BIOINFORMATICS: GENOMES AND ALGORITHMS

Computer analysis of genetic information

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GENOMES AND ALGORITHMS

1. Genomic texts

2. Genes and proteins

3. Gene prediction

4. Sequence comparison

5. **Phylogenetic trees**

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5. Phylogenetic trees

- **The tree of life**

- The tree, an abstract object

- Building an array of distances

- The UPGMA algorithm

- Differences are not always what they look like

- The diversity of bioinformatics algorithms

- The application domains in microbiology

I think

B

D

C

A

①

Case must be that one generation then should be as many living as now. To do this & to have so many species in same genus (as is) requires extinction.
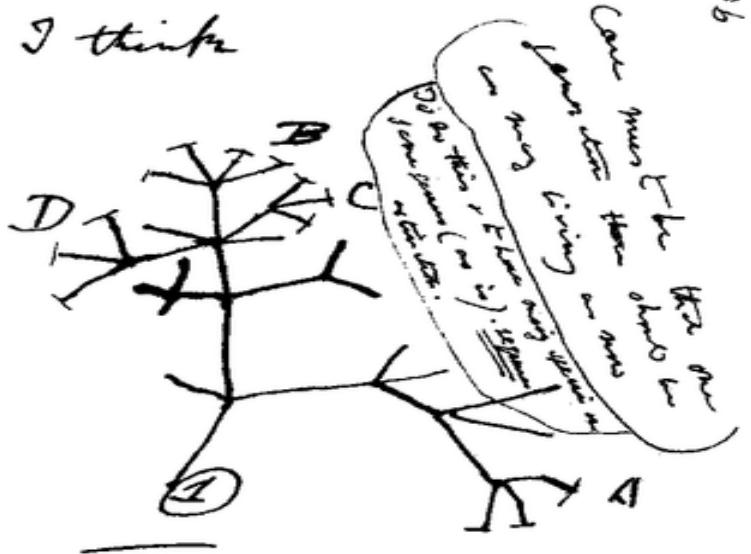
Thus between A & B immense gap of relation. C & B. the finest gradation, B & D rather greater distinction. Thus genera would be formed. — bearing relation
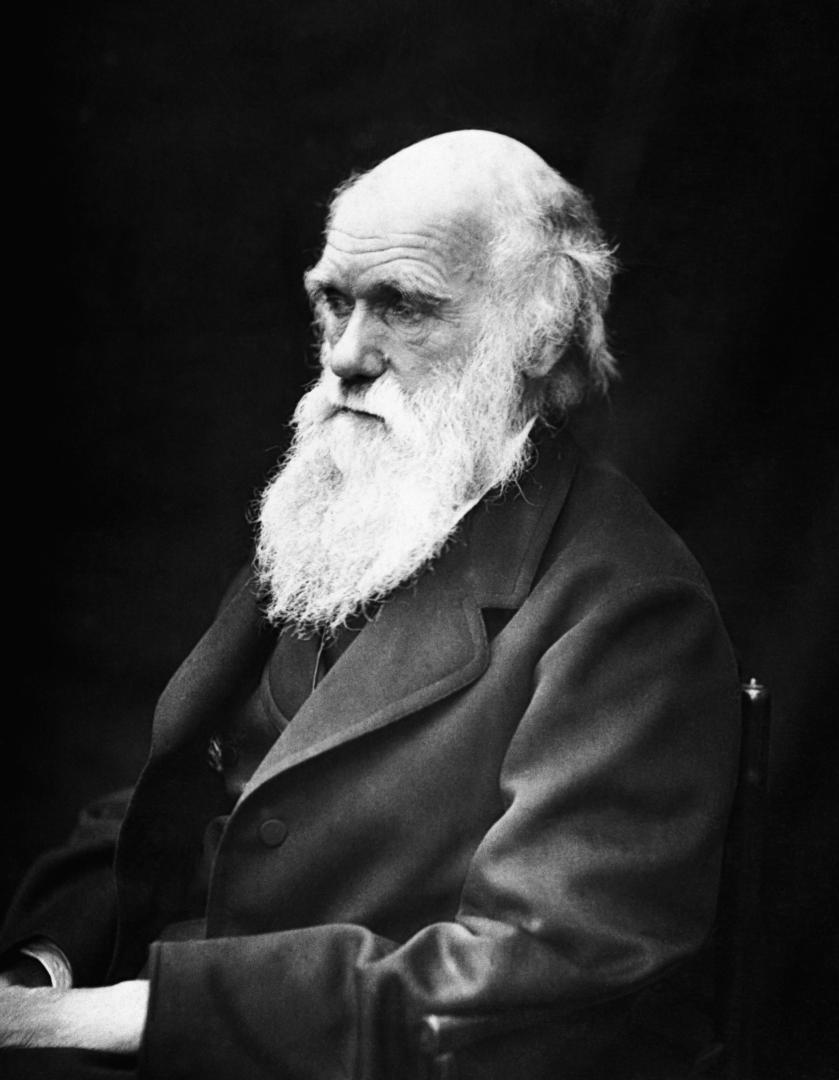
Evolution and the tree of life

