Réunion PhyloAlps #18

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Participants

- Frédéric Boyer
- Bruno Bzeznik
- Eric Coissac
- Anthony Hombiat
- Sébastien Lavergne
- Charles Pouchon

Latest updates

Data

- Feed the database PhyloNorway samples with adaptating PhyloAlps load samples script
- Update PhyloAlps sampling script according to Eric's XML assembling metadata file
- Collectors cleaning (1500 -> 300)
- Organizations cleaning (/2)

User interface redesign

- Box every piece of information
- Counter up on homepage
- Redesign the projects map
- Redesign navigation tabs
- Redesign breadcrumbs tab
- Responsive design
- Remove the Home module and move the registration feature to the Editor module
- Rename edit button to open button in Editor

Data model

- Add 3 kinds of annotations to Sample/Extract/Library/Sequence/Assembling/Assembly
  - Automatic Assembling logs from Assembling metadata XML file
  - Notes for commenting everything from Sample to Assembly with a severity level (Info/Warning/Error)
  - Advices for validating everything from Sample to Assembly

New features

- Sampleset
  - Add map to the sampleset template
  - Add session-wide sampleset

- Add associated samplesets in samples template
- Annotations
  - Add create/edit/delete annotations feature
  - Add annotations badges in hero
- DNA Assembly graph
  - Increase nodes and edges size
  - Immediatly display tooltip on edge hovering
  - Add progress indicator on loading
- Auto center project/sampleset/home maps on makers layer extent
- Display Extract/Library/Sequence/Assembling in organization template

User roles and permissions

- ProjectMember

  - Sampleset: add/change/delete
  - Annotations: add/change/delete
  - Sample: add/change/delete
  - DNA extract: add/change/delete
  - DNA library: change

- ProjectManager

  - Project: change

- Administrator

  - Project: add/delete
  - Person: add/change/delete
  - Organization: add/change/delete

Architecture

- Merge beta branch with master beta.phyloalps.org -> data.phyloalps.org
- Add reload metedata RESTful method with crc64 authentication

TODO

- Aggregate notices/advices from child item and display in parent template hero
- Use latest advice as the authoritative advice (which implies renaming the advices table "History of advices")
- Implement a complex quality indicator based on tables/advices
- Add the libraries number in sample tables
- Fix the sequencing status in the libraries table in the sample template
- Add play/stop toggle button to control the graph assembly rendering engine
- Fix the probing->graph->unfold->annotation order in the assembly tables of the assembling template
- Invert the wrong lon/lat geographic coordinates in some PhyloNorway samples
- Deal with samples that don't have a NCBI taxID
- Display some database stats on homepage