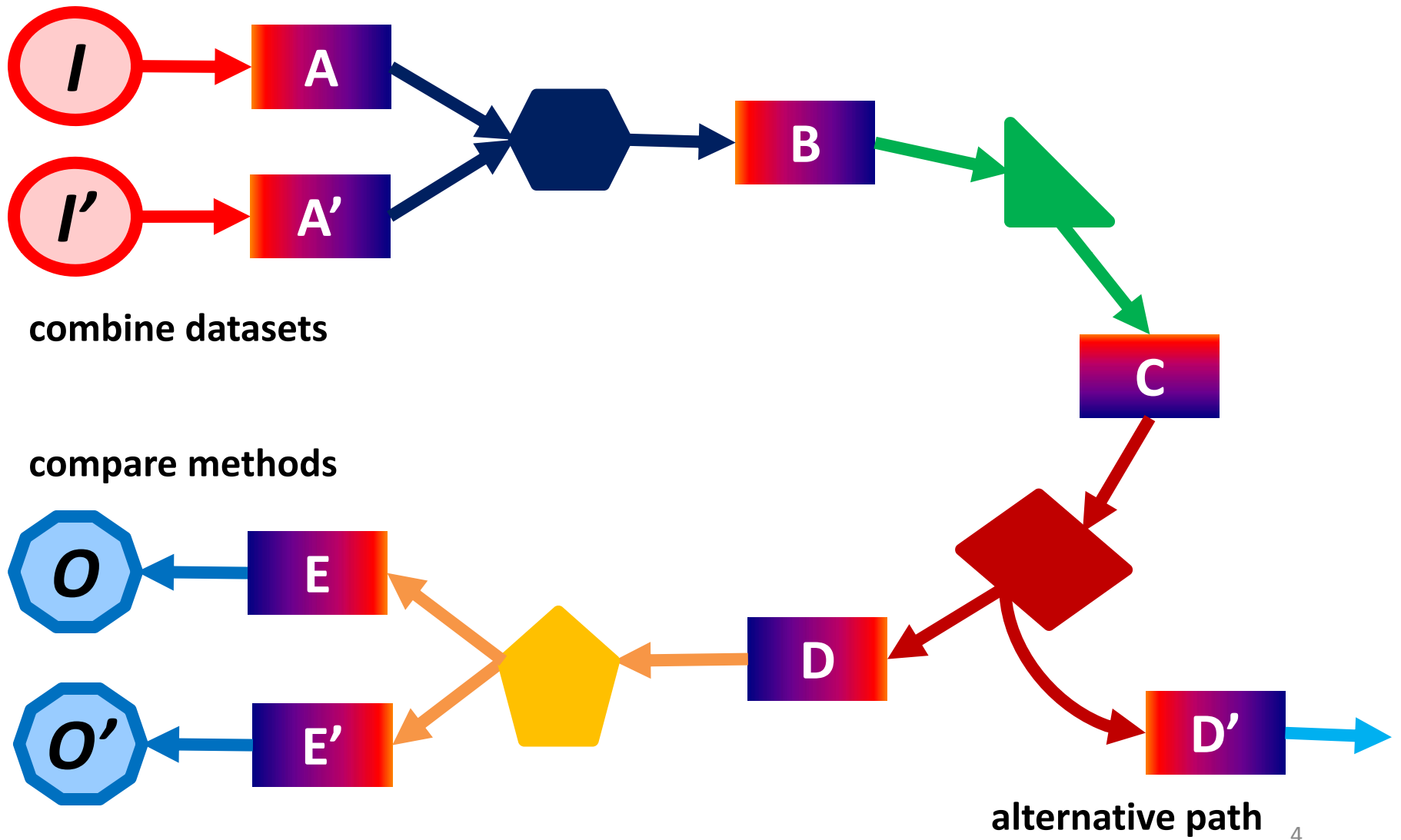
LabKey: Igra



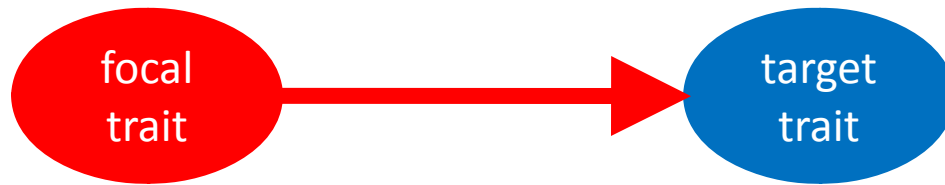
analysis pipeline acts on objects
(extends concept of GenePattern)



