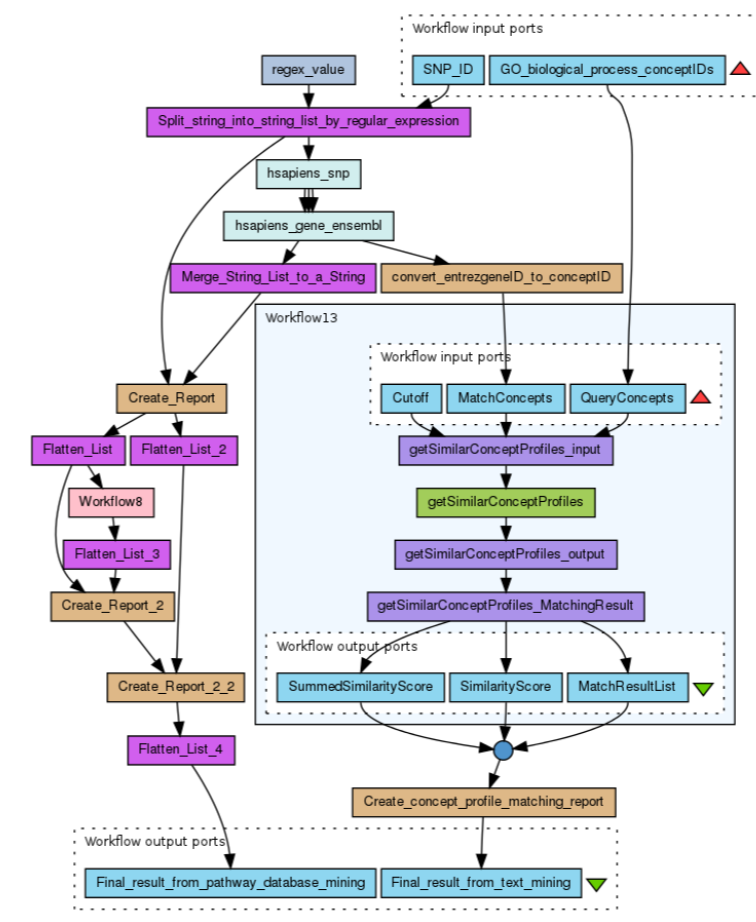


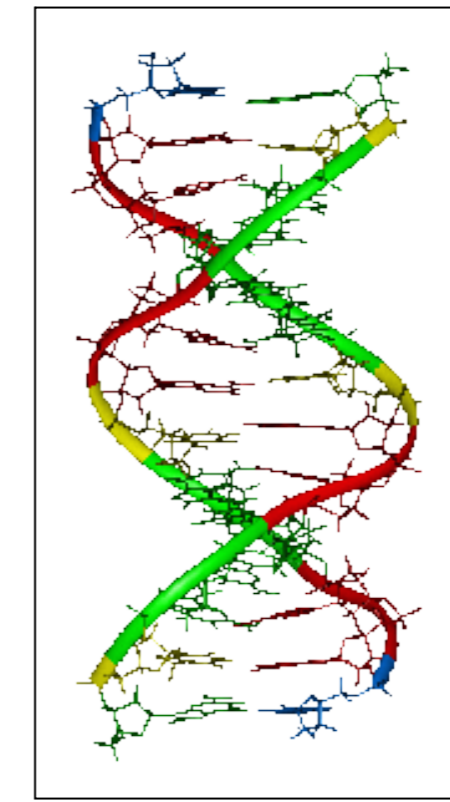
Understanding complex diseases requires complex computational studies. Workflows help perform these studies. To uphold scientific principles of reproducibility we develop tooling for digitally preserving computational experiments.



