

Mon - Insect systematics

Tues - Stats, Bayes, tetrads

Wed - Ethology, game theory

Thurs - Plants

Fri - Enzyme kinetics

Sat - Phylogenetic trees

Sun - Physiology

6:30

day before prac

USABO parking list

- Insects
- micro Campbell
- Raven's
- Systematics cards

8:30
7:00 - Insects + misc (specimens)
7:00 - Stats, Bayes, lotrads
7:00 - Ethology + Game Theory
7:00 - plant terminology + systematics
6:30 picnic → end, enzyme kinetics + basic spec
8:30 - phylogenetic trees
7:30
6:00
day before prac 6:00 — nothing

← card games
not teaching

Spec intro
Enzyme kinetics + Mich Menten
~~lotrads~~
plants I (90)
plants II (60)
Misc systematics
Statistics
~~Bayes~~
MCB problem solving
Ethology + game theory

Phylogenetics
Tetrad analysis
Entomology
Bayes + genetics

Physiology

Phylogenetic trees & comp bio lecture (beyond Campbell)

- UPGMA
 Neighbor joining
 Max parsimony
 Max likelihood
 Bayesian inference

rooted vs. unrooted

cladistics

autapomorphy
 synapomorphy

phenetic = classify based on phenotypic traits
 wiki: "largely obsolete" - but IBO will ask you to do it

phenetics: classify on phenotype, regardless of phylogeny
 does not distinguish between

define term as ancestor of cladistics

plesiomorphies - traits inherited ancestrally
 & apomorphies - traits that evolved anew

↳ can be misled by convergent evolution

fig. birds bats bears phenetics: wings! vs. nooooo.



of seconds since Big Bang:
 4×10^{17} sec

(DNK)

cladogram terminology

ancestral state
 derived state

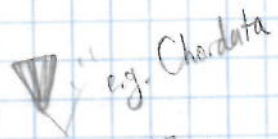
homoplasy
 plesiomorphy
 apomorphy

synapomorphy
 autapomorphy

2+ taxa ("together")
 → useful

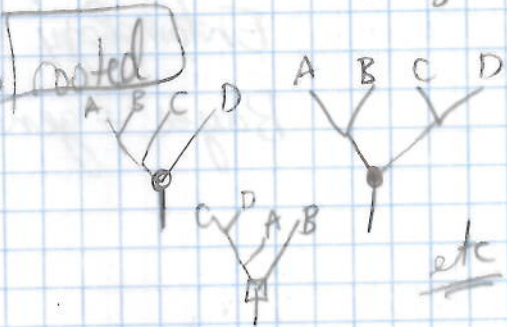
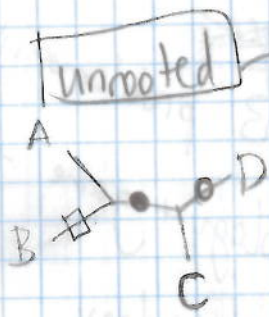
1 taxa ("self")
 → useless

monophyly
 paraphyly
 polyphyly



"neither"
 e.g. Detritivores

horizontal gene transfer
 relevance



$O(n^2)$ UPGMA

Bayes
 Max

Q: More ways to make unrooted or rooted trees? A: rooted

Exam

Counting

# taxa	# UR*	# R [✓] more
3	1	3 = 3
4	3	3 × 5 = 15
5	15	3 × 5 × 7 = 105
10		34,459,425
20		8,200,714,532,637,891,559,375 = 8 × 10 ²¹

of seconds since Big Bang:
4 × 10¹⁷ sec

of species
8.7 mil

(DNK) # rooted (n) = $\frac{(2n-3)!}{2^{n-2} (n-2)!} = \prod_{i=1}^{n-1} (2i-1)$

rooted (n) = # unrooted (n+1)

paper. 9 "The principal use of these #s will be to double-check algorithms & to frighten taxonomists"

So! To avoid searching through this massive space of possibilities we need... algorithms!

