# Identifying Adaptation to Hypoxia in Experimental Evolution

Arya Iranmehr
airanmehr@ucsd.edu

Bafna Lab
University of California, San Diego

November, 2016

# CLEAR

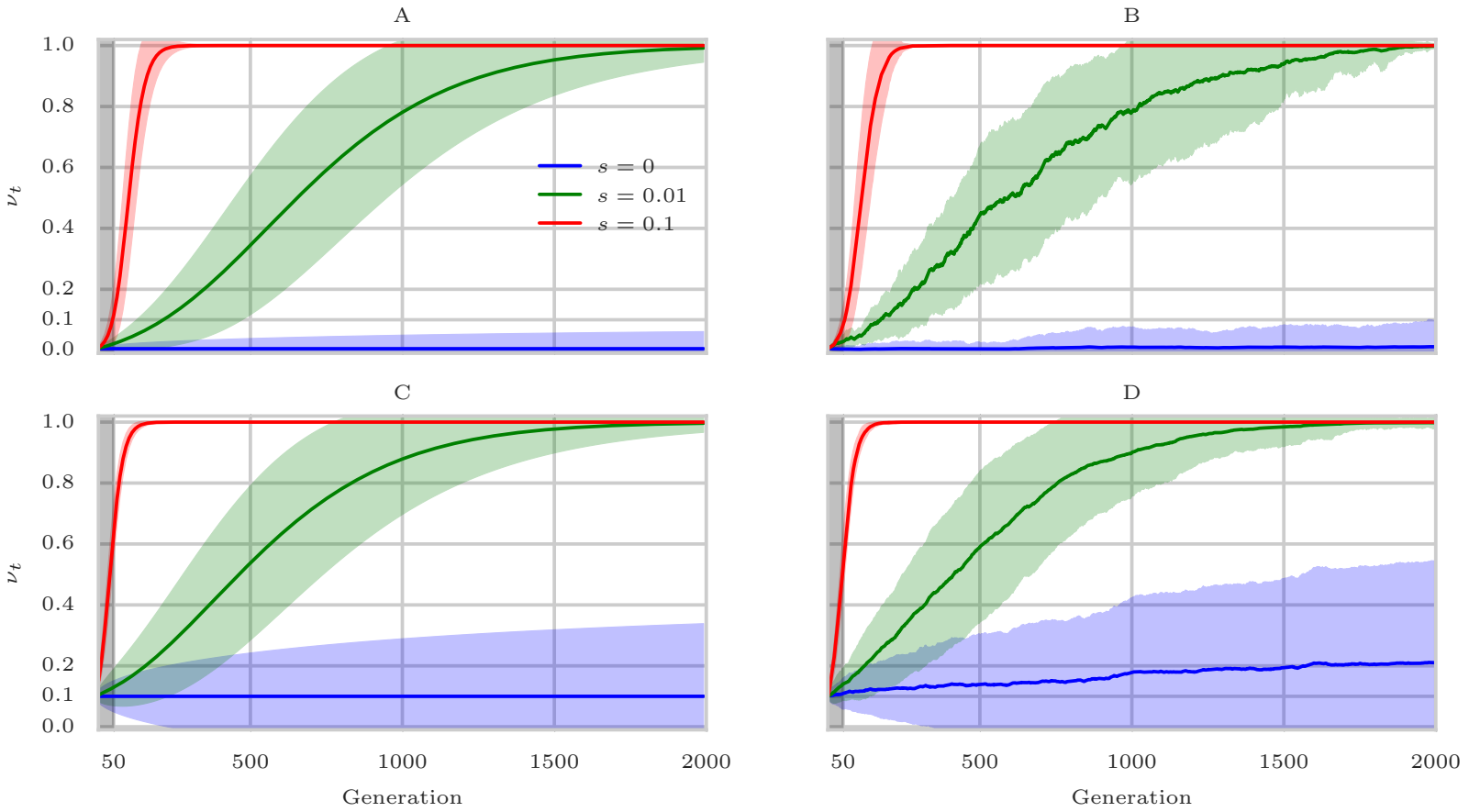
- takes read-count data (models uncertainties in allele frequency of pool-seq data).
- takes complete time-series (not restricted to 2 time-points)
- detects balancing and directional selection.
- works well for when selection is acting upon *de novo* mutation as well as standing variation.
- takes into account of background genetic variation (first detects candidate regions and then return variants).
- models demographic changes during (bottleneck, or expansion) EE.
- very powerful for detecting directional selection in short term EE.
- to be adapted for cross populations tests.

