

1	2	3	$\Sigma$ (7)

**Blatt 11**

(Abgabe am 1. Februar 2016)

**1. Theoretical Assignment - *Coverage statistics*****1a.****1b.****1c.****2. Theoretical Assignment - *Application of the arrival statistic for unitigs*****3. Theoretical Assignment - *On distances*****3a.**

Consider a tree  $T$  constructed with  $D$  and the four nodes  $i, j, k, l \in T$ . Since  $D$  is ultrametric, the following four inequalities have to hold:

$$d(i, j) \leq \max \{d(i, k), d(j, k)\}$$

$$d(i, j) \leq \max \{d(i, l), d(j, l)\}$$

$$d(k, l) \leq \max \{d(i, k), d(i, l)\}$$

$$d(k, l) \leq \max \{d(j, k), d(j, l)\}$$

W.l.o.g we can assume that  $d(i, k) = d(j, k) = d(i, l) = d(j, l)$ . With that assumption we can rewrite the inequalities as

$$d(i, j) + d(i, j) \leq d(i, k) + d(j, l)$$

$$d(k, l) + d(k, l) \leq d(i, l) + d(j, k)$$

And also the following inequality is valid:

$$d(i, j) + d(k, l) \leq \max \{d(i, k) + d(j, l), d(i, l) + d(j, k)\}$$

As one can see, that is the Four-Point-Condition (4PC) and a metric fulfill 4PC if and only if it is additive. So  $D$  is a tree metric  $\square$

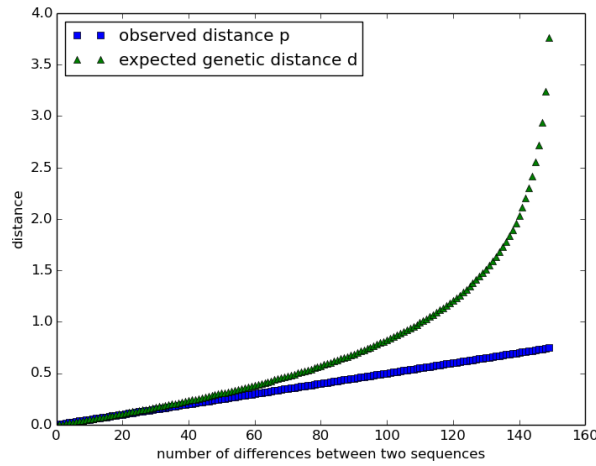


Figure 1: Behavior of observed distance  $p$  and expected genetic distance  $d$  of two non-saturated sequences. Both sequences are of length 200.

To show the back direction one consider the four elements  $A, B, C, D \in X$  of a taxa  $X$  and the following distance matrix:

$$D = \begin{bmatrix} & B & C & D \\ A & 7 & 6 & 5 \\ B & & 3 & 6 \\ C & & & 5 \end{bmatrix}$$

One can see in the script of this lecture that  $D$  is a tree metric. But the Three-Point-Condition (3PC) is not fulfilled as can be easily shown. To fulfill 3PC the following inequality has to be valid:

$$d(A, B) \leq \max \{d(A, C), d(B, C)\}$$

but

$$7 \not\leq \max \{6, 3\}$$

So  $D$  does not fulfill 3PC and thus  $D$  is not ultra metric.  $\square$

### 3b.

There are different methods to estimate the (evolutionary) distance between two sequences. The easiest one is to simply calculate the Hamming distance. This is called the observed or  $p$ -distance.  $p$ -distance is just suitable for closely related species, since it is not able to detect superimposed mutations, i.e. mutations that happened at a position that was already mutated, previously. A correction for observed distance was formulated by Jukes and Cantor. The Jukes-Cantor transformation corrects the  $p$ -distance to take, among others, superimposed events into account. This correct distance is called the expected genetic distance  $d$ . An important note is that JC transformation does not work for sequences that are saturated w.r.t. each other. So Figure 1 shows the relationship between  $d$  and  $p$  for non-saturated sequences of length 200. As one can see the observed distance  $p$  is constantly underestimating the genetic distance for more distant sequences. Especially, if both sequences are close to be saturated, the difference between  $d$  and  $p$  shows that

$p$  cannot give a reliable result. So for sequences/species that are evolutionary close to each other both measurements  $d$  and  $p$  give almost the same result. But the further away the last common ancestor of both sequences the larger is the difference between observed distance and expected genetic distance.