Introduction to Bioinformatics for Computer Scientists
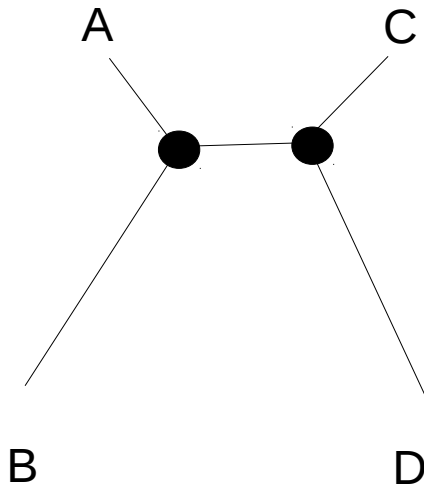
Lecture 9a

Outline – Lecture 9
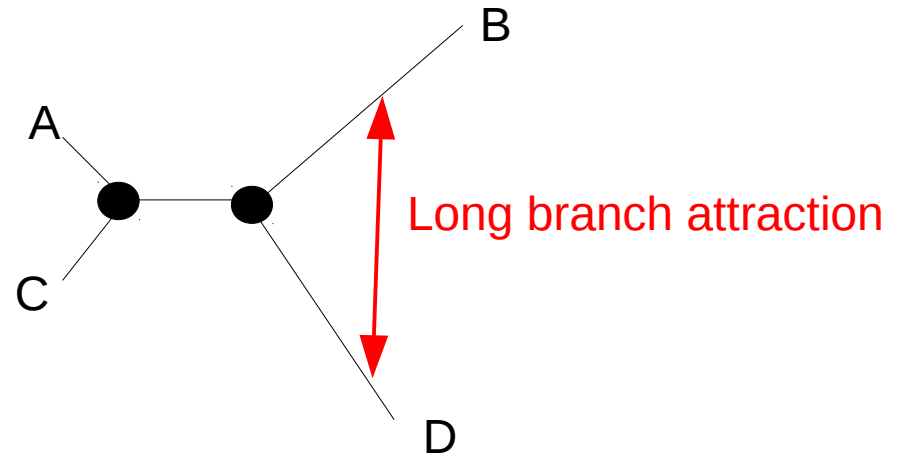
- Lecture **9a**:

  Maximum Likelihood – motivation

- Lecture **9b:**

  Computing the Likelihood on a tree

- Lecture **9c**:

  Computing the Maximum Likelihood on a tree

Parsimony & Long Branch Attraction

- Because parsimony tries to minimize the number of mutations it faces some problems on trees with long branches
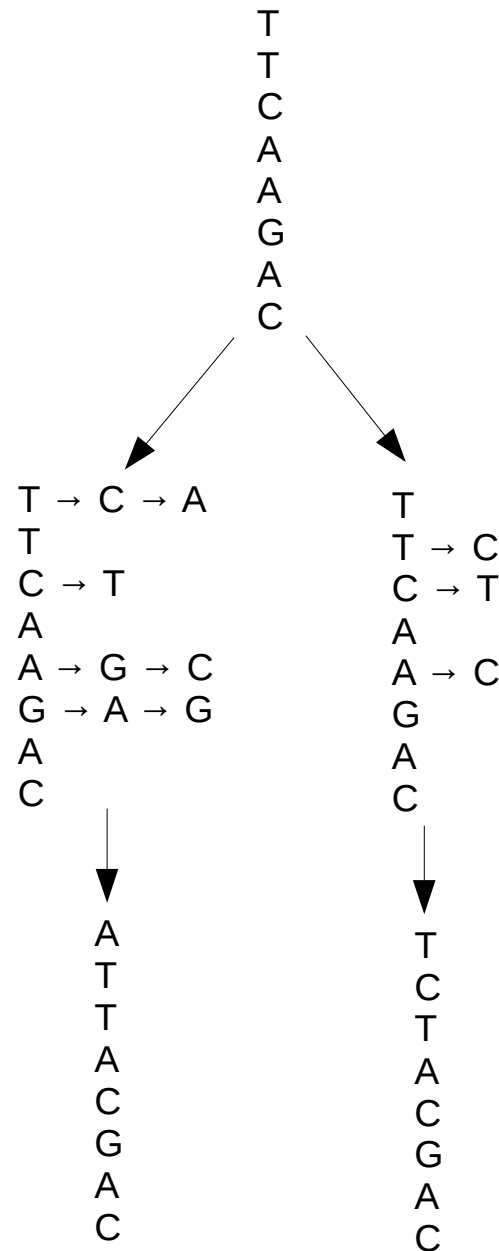