Speciation

S1

S12

S11

S111   S112   S1211   S1212   S122

Time
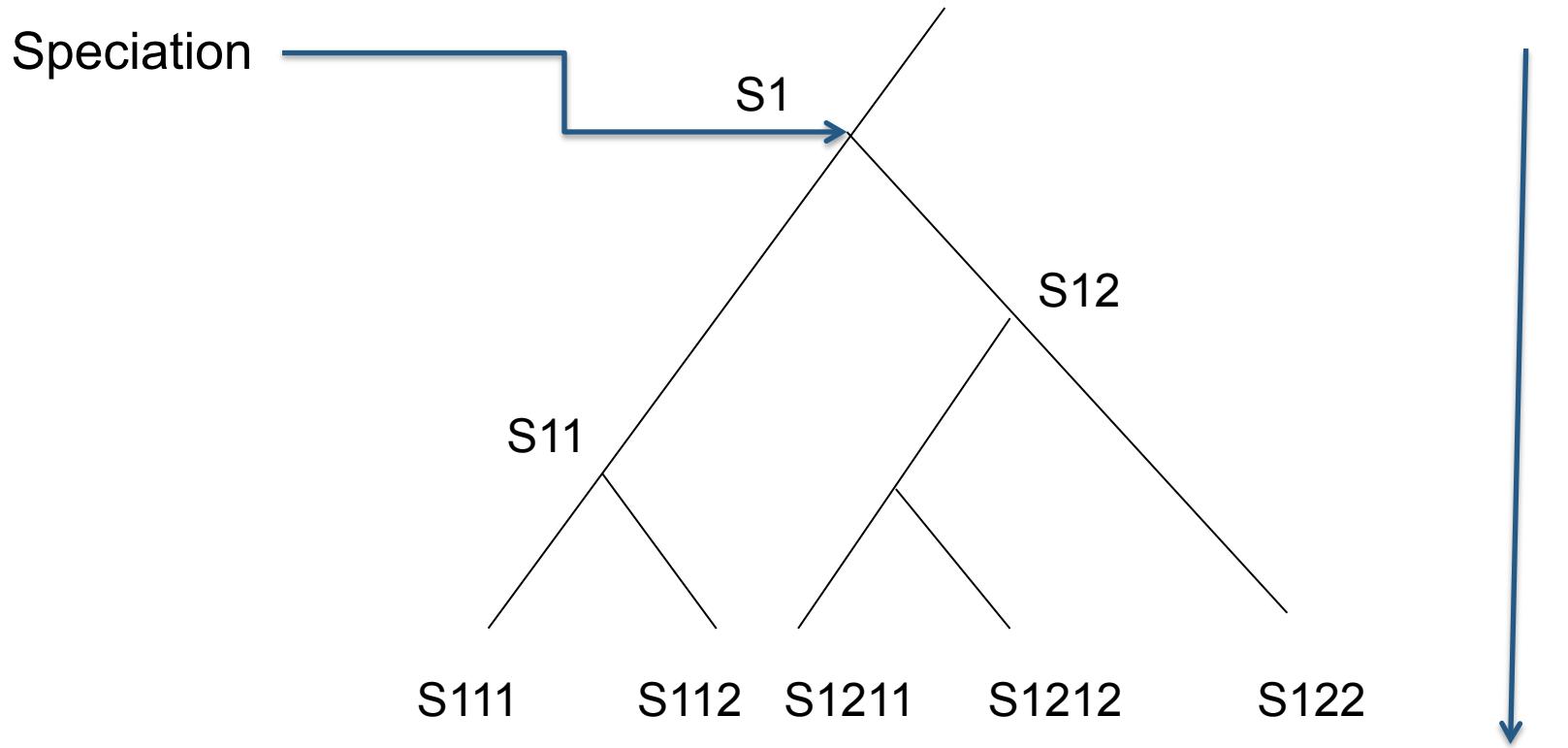
The problem of phylogenetic tree reconstruction

- With the information <u>presently available</u>, can we reconstruct phylogenetic trees?

