EVOLUTION 1993

Pseudofossils

- take two complete sets and use resampling

Mutation

EA Kellogg

55 - pol III

- what tissue type
- if from somatic then mutations may not be passed on...

pseudogenes undergo concerted evolution

- is concerted evolution guided by tx?

- biased gene conversion?

-

EVOLUTION 1993

Michael Donohue: RANDOM vs OUTGROUP

- sequence bias?

① need diff. types of RANDOMS

PR Sochondoun

Zebrafish

Examples
- aphids/homoptera
- rhizobium
- rickettsias
- vents

Nancy Moran

- says these are beneficial
- homoptera - almost all feed on sap
- two subordens -
- says they are dependent on symbionts
  - probably by supply essential aa.
- aphids in mycetocytes
- transmission
  - mothers to offspring before birth
  - transovarial
  - soldiers don't have symbionts
- phylogenies
  - used those w/ good host phylogeny

..

① - all endosymbionts from 1 clade
- complete congruence betw. host & symbionts

② claims that divergends times should be parallel

③ got fossil dates

④ are rates constant in each branch
- seems so - relative rate

(4)

2%/50 my

- may be faster in endosymbionts

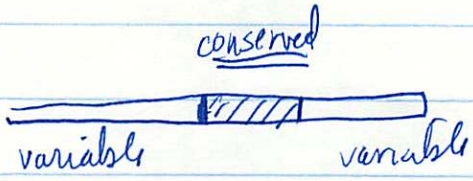
- medflies
- whiteflies } v. diff bacteria

Replacement?

① makes sense bec. multiple types of symbionts

Bindin

- sperm surface protein

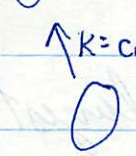


- variation within & among species

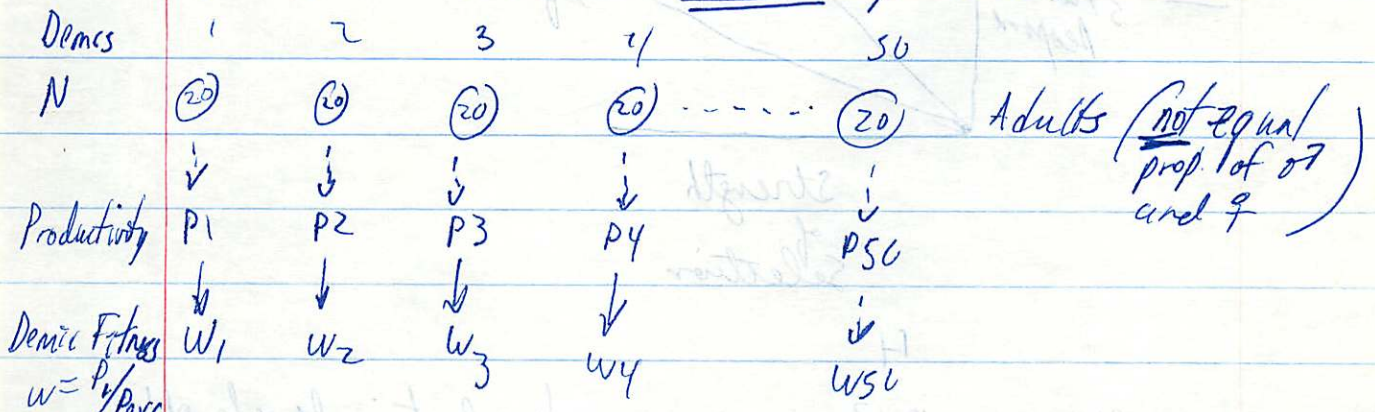
- aa replacement = 2x silent subst.
- intraspecific variation