**Obese Person**  
We know what is wrong here



Workflows to find genetic background



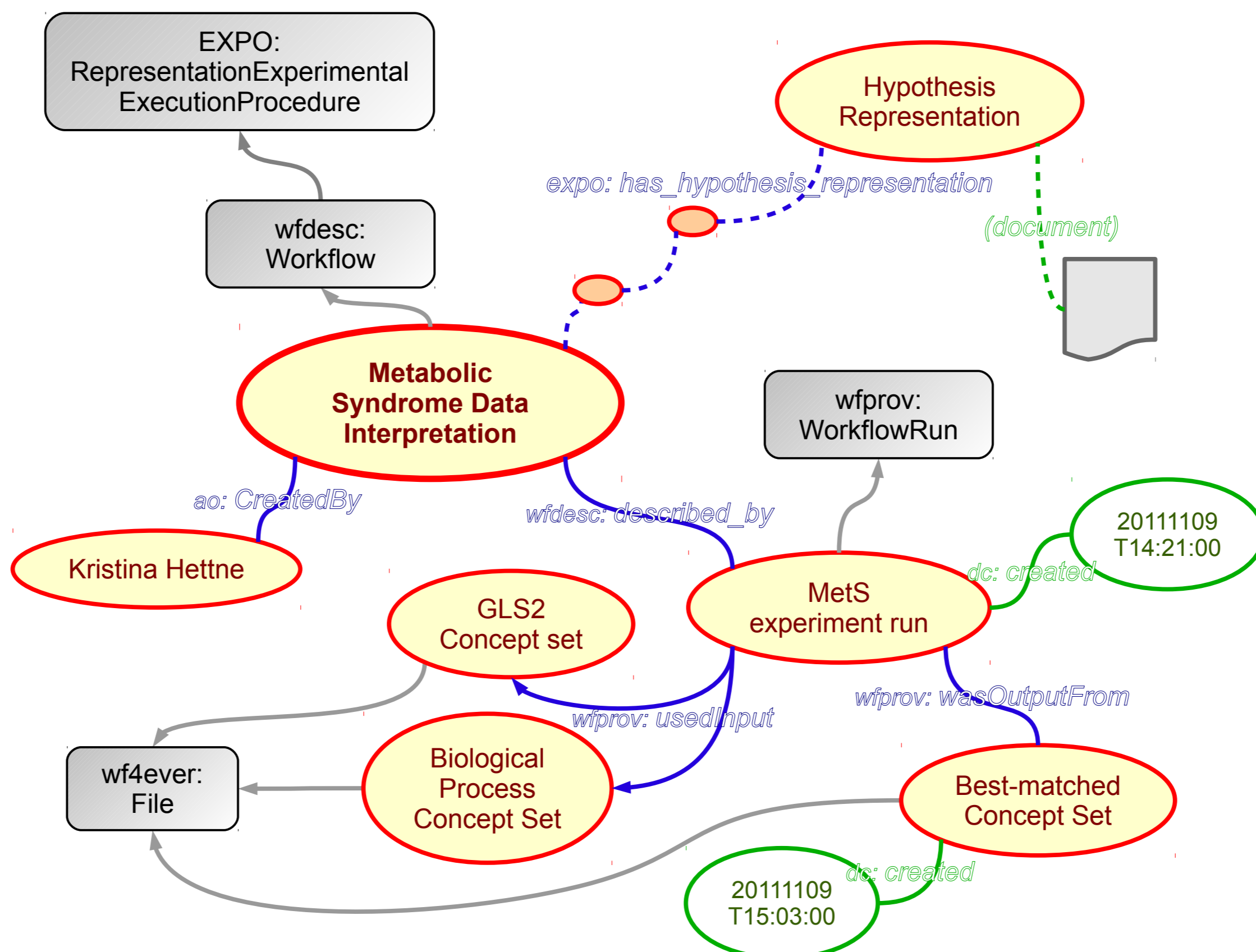
**Our Genes**  
What is wrong here?

Requirements are drawn from the study of Metabolic Syndrome. The other test domain is Astronomy.

### Example Research Object

An instance of a Workflow was used to perform a text mining run on two 'concept sets', resulting in best-matching biological processes per gene. The workflow was created by Kristina Hettne.