pipeline is composed of many steps



causal model selection choices in context of larger, unknown network



causal



reactive

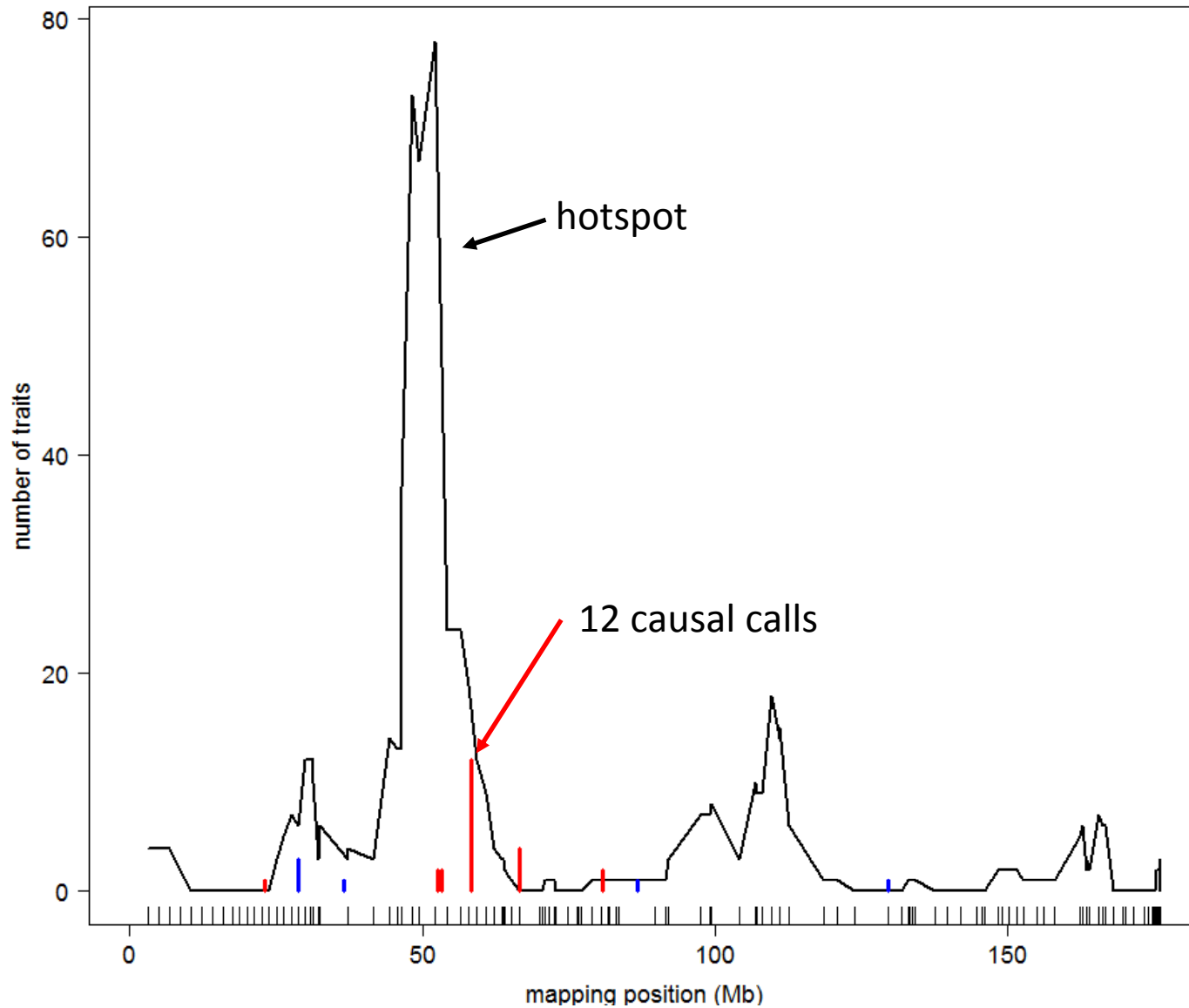


correlated

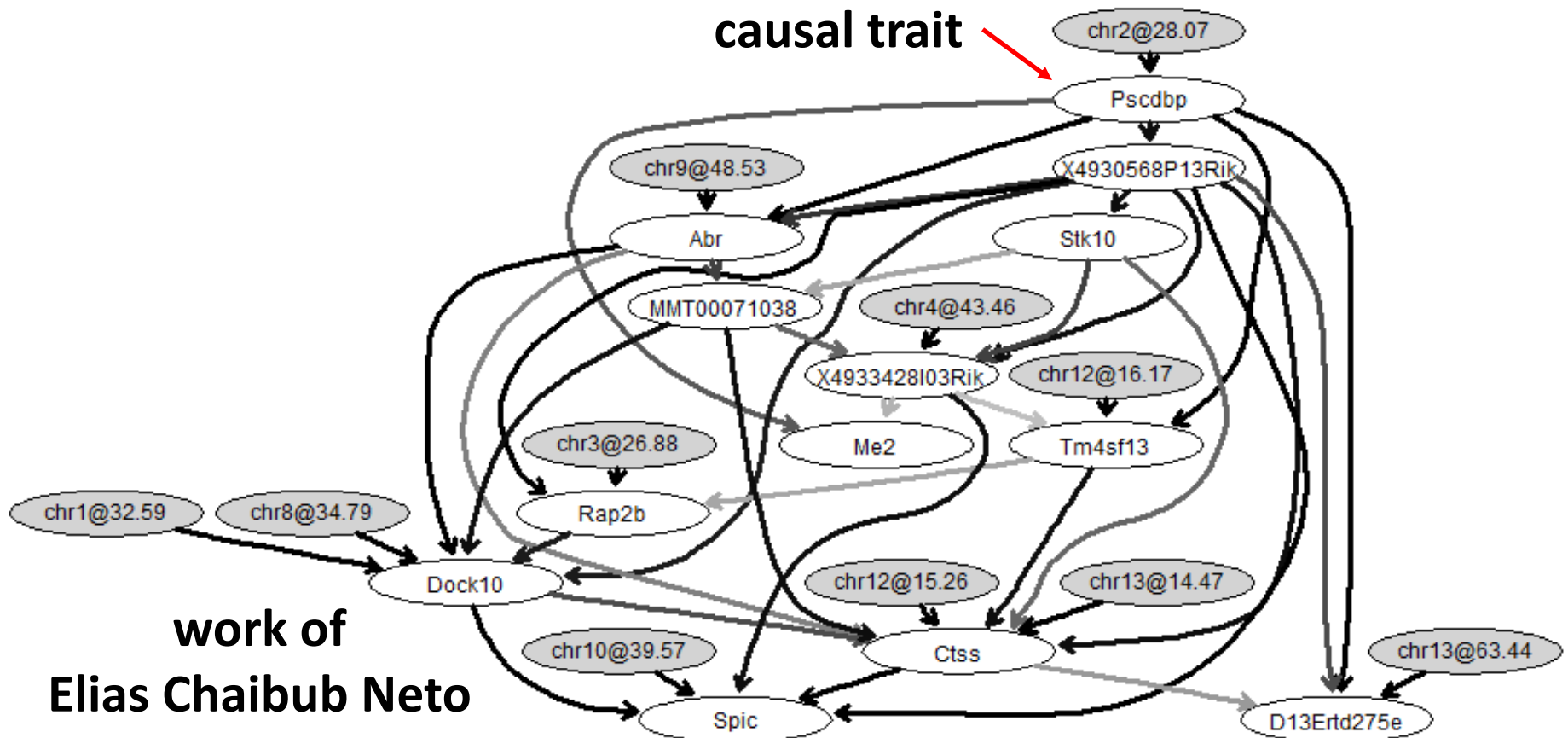


