Status of dead positives recovery

Meeting notes

Gus, Gisella, Andrea

2015-01-20 (Tuesday)

Contents

1 Discussed

- Methods
  - need to be collated into one doc
- Status of LD analysis and how to choose cut-off
  - look at tryp paper and email Mark regarding this
- Status of hapFLK (haplotype analysis) and state of results
  - email to author is sent and waiting for response
  - contacting Noonan and/or Jeff Townsend regarding this
- Structure of paper
  1. Development of the base SNP set
     - a process I am not clear on at the moment
  2. Linkage Analysis
  3. Functional Annotation of filtered SNPs
  4. Discussion
     - establish the ability to do this scale of work in *G. f. fuscipes*
     - limits of the dataset as it now stands
     - Never-the-less, hypotheses can be formulated and here they are. . .

2 Current/future plans

Gisella:

- [X] email Washington group about methods of Seq prep and analysis
- [X] email Aksoy group about linkage status of *G. m. morsitans*

Andrea:

- [ ] Re-run RAD pipeline showing Gus whats going on and writing up the pieces.
- [X] Contact Noonan and/or Townsend regarding `hapFLK` stuff

Gus:

- [X] email Mark about Tryp LD analysis in his paper
- [ ] read Tryp paper for same
- [ ] install latest `Stacks` version on `louise` and make runable by Andrea
- [ ] return `hapFLK` script to original code and copy altered version to new name
- [ ] Generate descriptive statistics and figures of the LD results as a whole rather than by contig where possible
- [ ] upon decision of which near-by genes are "interesting" send summary of info known about them to Aksoy group for ideas.