B. Farrell

Michael Wade



- Imposed interdemic selection
- Fitness - counted # of adults produced



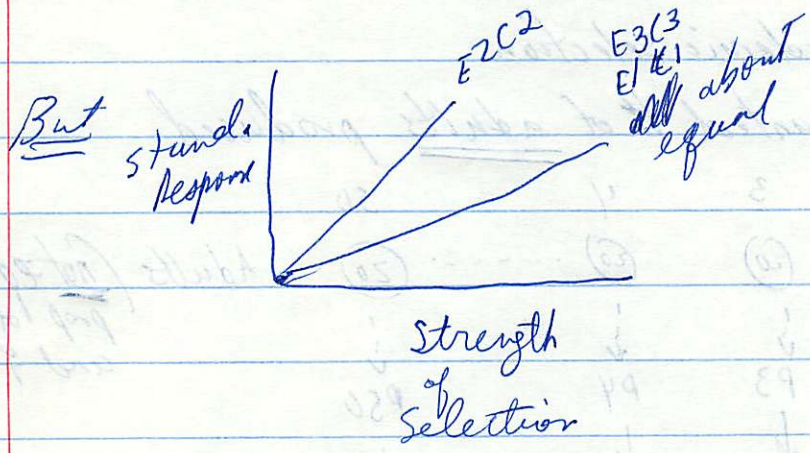
W(20) = # of indiv. to contrib. to next generation
= extras go to migrant pool
= missing come from migrant pool

Control = random w/ same amt. of migration

Three treatments

E1-C1 Interdemic Selection Every Generation
E2-C2 " " " Other "
E3-C3 " " " 3 "
(Random otherwise)

Thus forces of interdemic selection would be strongest in E1-C1 and whatever this selection causes it would be largest here.



	H	
E1C1	0.12	- response to selection levels off
E2C2	0.54	- response to selection doesn't level
E3C3	0.139	

Relaxed Selection

Sponsor F. Moore

When is it shifting balance?

Epistasis

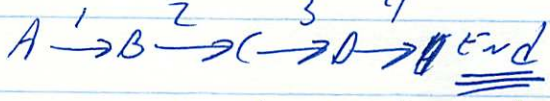
see Lenski 1988 Evolution. T4 phage.

Mechanisms

large scale: homeotic

Small scale:

Metabolic control theory



1, 2, 3, 4 all contribute to end.

Correlation selection

- two traits, both affect each other

Evidence

Allozymes (PGI, G6PDH

- osmotic stress in copepods

says diff organisms have diff amts of epistasis or ease of detection } but similar things were not compared

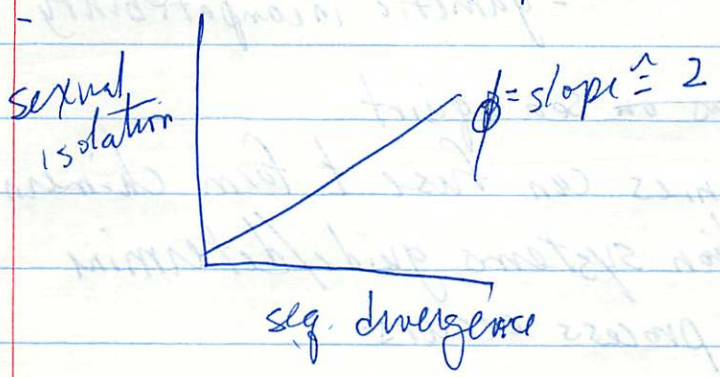
Demographic history affects repeat variants

Cohen

Promiscuity in bacteria

① sequence divergence
② restriction modification

sexual isolation is prop. to G_0 divergence



more sequence divergence ⟶ more sexual isolation

Recombination cannot limit sequence divergence

R. Grossberg

Allorecognition
- "w/ few total / loci - there must be a high level of variation"

Three possibilities
① neutral - unlikely bec. too many alleles
② selection
③ indirect - e.g. neg. assort mating
- gametic incompatibility

e.g. Monse MHC mating studies

~~Botryllus~~? - ~~grows on~~ sea squirt
- indiv. colonies can fuse & form chimera
- allorecognition systems guide/determine whether process occurs-

