ddRAD advice

Gus Dunn, Dan

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# My planning

* balancing *number of loci* vs *depth of per loci coverage*:
  + what is my sequencing budget?
  + What is my question set?
  + Because *selection* **AND** *population genetics* are part of the project needs, shooting for conditions that favor more loci with as high a sequencing coverage as we can afford is probably the best route.
* There are equations for choosing size selection cutoffs that take into account the above considerations associated with the protocols (she says)
* I have not seen the protocols yet

# Andrea’s data

* If I am to use her data in my questions:
  + I need to know exactly what she did in terms of size selection
    - *the size selection is how you target the same loci*
  + I need to determine whether the conditions she used are even *compatible* with the questions **I** want to ask.

# pyRAD

* She likes/loves it compared to STACKS which was used before
* it is pretty comprehensive in its coverage of the entire analysis stack
* Daren is great and responsive
* I would like to volunteer to help in its development

# Action items

## ddRAD cost info

1. [\_] cost per library
2. [\_] cost per lane
3. [\_] lane capacity

## Gisella

* [\_] ask about the sequencing budget

## Daren

* [\_] email of introduction and interest

## Andrea

* [\_] ask for write up of protocol/size selection

## Louise

* [\_] install pyRAD and dependencies

## Dan

* [X] ask to shadow some of the mentoring sessions with Yiota