\* weighted disambiguated term lists

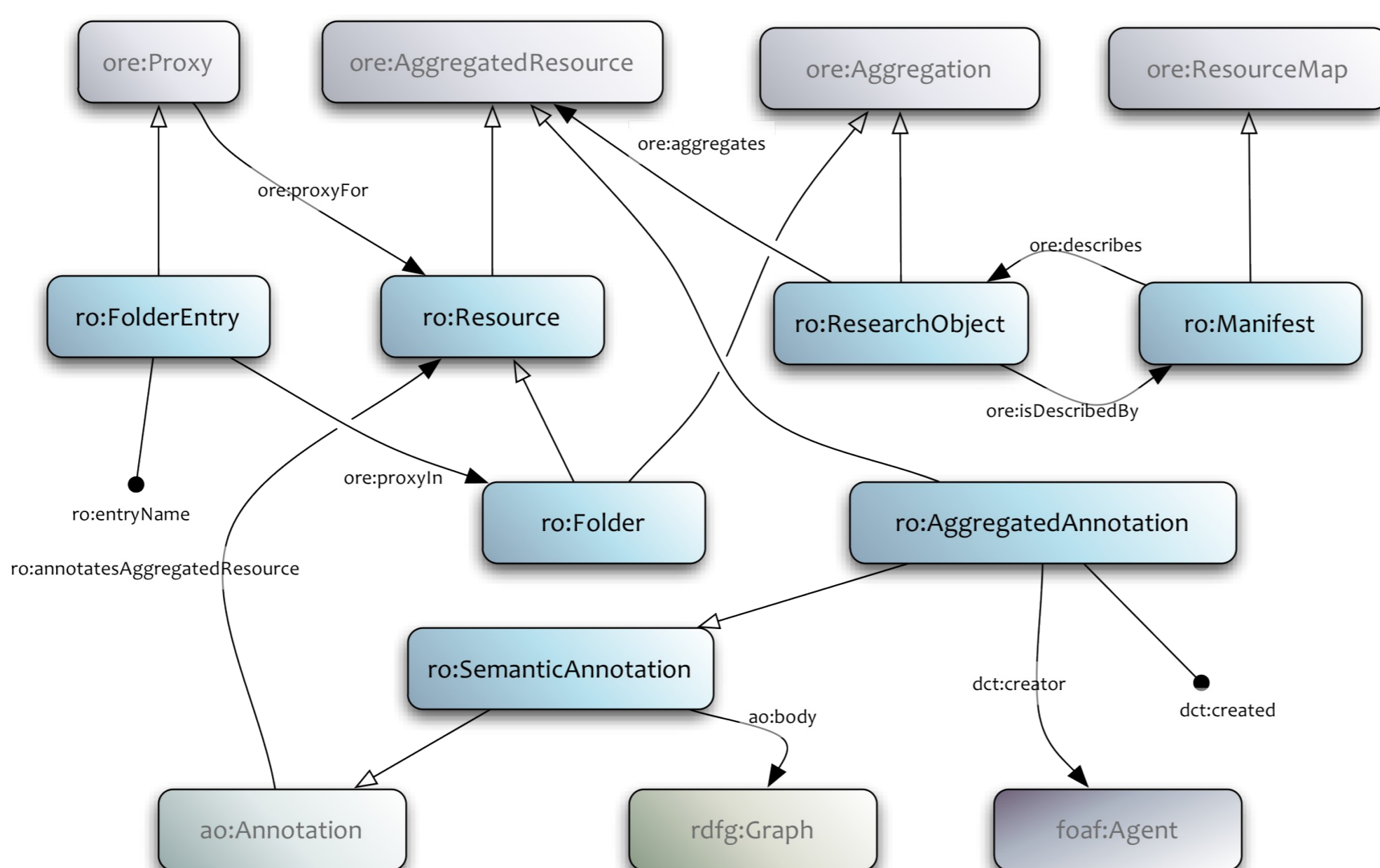


A possible extension for experimental science is the Experiment Ontology (EXPO)\* to link to for instance experimental design or a hypothesis.

\* Soldatova et al. Bioinformatics. 2006, 22(14):e464-71. PMID: 16873508

A Research Object is a bundle of resources. The Research Object Model reflects that and allow resources to be annotated. Tools perform these annotations 'under the hood' for users.

OAI-ORE: Open Archives Initiative Object Reuse and Exchange; foaf: Friend of a Friend Ontology; ao: Annotation Ontology



Preserving digital Research Objects including workflows will help reuse of methods, data, and interpretations across experiments. **wf4ever architecture** uses Semantic Web models to represent and expose its content **Semantic annotations** enables us to understand preserved computational experiments.

### Acknowledgements

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Check our web page and wiki:  
<http://www.wf4ever-project.org/>  
 Release Version 0.1 of the RO model:  
<http://www.wf4ever-project.org/wiki/display/docs/Research+Object+Vocabulary+Specification+v0.1>