Correct tree

Long branch attraction

Wrong tree inferred by parsimony
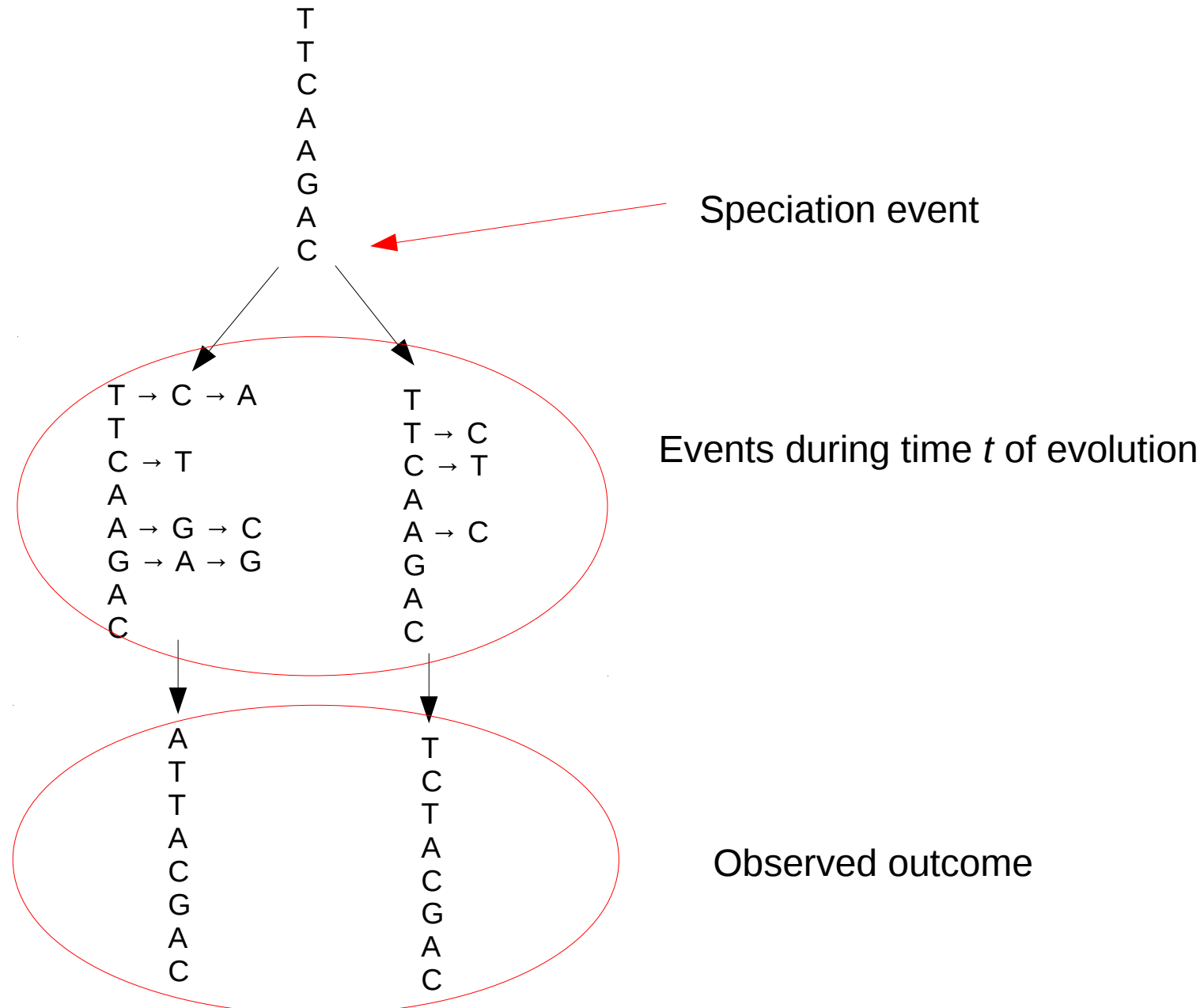
Parsimony & Long Branch Attraction

