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biofinity.unl.edu

Our Answer to the Challenge

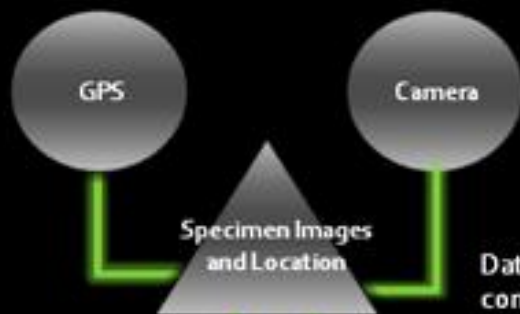
What is Biofinity?

- 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).
- 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-biosphereog/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



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.



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.



Day One Update

- Specimen data collected by data partners in the field are uploaded to The Biofinity Project database.
- Subscribers to the 'Unclassified Specimen' RSS feed are able to classify these specimens, allowing them to be included in The Biofinity Project Taxonomy.
- Coming next: specimen samples to be taken at eBiosphere and classified by RSS subscribers.
- Follow the specimen feed at:
<http://biofinity.unl.edu/service/rss/specimens.rss?ID=-1>

Day Two Update

- Unknown moth specimens from eBiosphere exhibits were uploaded into The Biofinity Project database from the iPhone application:
 - Data partners subscribing to the unclassified specimen feed provided classifications of 3 moths;
 - Specimens were classified in our database.
- Feeds remain active and are monitored as new specimen samples are uploaded using mobile devices in the “wild”.

Challenge Results

- Our response to the eBiosphere Informatics Challenge provides a proof-of-concept for our framework architecture;
- Our relational database and ontological data specification allows us to digest data from other sources (NCBI Taxonomy);
- Using distributed / cloud computing techniques we have successfully deployed our technology to mobile / wireless devices to extend our model to the 'human network';
- We have identified improvements that can further enhance our model before its general availability at TDWG in November.
- We enjoyed the Challenge!