

M. Kreitman: weak selection + codon bias

Weak selection in two different systems

- codon bias
- gene regulatory evolution



If biased at all codons (on average)
then use AAG

◦◦ AAG = preferred codon

What causes bias?

bias correlated w/ expression level
" " " tRNA abundance

Weak selection

- has little effect on polymorphism
- test... do mutation to a preferred codon have diff. polymorphism than mutations from a preferred codon

mutator to	pref unpreferred	unpref ↓ pref.
polymorphic	13	3
fixed	13	8
% polymorphism	50.0	27.3

PGI = high codon bias

Always an excess of preferred

but when look at subs. in each species - in simulans there have been equal # of pref. & unpref. but in melanogaster there have been 32 vs 6 (more unpref. preferred). Suggests that melanogaster has more unpreferred b/c. selection hasn't worked as well in melano.

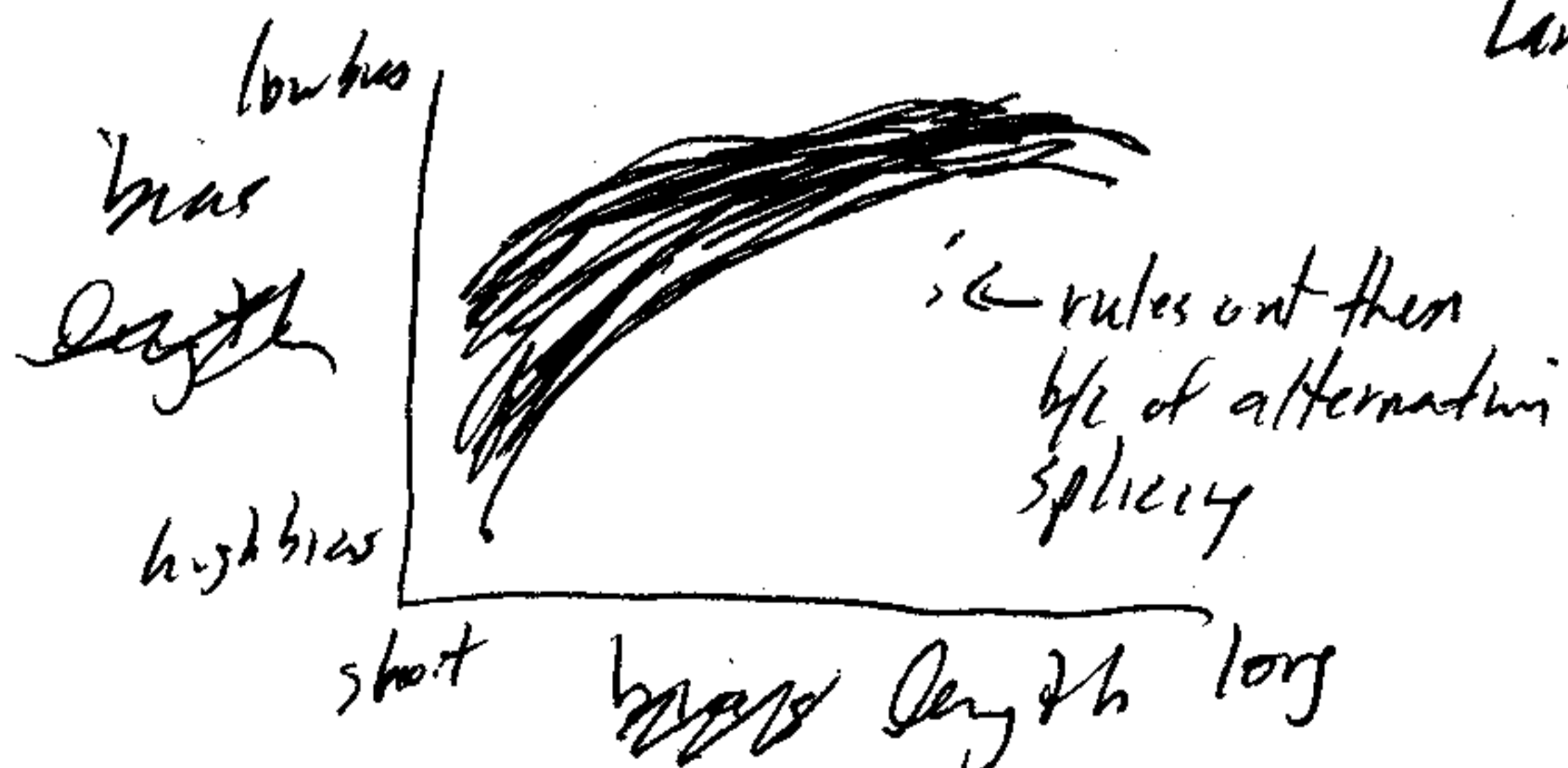
mel sim outgroup

Does codon bias change?

Codon bias conserved overall but bias w/in individual genes & S's. } but do this for whole gene

why codon bias change in individual genes? } but this - chrom. location & S and recomb. rates vary w/ genome position

5' 3'



Large genes cannot support codon bias

Why?

- translational speed
- ~~translational accuracy~~
- Hill Robertson interference - long genes have more traffic.

short genes



med genes



long genes



Only short genes have good relationship between codon bias + recomb

Regulatory Evolution - Even Stopped

- lots of info about enhancers
- seems to be flexible - multiple ways to do same thing



Evolution of Enhancer

- length Δ s
- some binding sites completely conserved

Says consensus is usually strongest.

This would allow for compensatory changes.

- No site
- weak site - non-conserved
- strong site - conserved

CCCAAA
GGGTTT