Gametophytic incompatability -
- can maintain many alleles w/ low N
- but doesn't work here

Colonies sharing one or both alleles will fuse

DW Hall

Gene conversion & meiotic recombination

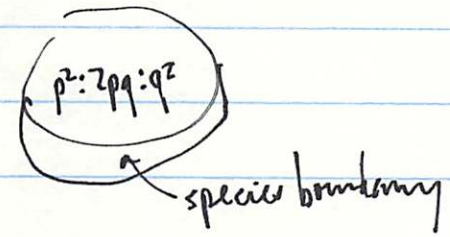
Meiotic reproduction vs Apomictic

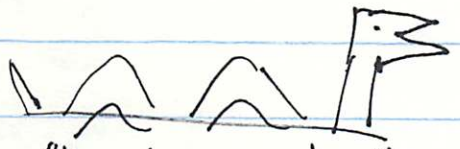
Bengtsson $A_1 \neq A_2$

Biased gene conversion – $A_2 \rightarrow A_1$

Felsenstein

Evolutionary Theory circa 1970





① Is there a post neo-Darwinian evolutionary synthesis?

1972 - Ewens

- Nei's Genetic Distance

1993 - Population Samples

① Human mt Eve

② Nuclear too

③ Kingman - coalescence $4Ne/K(K-1)$

④ Create tree

2 types of variability = mutational & coalescence

⑤ Likelihood

$L = \sum_{\theta} Prob(G/\theta)\, Prob(Data/G)$

$Prob(G/\theta)$ = probab. that a given genealogy

$Prob(Data/G)$ = probab that w/ the data would f.t.t.

Can use Markov-Chain Monte Carlo methods to get estimate

Hastings-Metropolis

① Start w/ tree

② Modify it - randomly

Important Factors

① Genetics

- drift
- mutation
- recombination ← subdivide sequence into regions
- gene conversion
- selection in favor of advantageous alleles
- selection agst. deleterious
- balancing selection

Genomic

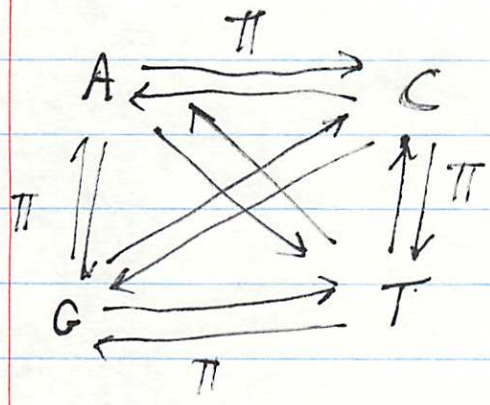
- Uneq. X-over
- transposition
- inversion
- translocation
- fusions
- duplication

Genomic analysis of selection
- QTL mapping
- get gene frequencies for genes that affect a character

Morphometrics

Species selection?

Is this a new evol synthesis?



- K = trans. transversion ratio

π = % base

Testing models

① mtDNA

② get MLE tree score

② compare to tree score w/ no assumptions

③ simulate evolution on that tree w/ model

ISN'T THE MODELING ANSWER TO FIT A TREE?

② new model
- γ distribution of rates

③ can estimate K, γ w/o tree

④ not much diff. in MLE score among trees

Senescence

① more mutat. than incr. early

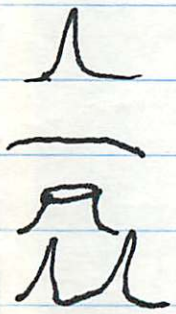
② deleterious mutations

③ pleitropy

D. Swofford Exploration of Tree Space

Types of tree methods:
- Algorithms - UPGMA, Neighbor-joining } can't say much about reliability of tree
- Criterion Based - MLE, parsimony

Landscapes



① one major peak - even close trees OK
② flat --- most trees equivalent & very diff.
③ plateau -- eg parsimony
④ multiple peaks ...