# Objectives I: Analyze long-term EE using CLEAR

Given 21 populations of Normaxia, Hyperoxia and Hypoxia at generations 4,17 and 200, we would like to perform comprehensive scan to identify gene sets , pathways, genes and specific alleles showing signal of selection.

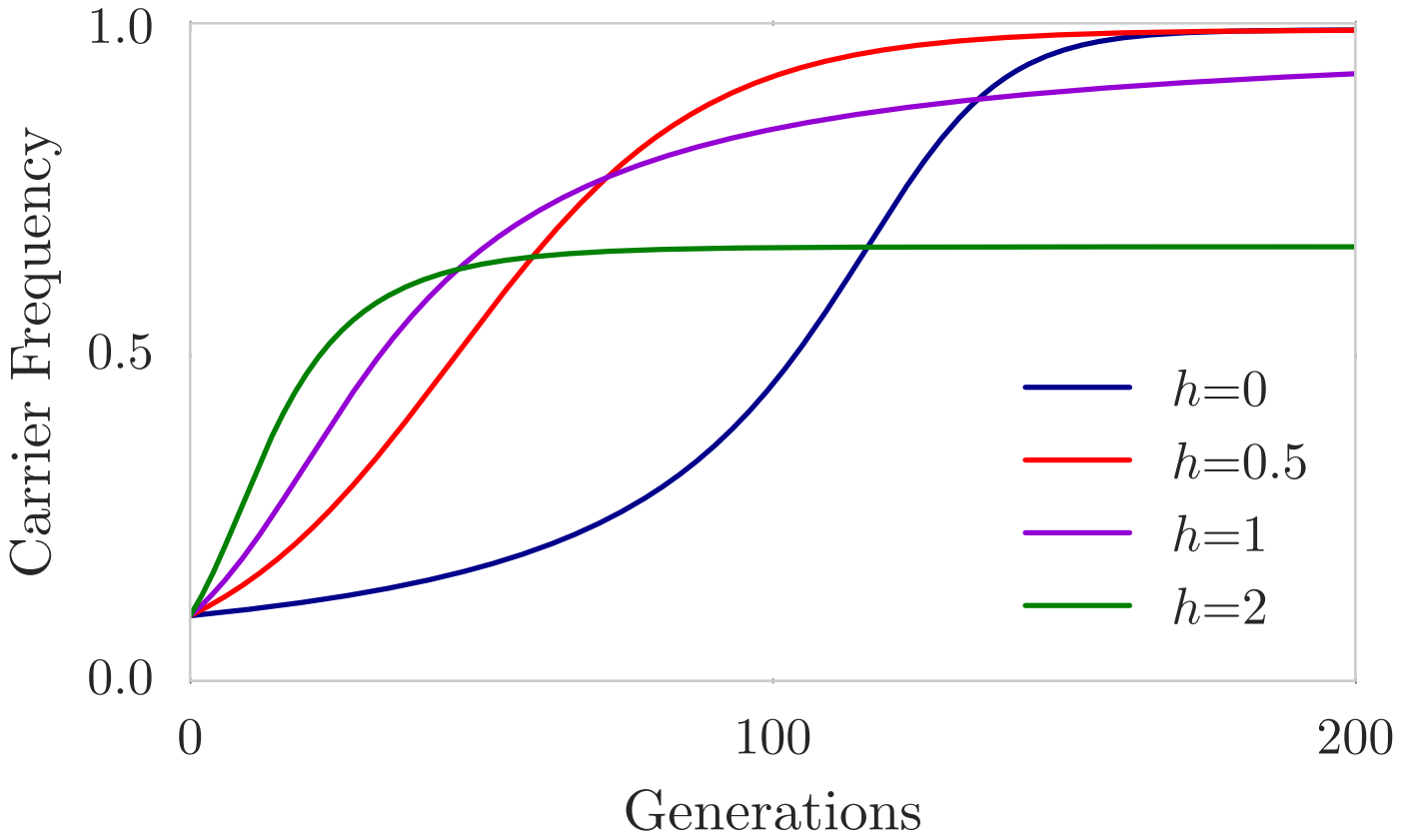
# Objectives II: replication using short-term EE

Given that CLEAR is powerful in detecting directional selection short-term EE, can we detect same genes using smaller number of generations?



# Objectives III: Balancing selection

Given that CLEAR can detect balancing selection in long-term EE can we identify balancing selection?



Thanks!