# mGIG

11 May 2021

### **Agenda**

- 1. Webpage
- 2. Summary of STN proposal
- 3. Results of survey
- 4. Training
- 5. Pilot annotation project
- 6. Final points

#### 1. mGIG webpage

https://mgig.weebly.com/

Includes contact form



• Would it be useful to compile resources here? If so, send them to us!

### 2. Summary of STN proposal

**Co-authors**: Alice Dennis, Angus Davison, Kara Layton, Luis Chueca, Joris Koene, and Maurine Neiman

Submitted 31 March. Results approx. August.

- Centered on research topics from you:
  - Conserved features of shell formation
  - Genomic basis of sex and sexual systems
  - Evolution of color variation
  - Basis and patterns of repeats across taxa
  - How unique or conserved are immune defenses
- Main goals:
  - Web resource for manual gene curation and
  - Training annotation and assembly
  - Conferences annual meetings and/or conference symposia

#### 3. Survey results

36 respondents

15 countries

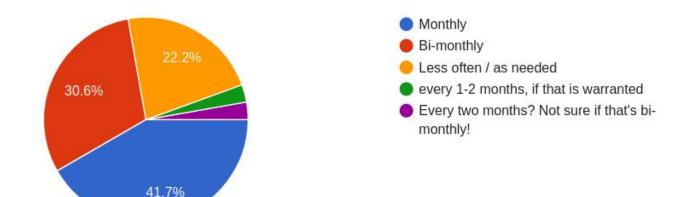
Varied career stages

Meet every 2 months

Alternate time zones

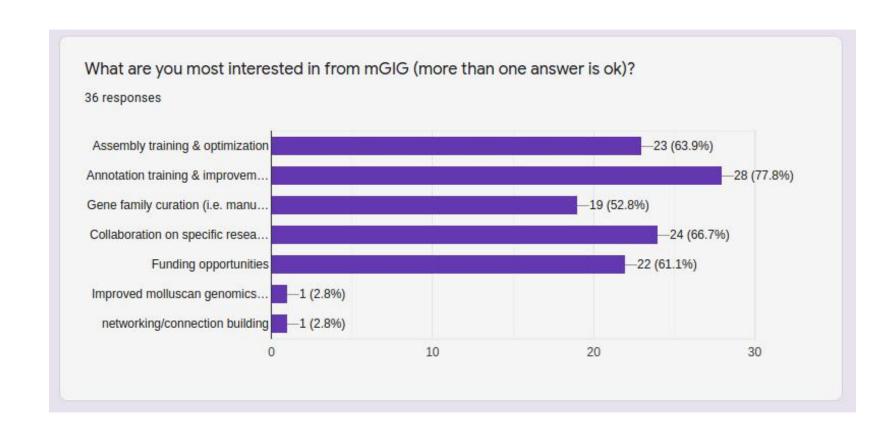
How often would you like to attend mGIG meetings?

36 responses



### 3. Survey results

What do we want?



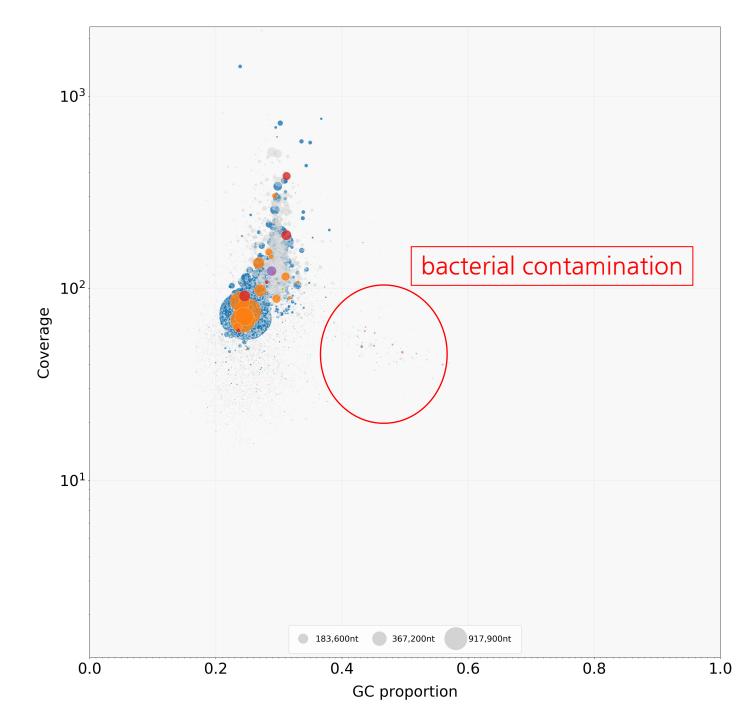
# 4. Training

### 4. Training

Already happening:

**BlobToolsKit**: two training sessions. Link to recordings on Slack and here:

https://www.youtube.com/channel/ UC6QimXygwjaX2CGZ8cgjNxw



### 4. Training

#### Next:

Assembly "optimization" and evaluation

Luis - spreadsheet to evaluate assemblies

Organize meetings to discuss these

## **Training**

#### Near future:

Repeat annotation. REPET

https://urgi.versailles.inra.fr/Tools/REPET



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#### REPET

#### REPET

The REPET package ( Flutre T. et al. 2011 , Quesneville H. et al. 2005 ) integrates bioinformatics programs in order to tackle biological issues at the genomic scale. It is distributed under the CeCIL license and deposited to the Agence de Protection des Programmes ( APP ) under the Inter Deposit Digital Number FR 001 480007 000 R P 2008 000 31 235.

To download the last <u>REPET package v3.0</u> . What's new in this release <u>CHANGELOG</u> (19.10 kB) ?

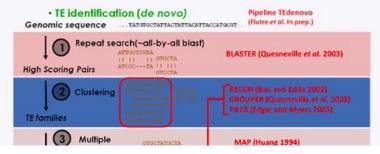
**NEWI** For a quick install, REPET and its dependencies are containerized in a free docker image downloadable

Previous releases are available here

- Version: 3.0
- · Editor: URGI
- DOWNLOAD

Its two main pipelines are dedicated to detecte, annotate and analyse repeats in genomic sequences, specifically designed for transposable elements (TEs).

TEdenovo: this pipeline starts by comparing the genome with itself using BLASTER. Then it clusters matches
with GROUPER, RECON and PILER, clustering programs specific for interspersed repeats. For each cluster, it
builds a multiple alignment from which a consensus sequence is derived. Finally these consensus are classified
according to TE features and redundancy is removed. At the end we obtain a library of classified, non-redundant
consensus sequences.



### **Training**

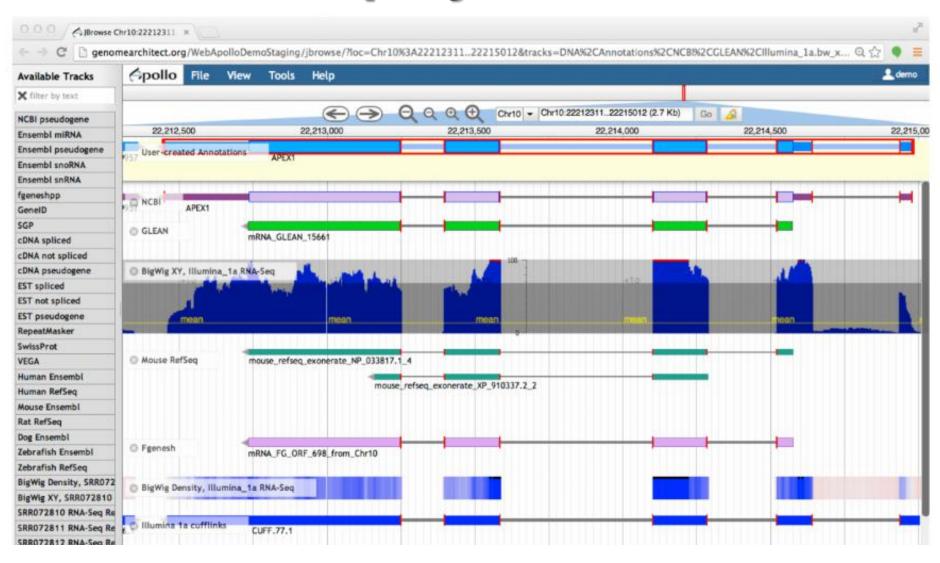
#### Annotation -

This will be the next step.

Perhaps a few rounds of Assembly Discussions first?

Seeking people who would like to help with this

### Pilot annotation project - Robert Waterhouse



### **Last points**

- Upcoming GIGA conference Mollusc genomics session
- Job postings SLACK
- Structure of mGIG
- Other points/ questions?
- Next meeting early July
- Before that: Assembly discussion groups
- Slides, minutes, and recording will go on SLACK and adennis5.wordpress.com