Tree-Space Exploration

① tree searching strategies

11 taxa
- ⓐ exhaustive

25 taxa
- ⓑ branch & bound (terminate paths)

473 taxa
- ⓒ stepwise addition
- ⓓ nearest neighbor interchange
- ⓔ random addition sequence

Taxon Sampling Paradox

Phylogenetic Methods

① mtDNA in humans

- Vigilant et al
- Swafford et al correction --- not enough trees
- Blair Hedges et al
- Stoneking et al 1992
- Rzhetsky & Nei 1992
  - Minimum evolution method
  - Swafford used this for mtDNA

DHillis - Don't Trip Over Your Bootstrap

Non-parametric bootstrapping : building pseudosamples of original data

Precision = reliability of bootstrap mean proportions given finite # resamples

Accuracy : prob. that inferred clade is real

Simulations

- 100 simulations
- inferences ... ~70% true
- bootstrap ... get wider distribution

for simulations - bootstrap doesn't relate well to repeatability

for TT - bootstrap better at accuracy
  - but only for mean
  - biased but usu. conservative

↓ unbiased but highly imprecise

M.J. Sanderson

Bootstrap
- confidence can be low in absence of conflicting data
- estimates of confid. are sensit. to # uninform. characters
- estimates of confid. may be inaccurate - Hillis
- may not apply to morph. data
- characters are not independently & identically distributed

IID Assumption

Why not?

① any structure ... (prot 3D)

How correct?

① random sampling ... not w/ molecular data
- sequence ... RFLP ... RAPDs

② distribution of synapomorphies
- if synapomorphies spread among sampling methods (enzymes) get better probabilities

Origin of evidence important

√Felsenstein

Bootstrap

① Assumes i.i.d

② Non-identical distrib. ; non-indep. distrib. — can sample in blocks

~~- multiple tests problem~~

- positive correlation .. when one site/character changes so does other

- not neg ... when one changes the other does less.

③ - multiple tests problem Bonferroni correction

Hillis & Bull ..

- He suggests "Felsenstein Zone" is not problem of ~~bootstrapping~~.

-

C. Aquadro

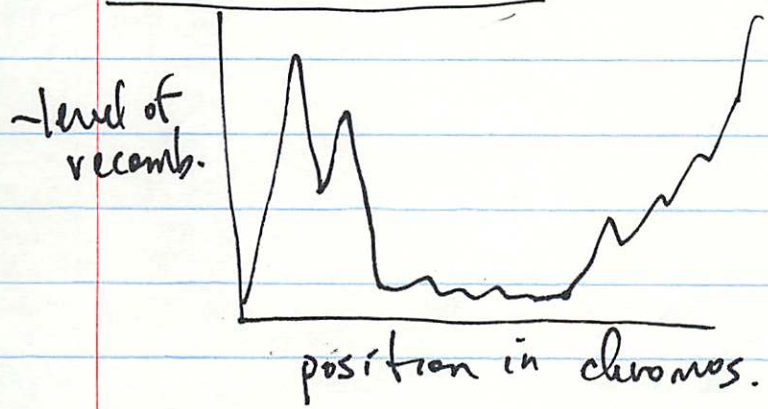
Drosophila -

- 4th chromo
- X chromo tip
- ~~rates of recomb~~

} low recomb.

- regions of low recombination → low variability
- " " " high " → high " "

Rates of recombination



— what about sequence divergence affecting recombination

Why?