- Settings under which parsimony recovers the wrong tree are also called **"the Felsenstein Zone"** after *Joe Felsenstein* who has made numerous very important contributions to the field, e.g.
  - The Maximum Likelihood model
  - The Bootstrapping procedure
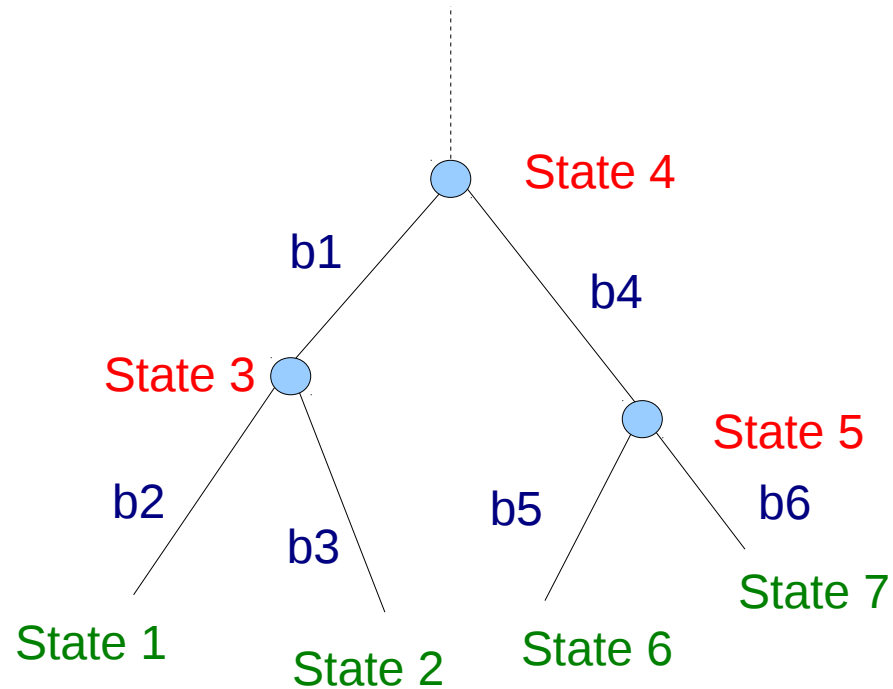- If you are interested in statistics, there are some on-line courses by Joe at http://evolution.gs.washington.edu/courses.html

Likelihood tries to fix this Problem

T
T
C
A
A
G
A
C

T → C → A
T
C → T
A
A → G → C
G → A → G
A
C

T
T → C
C → T
A
A → C
G
A
C

A
T
T
A
C
G
A
C

T
C
T
A
C
G
A
C

Likelihood tries to fix this Problem

T
T
C
A
A
G
A
C

Speciation event

T → C → A
T
C → T
A
A → G → C
G → A → G
A
C

T
T → C
C → T
A
A → C
G
A
C

Events during time *t* of evolution

A
T
T
A
C
G
A
C

T
C
T
A
C
G
A
C

Observed outcome

6

Lecture **9b** → How do we compute the likelihood on a tree?

Lecture **9c** → How do we maximize the likelihood on a tree?