- Methods {
- UPGMA
 - Neighbor-joining
 - Max parsimony — problem: not always good
 - Max likelihood
 - Bayes

(n²) UPGMA



- assumes molecular clock (ultrametric)
- creates rooted tree

(n³) Neighbor-joining



- no clock assumption
- creates unrooted tree

matrix distance methods; fast

Max Likelihood

- probability, Bayes
 - assumptions about types of mutations
 - want most probable
- creates rooted tree

Max Parsimony

- use parsimony principle
 - want: most parsimonious
 - score trees, but can't be exhaustive
 - creates unrooted tree
- can use more nuanced data (e.g. DNA) slow

Example: UPGMA

Game

currency: energy

energy: finite per turn (doesn't roll over)

abilities: might or might not consume energy

Win conditions

- Outsurvive everyone else (remove all producers)

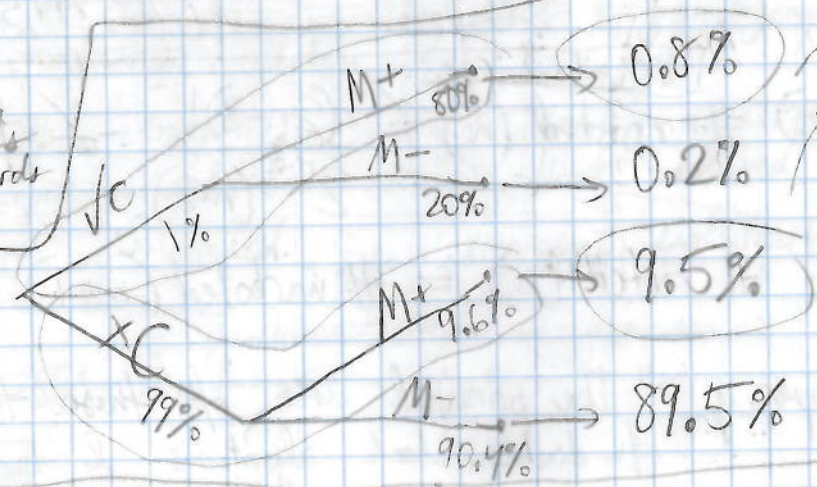
- Size victory: size > \$foo

piles (producers, C1, C2)

(A) 1% w
80%
GUESS 9.6%
factors (70-80%) mammo
only

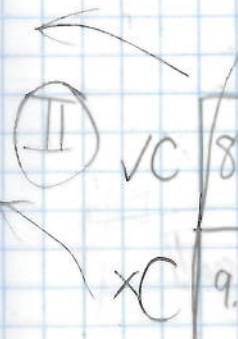
(I) Pr(C|M)

Cataclysm cards
Bioengineering cards



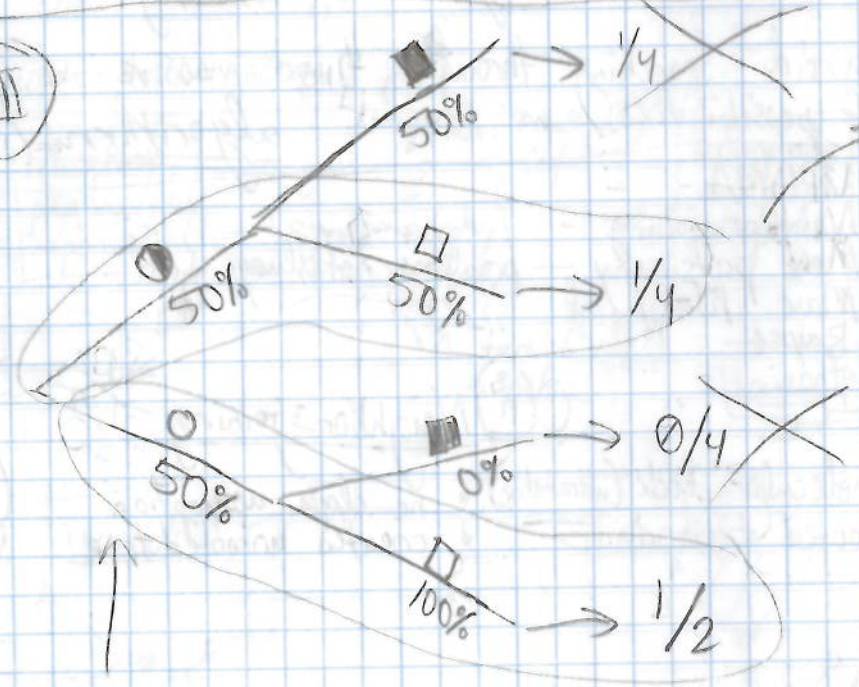
New Pr(vc)

$$\frac{0.8}{0.8 + 9.5} = 7.8\%$$



(III)