① low recomb. regions ↑ linked constraints

② recomb. mutagenic

③ selective sweeps

④ elimination of deleterious mutations — see Charles

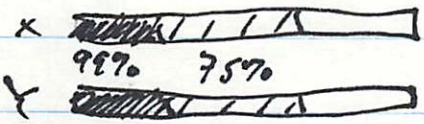
- neg. hitchhiking

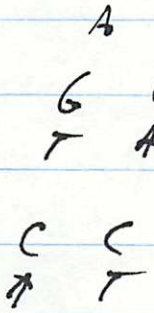
A. Bre—Walker

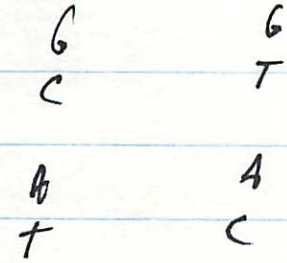
① variation in sequence composition
② GC=genes, SINES
AT=[illegible] LINES

③ recombination

Y chromosome = lower AT in non-recombining regions







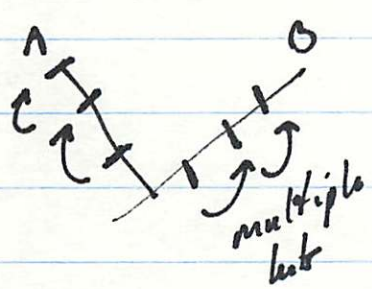
JEvans -
- Myrmica -
  - queen # & life history v. variable

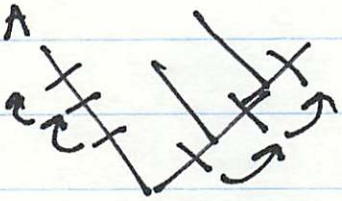
- Average relatedness within colonies
- Variance in queen-queen relatedness

$(CA)_n$

Goodnight & Queller
  Average relatedness of queens

Ratio of Nucleotide Evolution





- ADD TAXA AND CAN SEE MULTIPLE HITS MORE READILY.

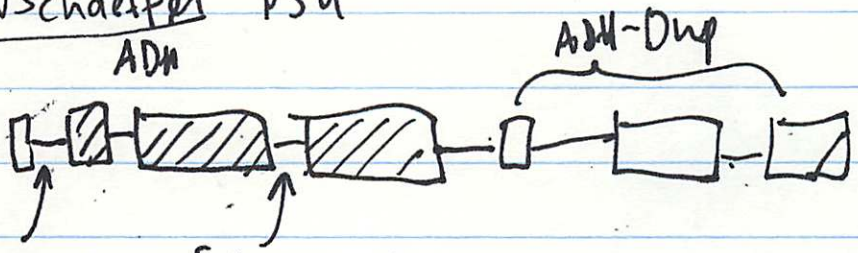
BODY MASS CORRELATES W/ SUBST. RATE

D. Gutfman Periodic Selection & Recombination
- Dykhuizen & ... JBac 1991
- showed that diff. regions have diff. phylogenies

sppA - one grpA highly divergent
gap - v. low divergence G3PDH *
paB - same geneology as GAP;
zwf - one gapA highly divergent

sppA - gap ... paB ... zwf

SW Schaeffer PSU



- clusters of linkage disequil.
- pairs of sites in link. diseq. are close in 1° structure

Thinks clustering due to epistasis from 2ary structure.

S Nuzhdin

① 10^{-4} transposition/generation

② mean transposition/~~population~~ individual
same in diff pops.

Why? - see Langley & Charlesworth
- Selection - Deleterious, ectopic exchange
- Regulation - host & self

10/32

If all capable
10 new
22 old
prob. of new = 10/32

D. Hartl
- Use lines of Charlesworth
- assumes that no selection in small populations

Mutations only expressed in bad environs.

