Boots

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Bootstrap

and phylogenetic trees

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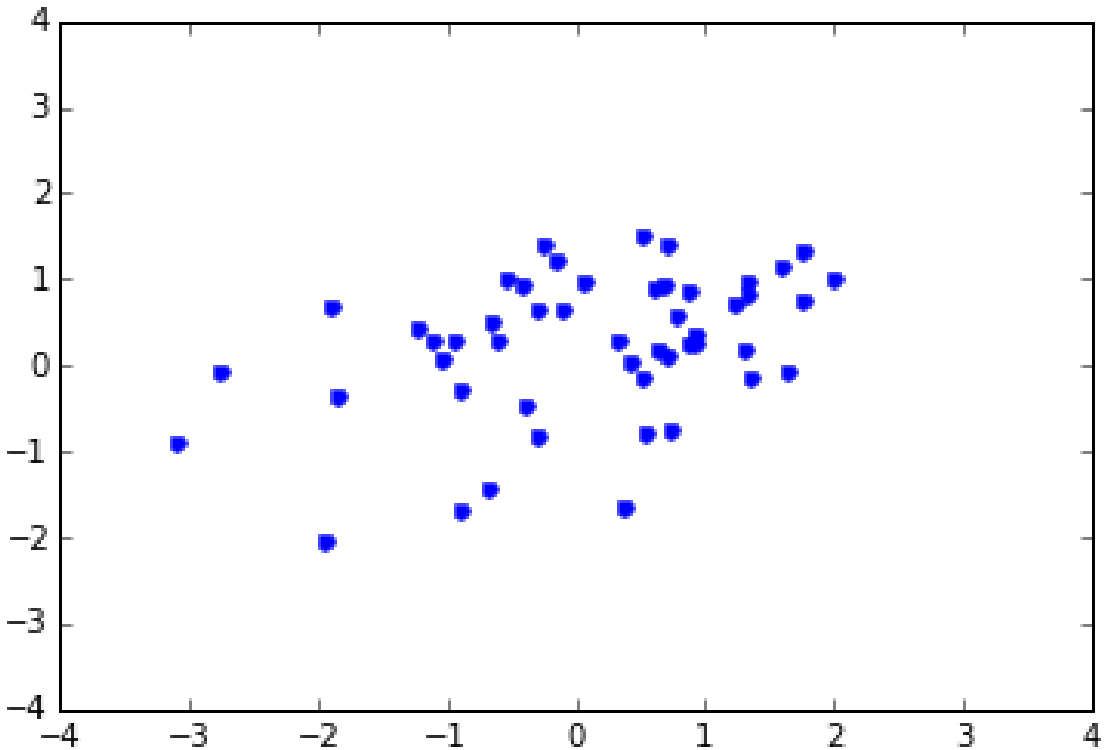
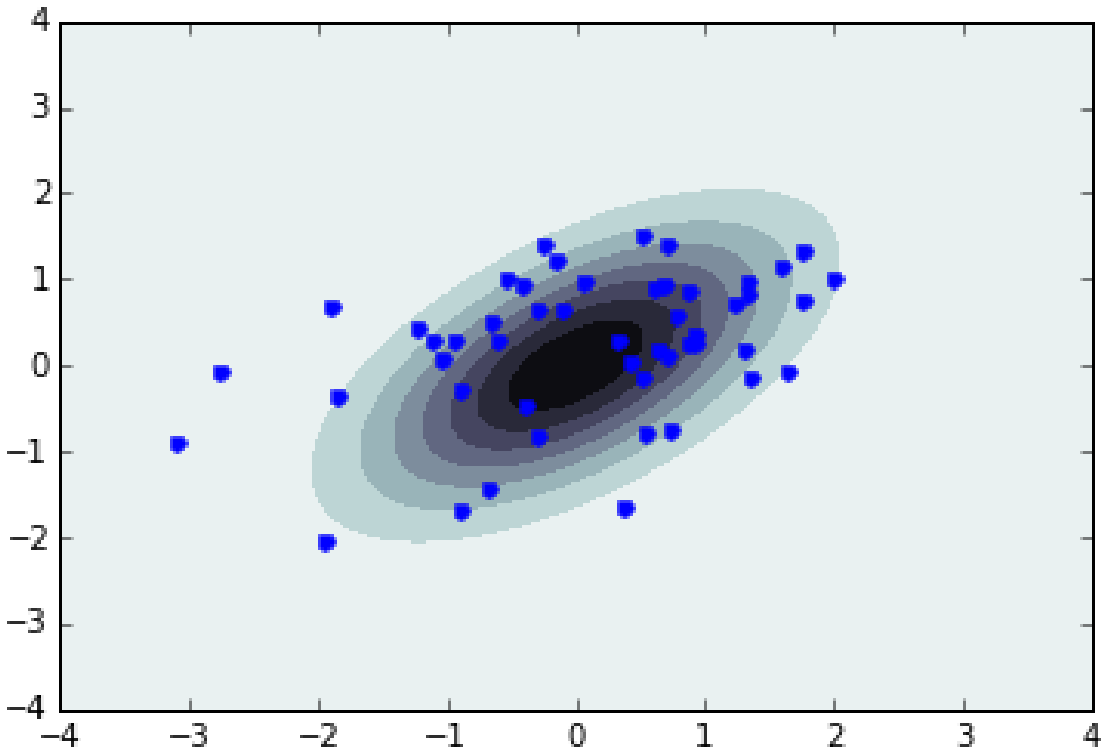
What does it mean