uncorrelated

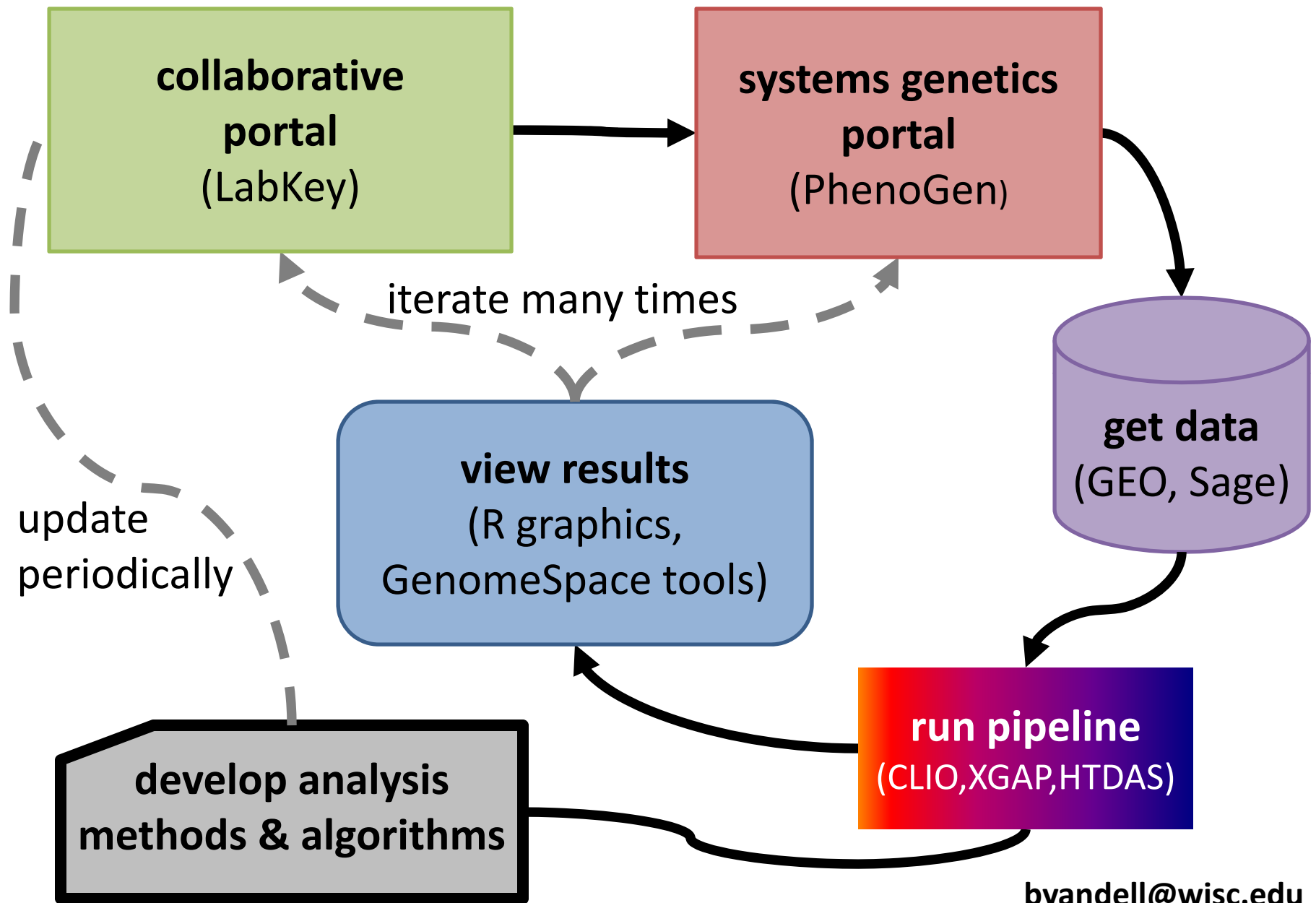
BxH ApoE-/- chr 2: causal architecture