RM Dawley
- 10% variation in DNA content
- but all from indiv. lines of each species

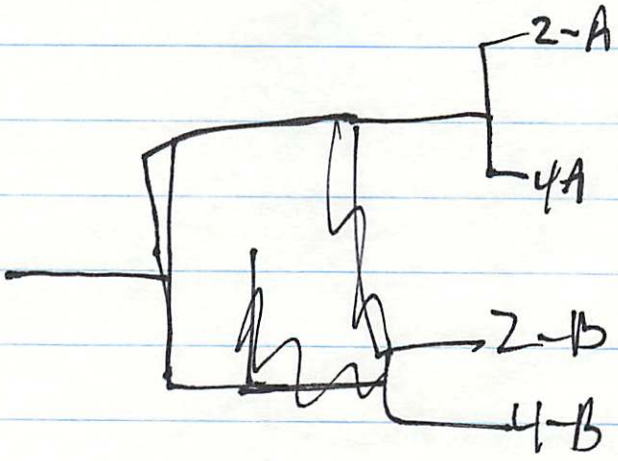
homoplasy -
Mytilus edilis
Heteroplasmy - type C / type A
Homoplasmic individuals - fo. type C very rare

Zouros - biparental inheritance of mtDNA

TCrease - Daphnia pulex

- ameiotic reproduction vs. meiotic

intergenic spacer - have RNApol promoter



Bats

Morphology

- Chiropt & Dermopt appear similar
- visual & penal morphol - Pettigrew et al suggest non-monophyly of bats

Smith & Madkour

Molecular.

- 12S, COII, IRBP, Epsilon globin ...
  - Chiroptera one order
  - Dermoptera not monophyletic w/ Chiroptera

Glires? = Rodents & Lagomorphs

- Morphology suggests so
- Molecular doesn't

NO COMMENT ON RELIABILITY.

use sis orders

Rodents — over 1/2 species of mammals

- morphology suggests monophyletic
- molecular - L-t branches LME
  - some weird stuff
- many proteins - w/ birds/marsups. as outgroups
  - Alpha-lactalbumin

R. Honeycutt - Eutherian mammals

Eutherians

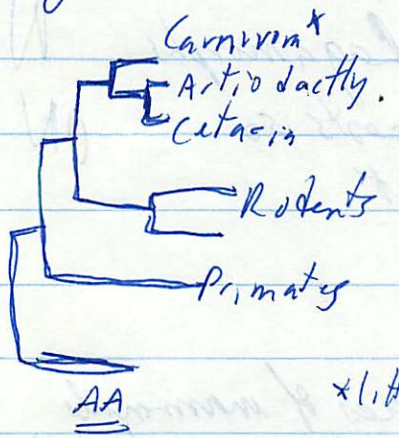
- Three clades from morphology - Novacek & MacPhee - Flynn
  1. rodentia / lagamorphs
  2. chiroptera
  3. elephants

Book

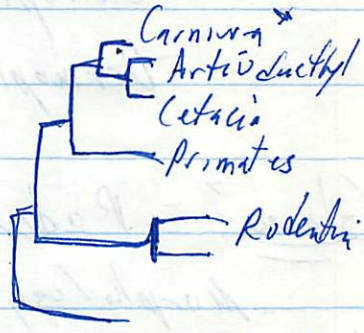
- Molecular data NOT congruent - Goodman

mtDNA

- 6 complete genomes -



AA



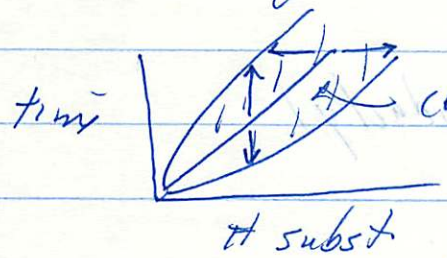
DNA total

* little morphol. support

- unequal weighting schemes help (only transversions and only 3rd position)

Hill's - Molecular Clocks

Given a linear relationship - can time of divergence be predicted from molecular



confidence limit due to Poisson distribution of ratio.

Restrict. Site - does fit

Sequence data doesn't fit clock perfectly - variance greater than expected

(may be due to non-independence)

Real data

- confid. limit of regression

example of this for rRNA.