Tall boots may have a tab, loop or handle at the top known as a bootstrap, allowing one to use fingers or a boot hook tool to help pulling the boots on. The saying ”to pull oneself up by one’s bootstraps” was already in use during the 19th century as an example of an impossible task. The idiom dates at least to 1834, when it appeared in the Workingman’s Advocate: ”It is conjectured that Mr. Murphee will now be enabled to hand himself over the Cumberland river or a barn yard fence by the straps of his boots.” In 1860 it appeared in a comment on metaphysical philosophy: ”The attempt of the mind to analyze itself [is] an effort analogous to one who would lift himself by his own bootstraps.” Bootstrap as a metaphor, meaning to better oneself by one’s own unaided efforts, was in use in 1922.

Take a sample

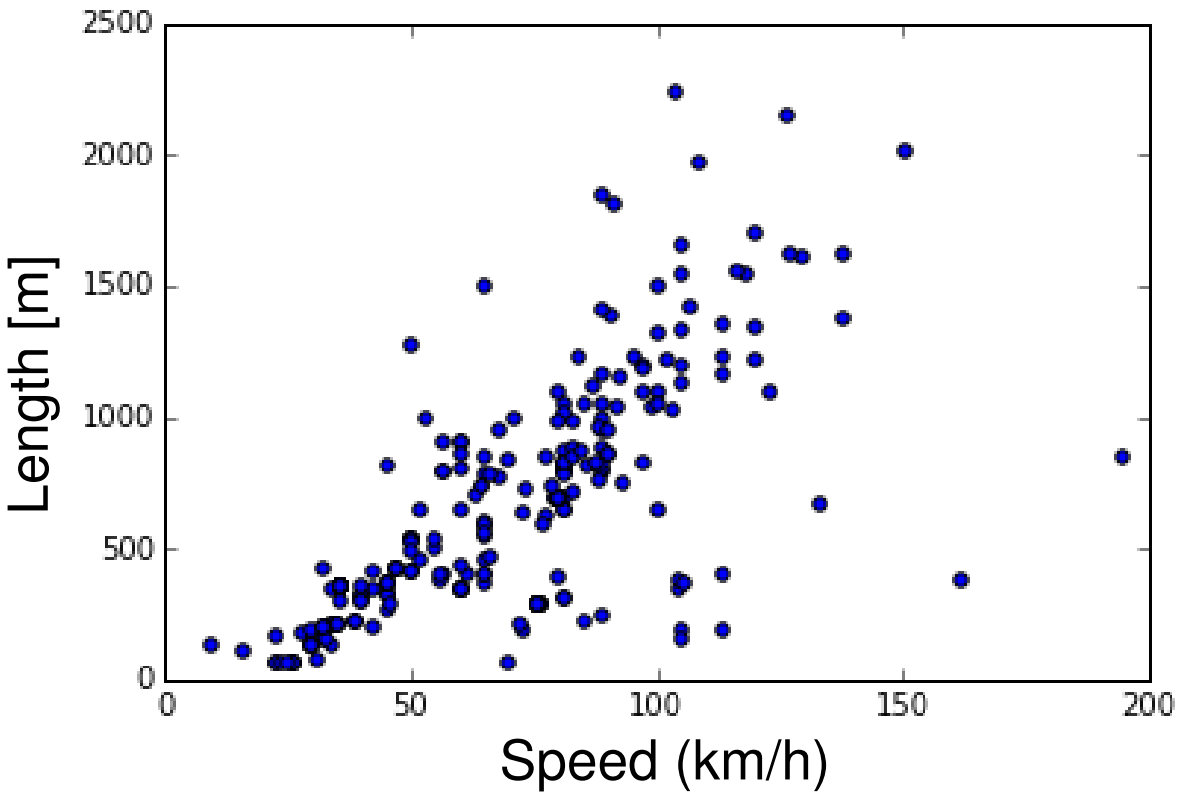


Take a sample



Roller Coaster

Length and Speed of Roller coasters



Standard Analysis

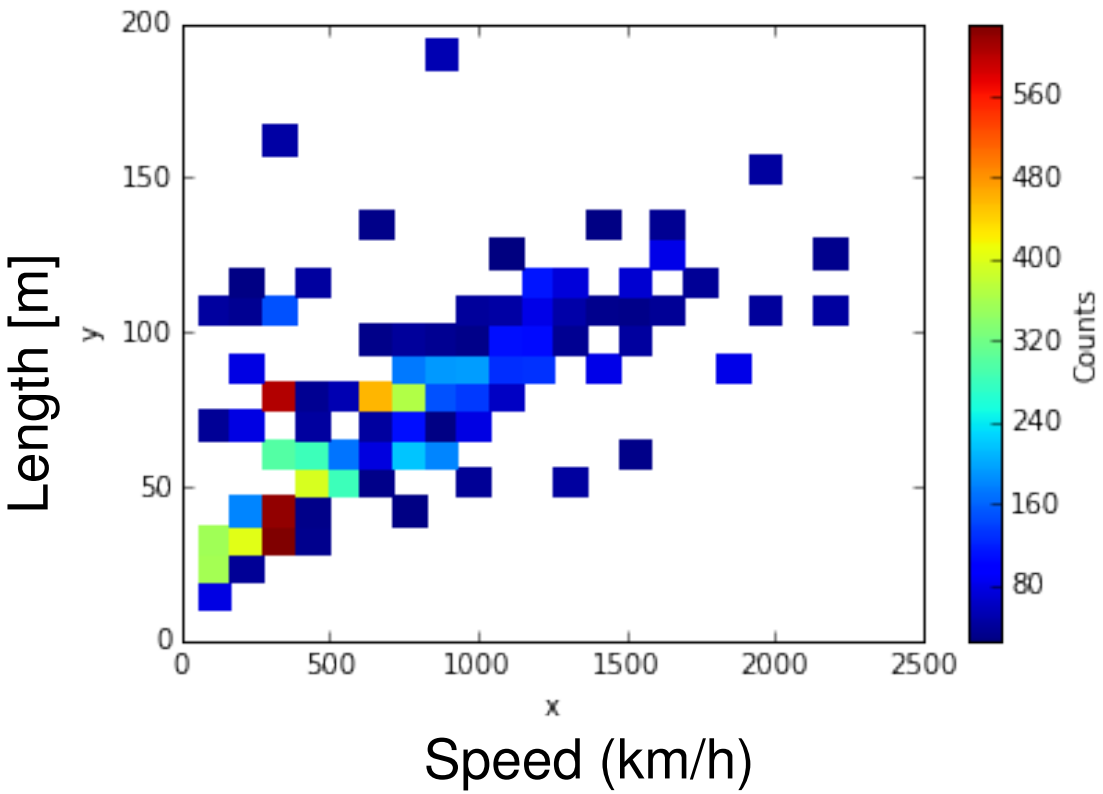