- Make use of phenotypic information

  or/and

- Make use of genotypic data

H = Humerus   U = Ulna

R = Radius   CMP = Carpals, Metacarpals and Phalanges

http://evolution.berkeley.edu/

Molecular evolution

…AACGTATTGCATTAGGTAGT…

S1

S12

…AACCTATTGCATTAGGTAGT…

…AACGTATAGCATTAGGTAGT…

S11

S111   S112   S1211   S1212   S122

…AACGTATAGCATTAGCTAGT…

…AACCTATTGTCATTAG-TAGT…
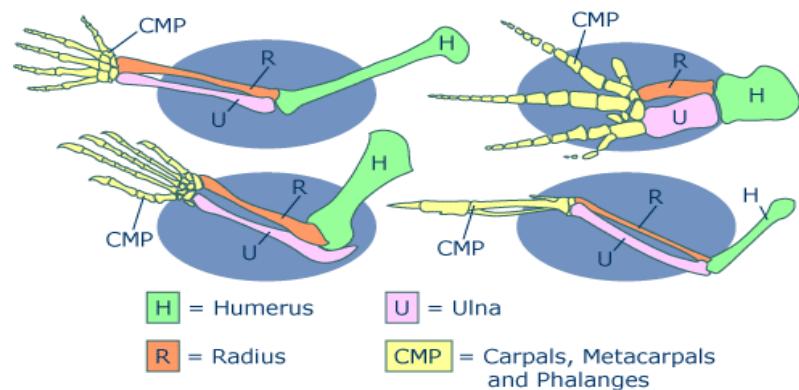
…AACGTATAGCATTAGCTACT…
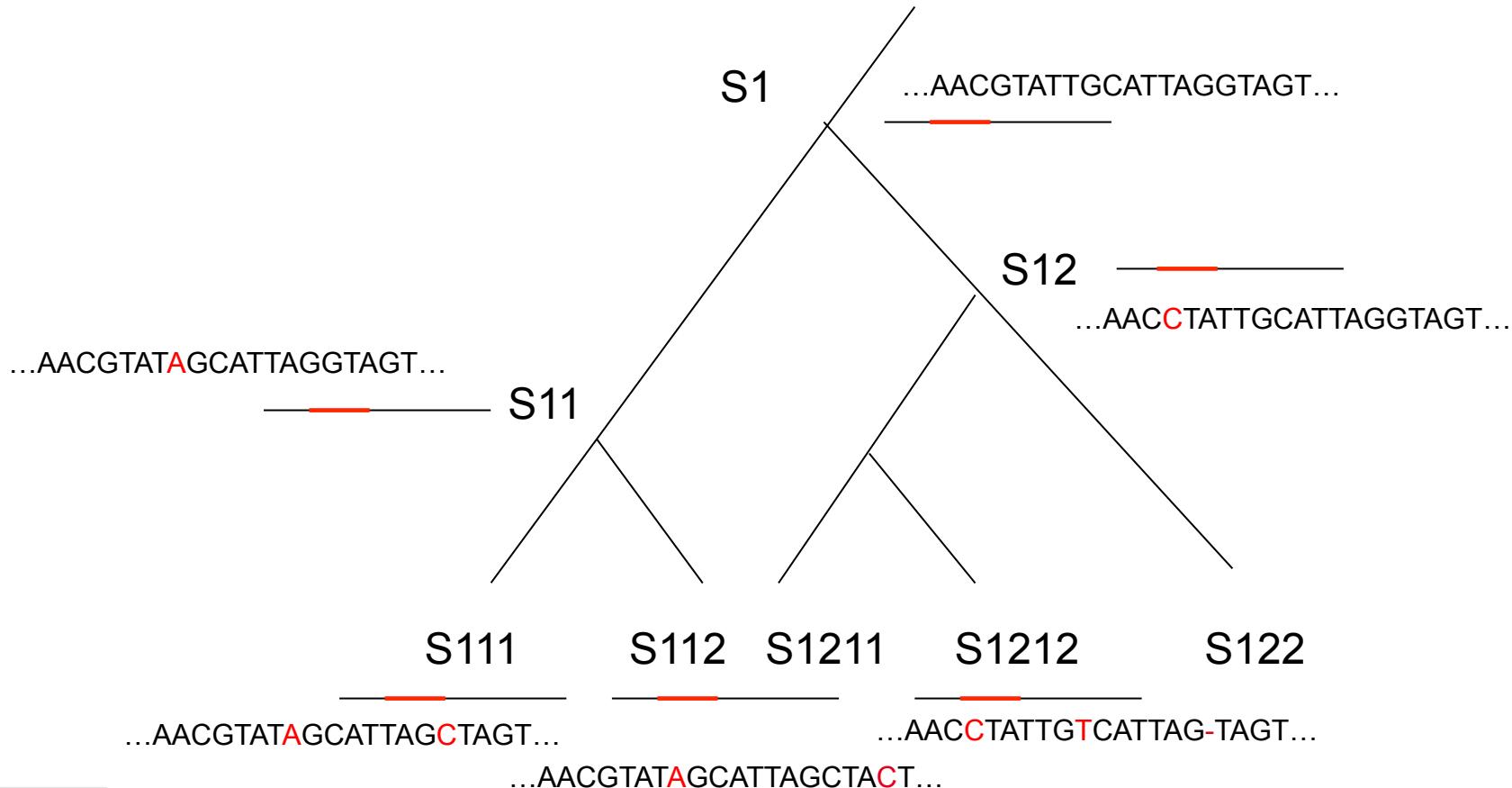
Substitutions and insertions/deletions

...ACCTCT**–A**ATCTATTCGT**A**CTGCTATT...

...ACC**T**CT**G**AATC**C**ATTCGT**–**CTGCTATT...

Available genotypic data

- Genomic sequences

…AACGTAT**A**GCATTAG**C**–TAGT…
…AAC**C**TATTG**C**CATTAG**T**TAGT…
…AACGTAT**A**GCATTAGC–TA**C**T…

- Proteic sequences

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p.6 : Understanding Evolution. 2015. University of California Museum of Paleontology. Février 2015 http://evolution.berkeley.edu/