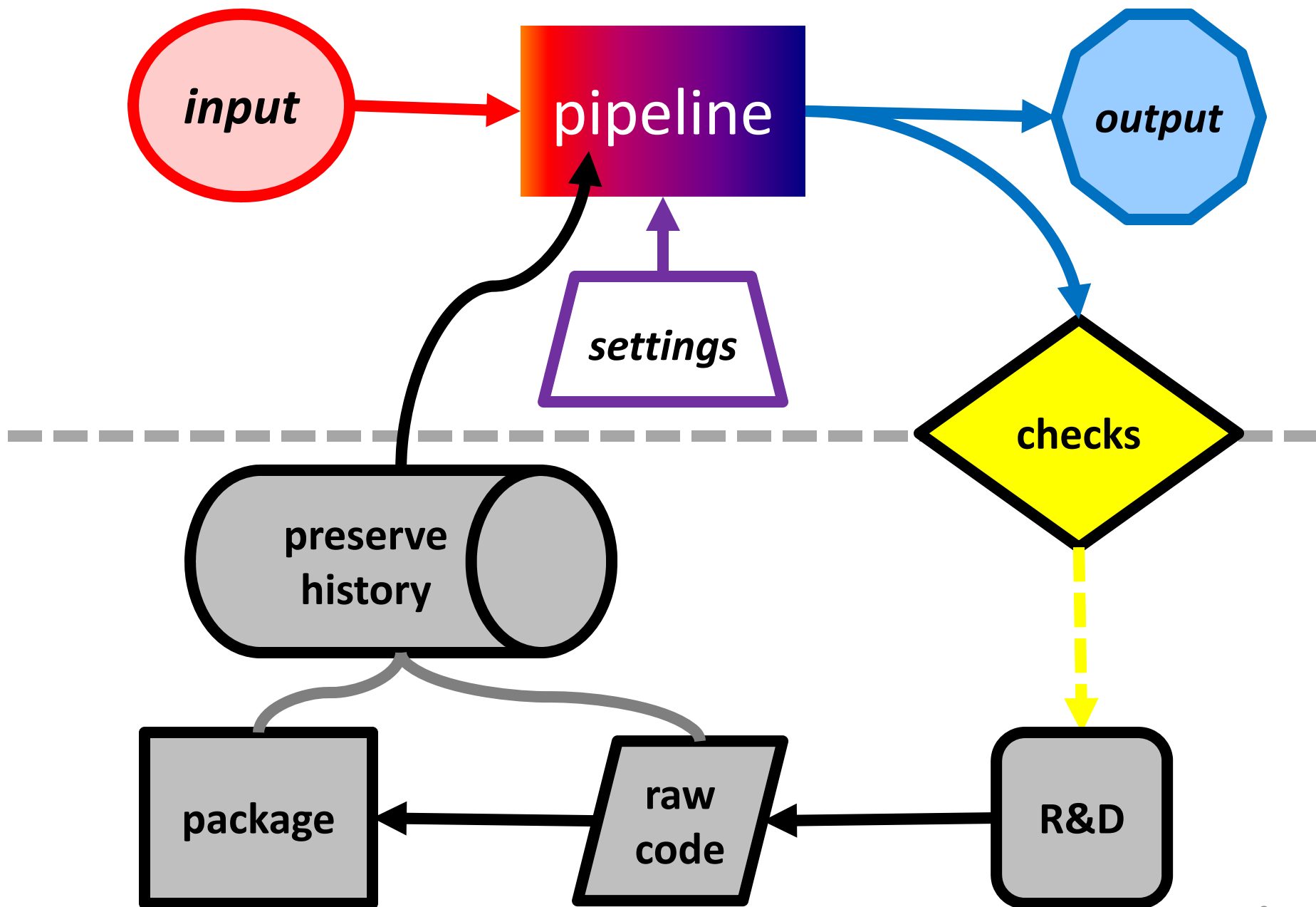
BxH ApoE-/- causal network for transcription factor Pscdbp