```
scipy.stats.describe(v)
```

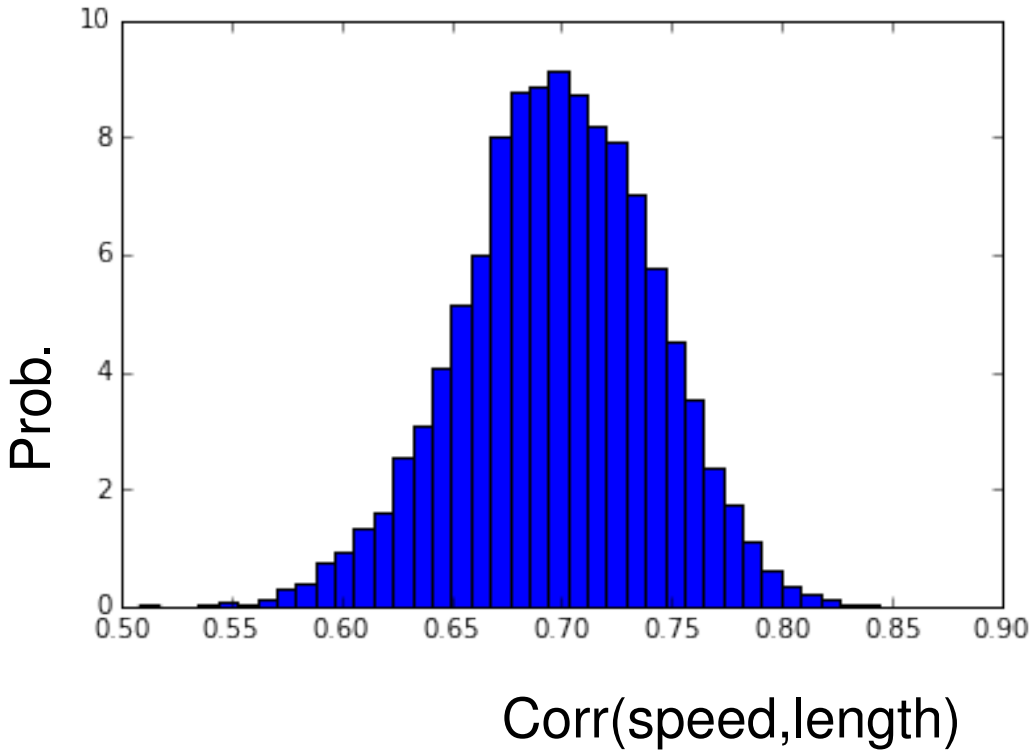
```
DescribeResult(nobs=260, minmax=(array([  9.72,  60.  ]), array([  194.4 ,
2243.02])), mean=array([  69.36838462,  648.00698077]), variance=array([
865.4759495 ,  196697.51442304]), skewness=array([ 0.56402121,  1.01759565
]), kurtosis=array([ 0.56345422,  0.73611374]))
```

```
bpx,bpy = zip(*v); scipy.stats.pearsonr(bpx,bpy)
```

```
(0.69629308341240093, 4.9366122614103826e-39)
```