Assumptions

① clock uniform across taxa

② dating band

Rodentia
Artiodactyla } didn't get much support for any of these orders.
Primates

(coII) Primates, Rodents, Artiodactyl

Variation at each codon position

Retention index higher in Artiodactyls ...
probably because less divergence

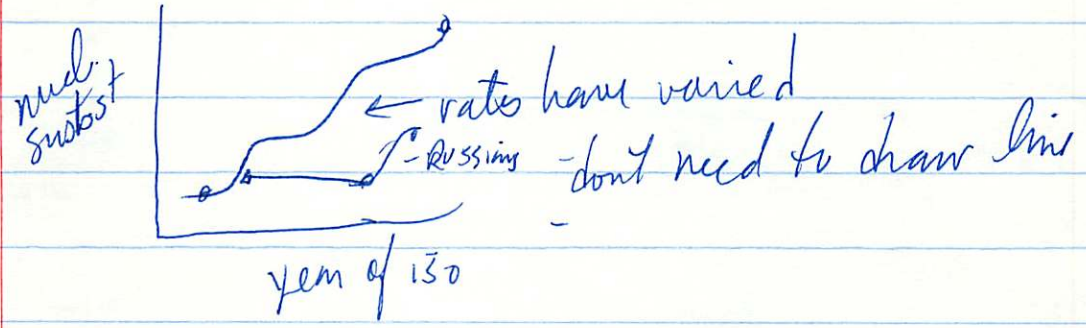
80% C-T
50% C-T

Rodents TS/TV = 2:1
Artiodactyls ≈ 8:1
Primates ≈ 18:1 (less divergent)

- Rate in rodents somewhat higher at 3rd position
- Rate of aa replacement higher in primates

NO STATISTICS

Influenza virus NS - Fitch &



S Palumbi

What are patterns of nucleotide states compared to physiology

A Martin

Shark physiology
- 6-800 mM Urea
- Rate of prot. evol. slow in cytb-nt
- Rate of silent subs at 4fold deg sites - slower

Diff. w/in taxa

Correlates w/ cytb rate (sil. subst rate)

globin
cytb

- Generation time ...??
- Metabolic rate ...??
- ~~Body size and rate~~
- Multiple regression

Metabolic rat
- $O_2 \rightarrow O^{\times}$ radical → damage
- mtDNA turnover
  - Gross et al mtDNA rat

Nucleotide Generation Time reduced by

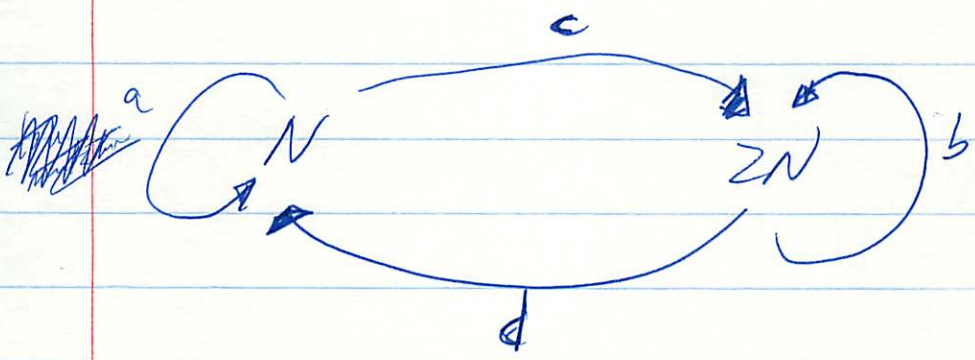
frequent repair

frequent division

high tumors

Sally says rate of beneficial mutations is higher in diploids. But diploid state limits mutations.

In multicellular organisms then the generation ~~of haploids~~ of mutations is common at haploid stage. Are mutations more common



Diploids
extra template
extra repair proteins
- if mutagen limiting their less mutation

a, b, c, d = mutation rates

d may be v. high

b may be low (diploid allows extra template)

a - high

c - low

what are diff. in mutation rates in haploids vs. diploids