

LD networks: unsupervised detection of polygenic selection



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Zuon GitHub

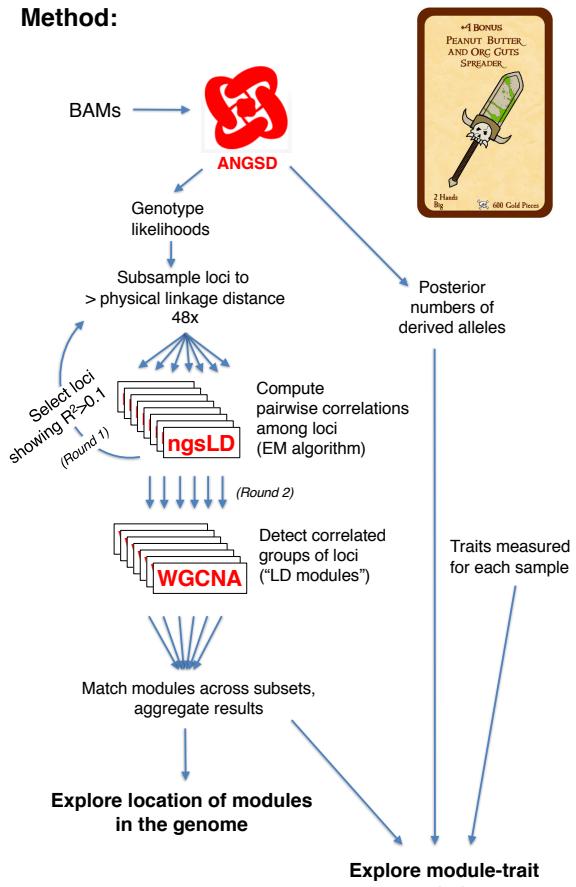
Main idea:



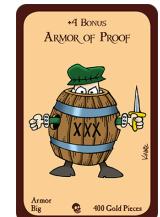
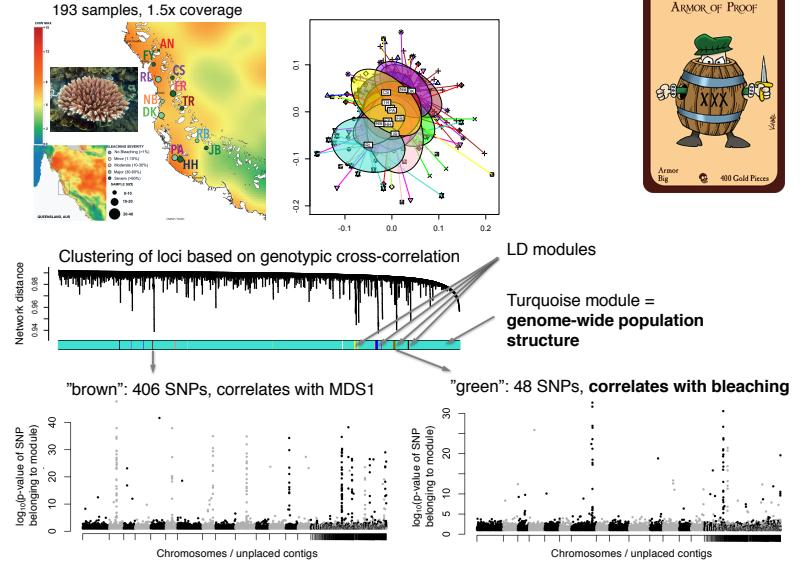
- Adaptation typically involves **changes of multiple traits** controlled by loci distributed throughout genome
- Selection should create **correlation between genotypes*** (i.e., LD) at these loci despite lack of physical linkage
- Let's **cannibalize** a correlation-based method for detecting gene co-expression networks to detect such groups of **co-selected loci**

* As long as selection pressure varies across species range

Method:



Case study #1: *Acropora millepora* coral

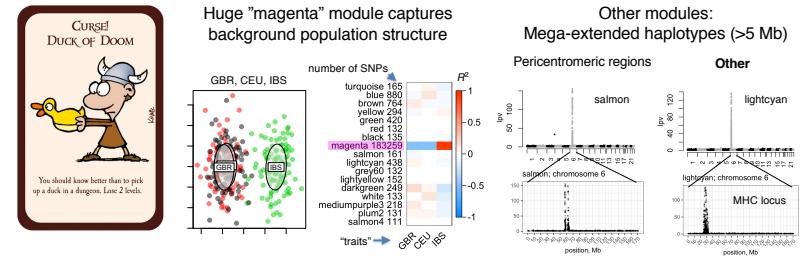


+4 BONUS
ARMOR_OF PROOF

Armor Big

400 Gold Pieces

Case study #2: *Homo sapiens* (297 samples, VCF from 1000 genomes project)



Emphasis art:
"Munchkin" card game

Designer: Steve Jackson

Artist: John Kovalic

munchkinsgames.com

Conclusions so far

- The method works as intended, powerfully detecting cross-correlated groups of loci based on a few hundred low-coverage samples;
- Type of detected signal depends on the organism
 - possibly, physically unlinked loci can only become correlated in organisms that can sustain very high selection pressure (e.g., highly fecund marine creatures)