Tree (III)



New Pr(●):

$$\frac{1/4}{1/4 + 1/2} = 1/3$$

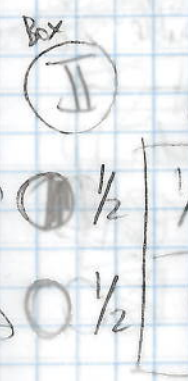


priors

event

update!

priors

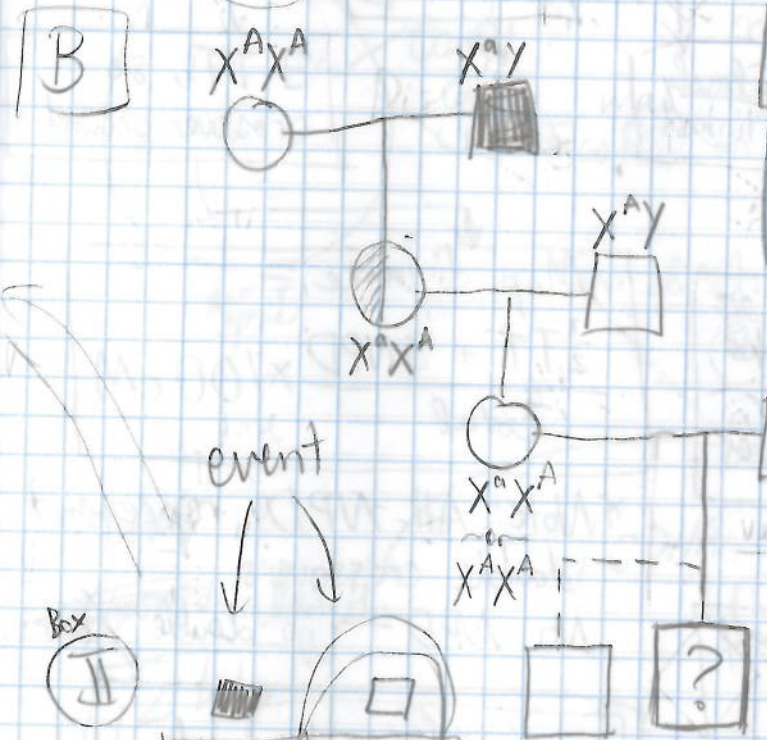


A 1% women @ 10 have bc-cancer
 80% of women w/ bc-cancer get mammo+
 9.6% of women w/o bc-cancer get mammo+
 GUESS factors (70-80%) mammo+. $P_r(\text{bc-cancer} | \text{mammo}+) ?$
 only 15% of doctors get this right

I $P_r(C|M) = \frac{P_r(C \& M)}{P_r(M)} = \frac{80\% \times 1\%}{80\% \times 1\% + 9.6\% \times 99\%}$
 $= 7.8\%$

II

	M+	M-	
VC	$80\% \times 1\%$	$20\% \times 1\%$	total: 1%
XC	$9.6\% \times 99\%$	$90.4\% \times 99\%$	total: 99%



III

	Carrier	Not Carrier	
Carrier	$\frac{1}{2} \cdot \frac{1}{2}$	$\frac{1}{2} \cdot \frac{1}{2}$	total: $\frac{1}{2}$
Not Carrier	$0 \cdot \frac{1}{2}$	$1 \cdot \frac{1}{2}$	total: $\frac{1}{2}$

update!

Bayes' Theorem

- A - Disease problem
- B - Pedigree problem

The method

1. Priors
 2. Event happens
 3. Update!
- COLORED

Visualization styles

- I** Formula
- II** Box
- III** Tree

$P_r(A|B) = \frac{P_r(B|A) P_r(A)}{P_r(B)}$

or,

$P_r(A|B) = \frac{P_r(A \& B)}{P_r(B)}$

ORIGINAL
 $\therefore P_r(\text{O is carrier}) = \frac{1}{2}$
 $P_r(\text{? is } X^A Y) = \frac{1}{4}$
 WITH OLDER BROTHER
 $\therefore P_r(\text{O is carrier} | \text{? born}) = \frac{P_r(\text{O} \& \text{?})}{P_r(\text{?})}$
 $= \frac{\frac{1}{4}}{\frac{3}{4}} = \frac{1}{3}$ **I** Formula

