phylogenetics

- why
- what
- how
- examples
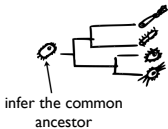
part 1
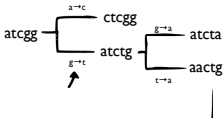why estimate a phylogeny?
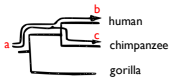
microbes

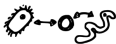an example tree

} relationship between species

infer the common
ancestor

```
                    a→c
                        ┌──── ctcgg
         atcgg ────┤              g→a
                        │    ┌──── atcta
                        └──── atctg ────┤
                              g→t        └──── aactg
                               ↑         t→a
```

b
c
a

human
chimpanzee
gorilla

linear gene flow

microbes can share
DNA horizontally
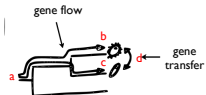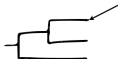
gene flow

b

c

a

gene transfer

d

part 2
what does a phylogenetic
tree look like?

branch

leaf or node

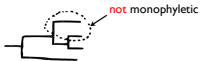internal node

root

phylogenetic trees
may be also be unrooted

monophyletic group

not monophyletic
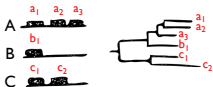
<u>part 3</u>
how to generate a phylogenetic tree?

need molecular data

16S rRNA
part of the ribosome

conserved across bacteria
and archaea

can use other genes though

tree may include both species
and gene relationships

tree requires interpretation

types of phylogenetic tree

cladogram

only splits are informative

phylogram

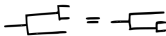branch length
is relatedness

a

b

relatedness of a-b
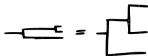is sum of branches

chronogram

build tree with constant
evolutionary time

some parts of a tree
are not-informative

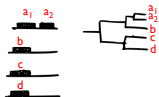rotation of branches doesn't
change anything

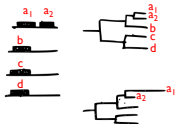nor does the length
of vertical branches
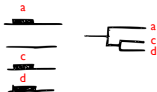
<u>part 4</u>
example trees

a
b
c
d

non ancestor

a₁ a₂

b
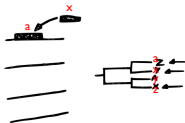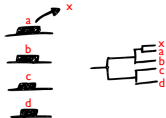
c

d

a₁
a₂
b
c
d

gene duplication

neofunctionalisation

gene loss

horizontal transfer into a

horizontal transfer out of a

summary

<u>why</u>
understand gene-flow and ancestry

<u>how</u>
molecular data (genes)
representing species

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