**work of
Elias Chaibub Neto**



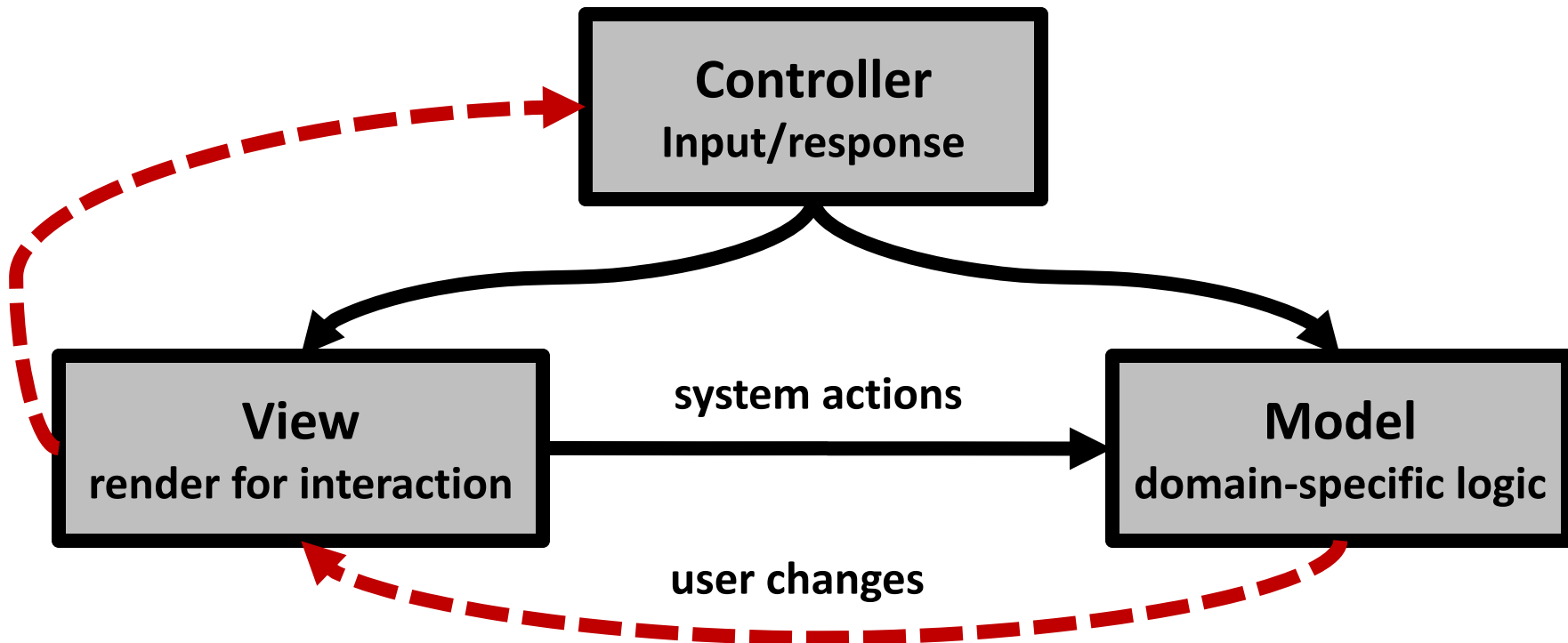
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Model/View/Controller (MVC)

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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 - Karl Broman
 - Mark Keller
 - Andrew Broman
 - Aimee Broman
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- Broad Institute
 - Jill Mesirov
 - Michael Reich

Systems Genetics Analysis Platform

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

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