Status of dead positives recovery

Meeting notes

Gus, Gisella, Andrea

2015-02-04 (Wednesday)

# Overview of Discussed

* Andrea’s write up of current results
  + *need to be collated into one doc*
* Status of LD analysis and how to choose cut-off
  + results of discussion with Mark
  + success in generating expected behavior of mean LD behavior vs distance
  + Gus’s proposed idea to identify “outlier” snp pairs (*see section below*)
* First figure should have a map of population locations as a panel
* Structure of paper *(****mostly*** *unchanged since last meeting)*
* plans for future

# Current structure of paper

***mostly*** *unchanged since last meeting*:

1. Development of the base SNP set
2. Linkage Analysis
   1. **(new)** linkage-based grouping of contigs by physical proximity
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…
   * **(new)** provides more information pertaining to the physical proximity of the supercontigs

# Gus’s proposal to identify LD “outlier” snp-pairs

1. for each group of SNPs bp apart: collect from bp distance window around :
   1. across genome
   2. across scaffold
2. calculate modified z-score (based on *median absolute deviation* rather than standard deviation: **MAD is more robust than SD for HTS-type data**)
3. flag any SNP-pair with
4. possibly randomize data and calculate FDR to evaluate performance.
   1. perhaps vary the window-size from step 1 to use FDR to chose window-size that minimizes FDR.

# 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*

**Gus and Andrea:**

* [ ] add methods in “final” style to growing document
* [ ] place document in shared location

**Gus:**

* [ ] add LD methods and results to document
* [ ] generate population-location map with zoom out to all Uganda
* [-waiting-] upon decision of which near-by genes are “interesting” send summary of info known about them to Aksoy group for ideas.