$P_r(\text{? is } X^A Y | \text{? born}) = \frac{1}{6}$

Tetrads Whole point: Study recombination
tetrad: output of a single meiosis \rightarrow spores

Yeast: ascomycete
 ascus

\rightarrow Spore parents are $\text{AB} \times \text{ab}$ (n)

Come in an ascus:

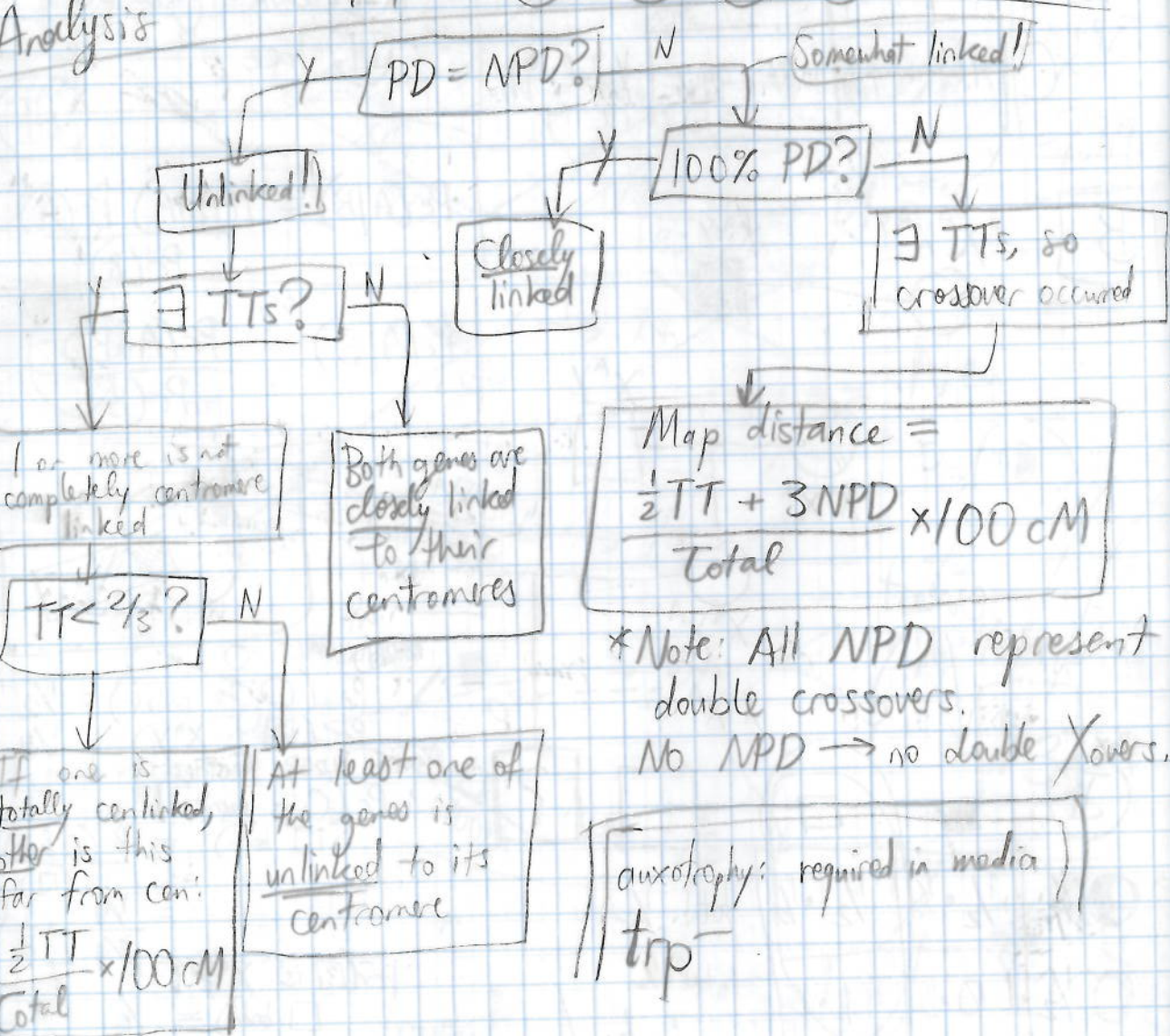


PD: $\text{AB} \quad \text{AB} \quad \text{ab} \quad \text{ab}$

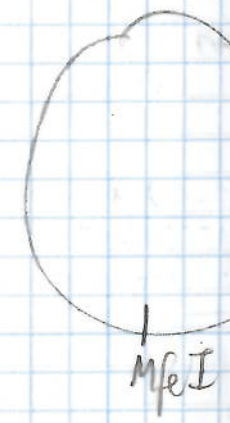
NPD: $\text{Ab} \quad \text{Ab} \quad \text{aB} \quad \text{aB}$

