Coloc-stats
– a unified web interface to perform colocalization analysis of genomic features

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2018 Galaxy Community Conference (GCGOSC2018), June 27–28, Portland, Oregon, USA

The problem
1. Functionally related GENOMIC FEATURES often tend to colocalize.

2. This assumption, however, is not often tenable in practice.

3. The genomic features we test for colocalization are not always independent.

4. The two questions can be tested using different null models.

5. The choice of null model greatly affects the conclusions.

So what should one do?
Run multiple tests with varying methods, parameters, and null models.

The challenge
1. Tools are available in different frameworks.

2. Requires single user interface with reproducibility and advanced tools.

3. Trying to coordinate seven research groups.

The solution
1. Too many chefs (developers) in the same kitchen.

2. Common workflow language (OWL) engine.

3. GALAXY w/ PyCLODSTATS

4. Galaxy framework: good

5. Code: good XML files; Galaxy workflow engine: no good

6. Too little time!?