ddRAD advice

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Contents

1 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

2 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.

3 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

4 Action items

4.1 ddRAD cost info

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

4.2 Gisella

- [_] ask about the sequencing budget

4.3 Daren

- [_] email of introduction and interest

4.4 Andrea

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

4.5 Louise

- [_] install pyRAD and dependencies

4.6 Dan

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