TT: $\text{AB} \quad \text{Ab} \quad \text{aB} \quad \text{ab}$

Analysis



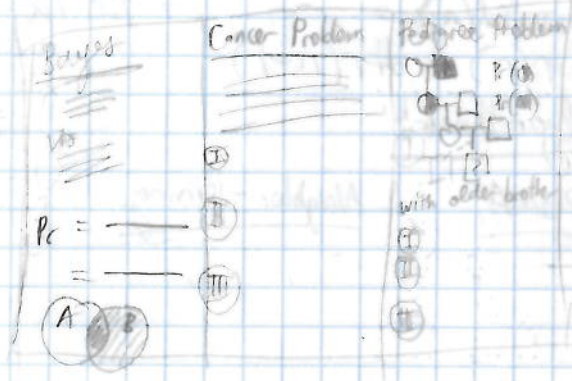
MfeI Eco



cDNA
~~Plasmid~~ 2 kbp

2 kbp





Insecta

Phylog. etc

Neoptera

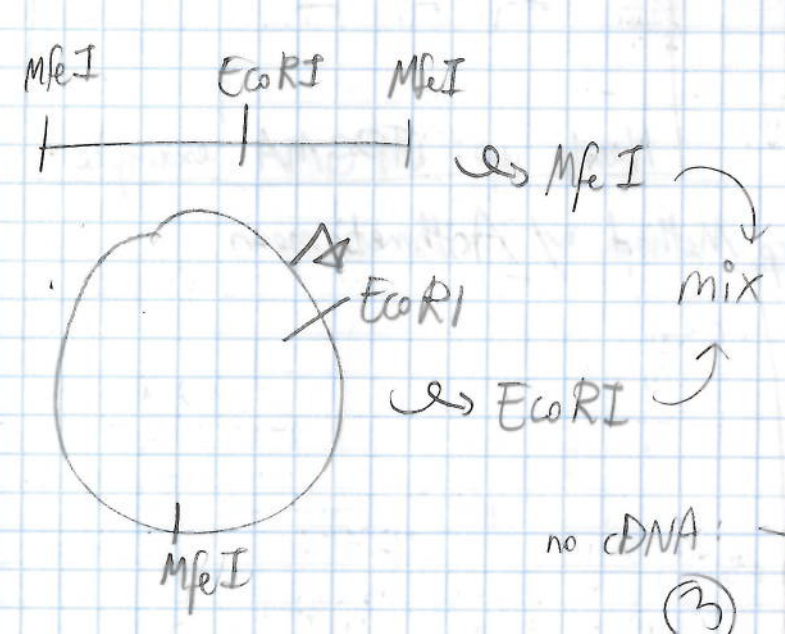
Dictyoptera

Ortho
p. thina
hemi

Exopt.

Coleo
Hymeno
Lepido
Dipter
Siphona

offset EcoRI:



②

$3.3 + 1.2 \text{ kbp}$

ins. backwards!

Sum: 4.5

no cDNA: → 2 fragments

③

~~2kb & 3kb~~

cDNA

~~Plasmid~~ length:

2 kbp

(2.0 kbp)

w/ cDNA → 4 fragments? 0.85 kbp

①

Messed-up recog sequence

→ ~~2~~

Anyways,

1.8 & 2.5 kbp

Sum: 4.3

Cladogram

terminology

homoplasy
plesiomorphy
apomorphy

monophyly
paraphyly
polyphyly

synapomorphy
autapomorphy

unrooted vs. rooted



#n

#rooted(n) = ~ ~ ~ ← YDN TK

#ur(n) = #r(n-1)

Algorithms!

UPGMA

Neighbor-joining

Max Parsimony

Max Likelihood

Next up: UPGMA example

UPGMA = Un Pair Grp Method w/ Arithmetic mean

① Characters

② Distance matrix

Repeat:

- Find least-distant pair
- Merge into new taxon
- Average for new DM