

biofinity.unl.edu
Our Answer to the Challenge

University of Nebraska
Dept of Computer Science
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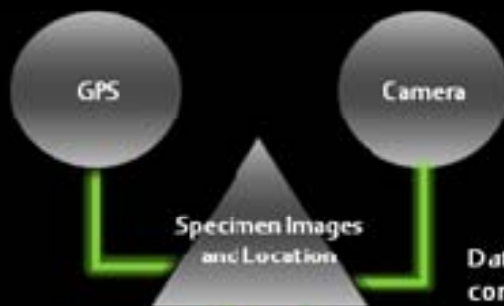
What is Biofinity?

- An NSF-funded project to federate genomics and biodiversity data
 - Currently holds fungal genomics data from the University of Nebraska and scarab beetle data from Instituto Argentino de Investigaciones
 - Currently working on incorporating NCBI genomics data and GBIF biodiversity data
- Provides a uniform interface to bioinformatics tools
 - Currently a Google Maps-based mapping tool, an iPhone-based browser and updater, and BLAST (sequence alignment)
- Started in October 2008; currently in pre-release stage

Our Response to the Challenge

- Data collected in field via mobile device (iPhone app), including comments, photo, and GPS data
- Data uploaded to ontology, and immediately viewed by RSS subscribers
- Subscribers add comments, amend classification, add genomic data, etc.
- Genomic data aligned against other sequences; hits automatically loaded into ontology
- New results automatically fed to RSS subscribers
- <http://biofinity.unl.edu/faces/e-biosphere09/index.xhtml>

Data are collected in the field or in the lab through various mechanisms (such as via a mobile device) and can include Images, sequences, or other information.



Data are processed as they are uploaded to The Biofinity Project. Processing involves converting data into a SCID compliant format, checking them against the ontology and running any automated processes. If the data contains any sequences, automated identification of the sample is done in the processing phase by running BLAST.



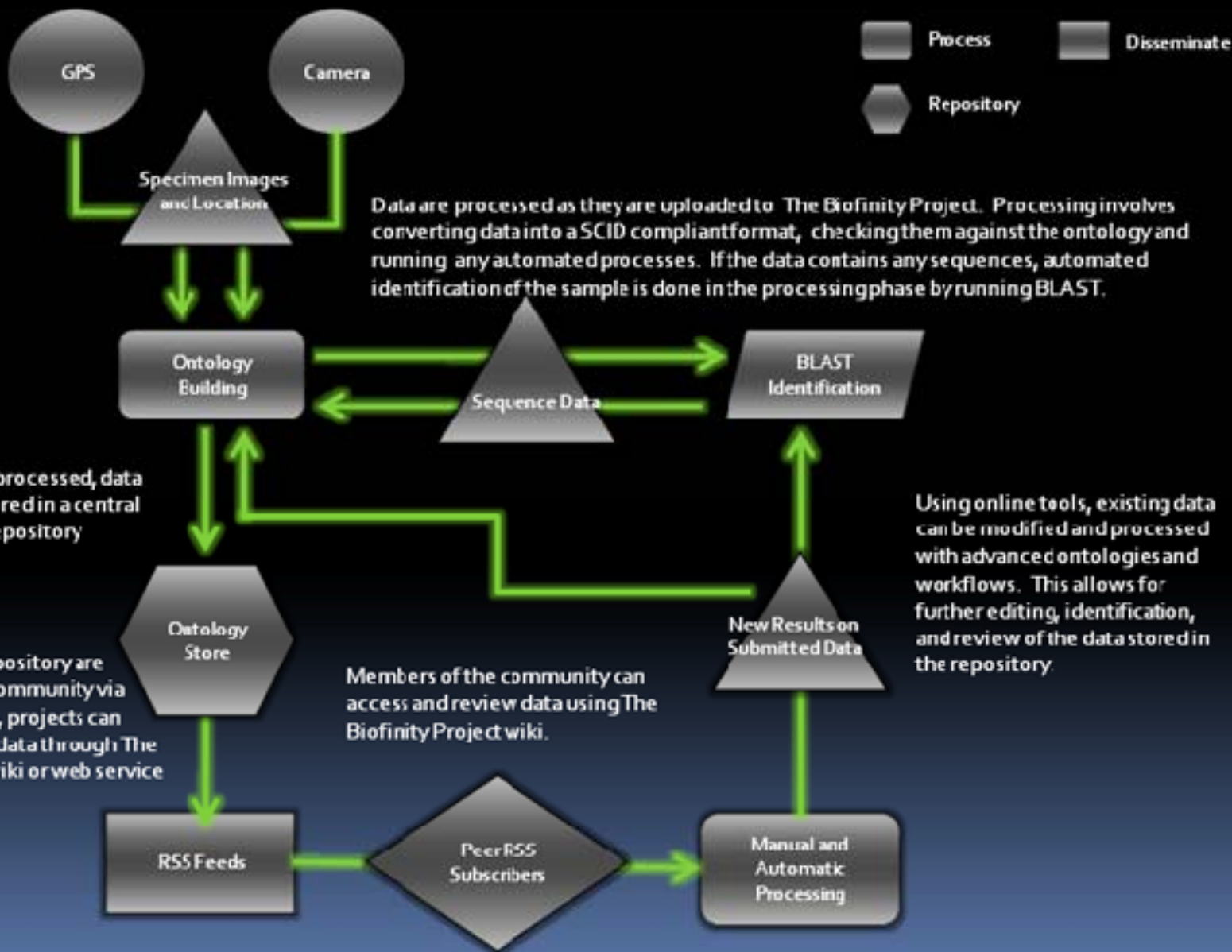
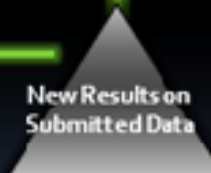
Once processed, data are stored in a central data repository



Changes to the repository are published to the community via RSS. Additionally, projects can access repository data through The Biofinity Project wiki or web service calls.

Members of the community can access and review data using The Biofinity Project wiki.

Using online tools, existing data can be modified and processed with advanced ontologies and workflows. This allows for further editing, identification, and review of the data stored in the repository.



What's Next?

- Prior to upcoming Biofinity Beta-Testers Workshop in Lincoln, Nebraska, October 11, 2009 (in conjunction with BIOT Oct 9-10):
 - Import NCBI and GBIF data to form a comprehensive mirror of these important data sets
 - New bioinformatics tools added via our application programmer interface (API)
 - New user interface to seamlessly integrate all connected data and tools