Bootstrap Analysis

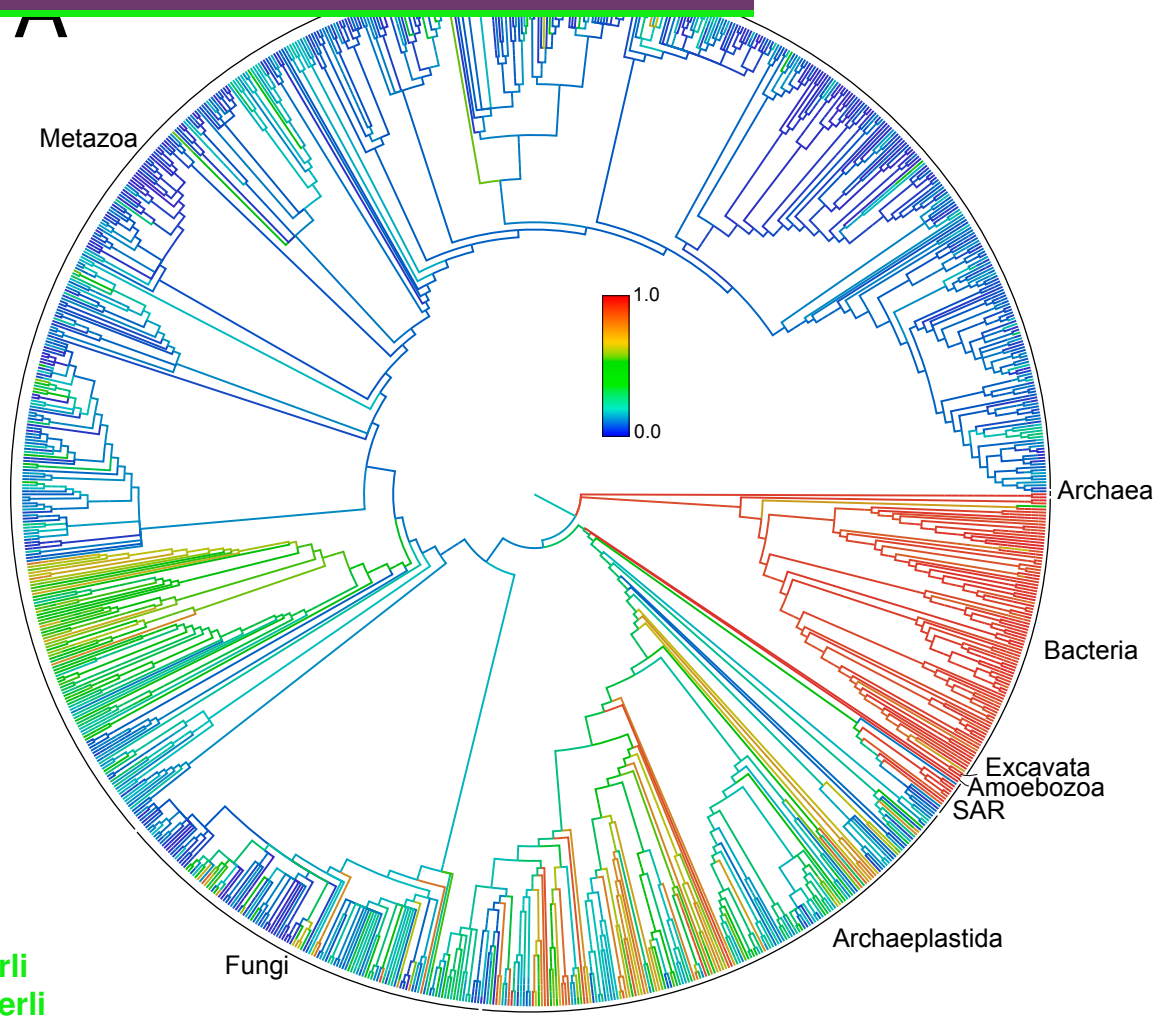




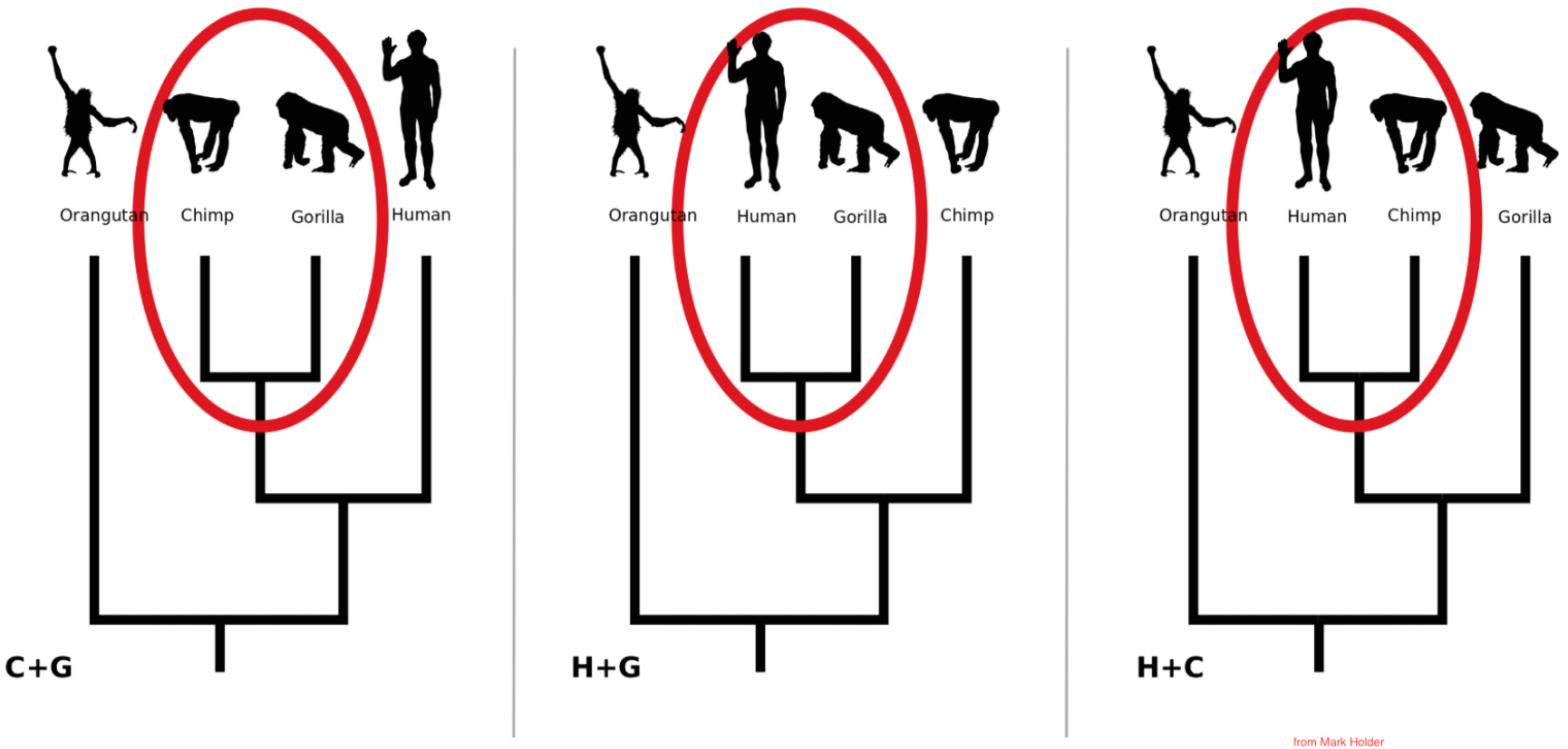
Bootstrap Analysis

```
In [52]: pp=(0.69629308341240093, 4.9366122614103826e-39);z = np.arctanh(pp[0])

In [65]: sigma = (1/((260-3)**0.5));sigma

Out[65]: 0.06237828615518053

In [66]: cint = z + np.array([-1, 1]) * sigma * stats.norm.ppf((1+0.95)/2)
         cint

Out[66]: array([ 0.73780954,  0.98232793])

In [67]: np.tanh(cint)

Out[67]: array([ 0.62781991,  0.75407188])

In [76]: scipy.cumsum(bins)/(scipy.sum(bins))

Out[76]: array([ 0.01811112,  0.03653619,  0.05527523,  0.07432821,  0.09369516,
                0.11337606,  0.13337091,  0.15367973,  0.1743025 ,  0.19523922,
                0.2164899 ,  0.23805454,  0.25993313,  0.28212568,  0.30463219,
                0.32745265,  0.35058707,  0.37403545,  0.39779778,  0.42187407,
                0.44626431,  0.47096851,  0.49598667,  0.52131878,  0.54696485,
                0.57292487,  0.59919885,  0.62578679,  0.65268869,  0.67990454,
                0.70743434,  0.73527811,  0.76343582,  0.7919075 ,  0.82069313,
                0.84979272,  0.87920626,  0.90893376,  0.93897522,  0.96933063,  1
         .        ])

In [83]: (np.array(range(40))*0.01 + 0.5)[3],(np.array(range(40))*0.01 + 0.5)[-3],

Out[83]: (0.53000000000000003, 0.87)
```

Phylogenies



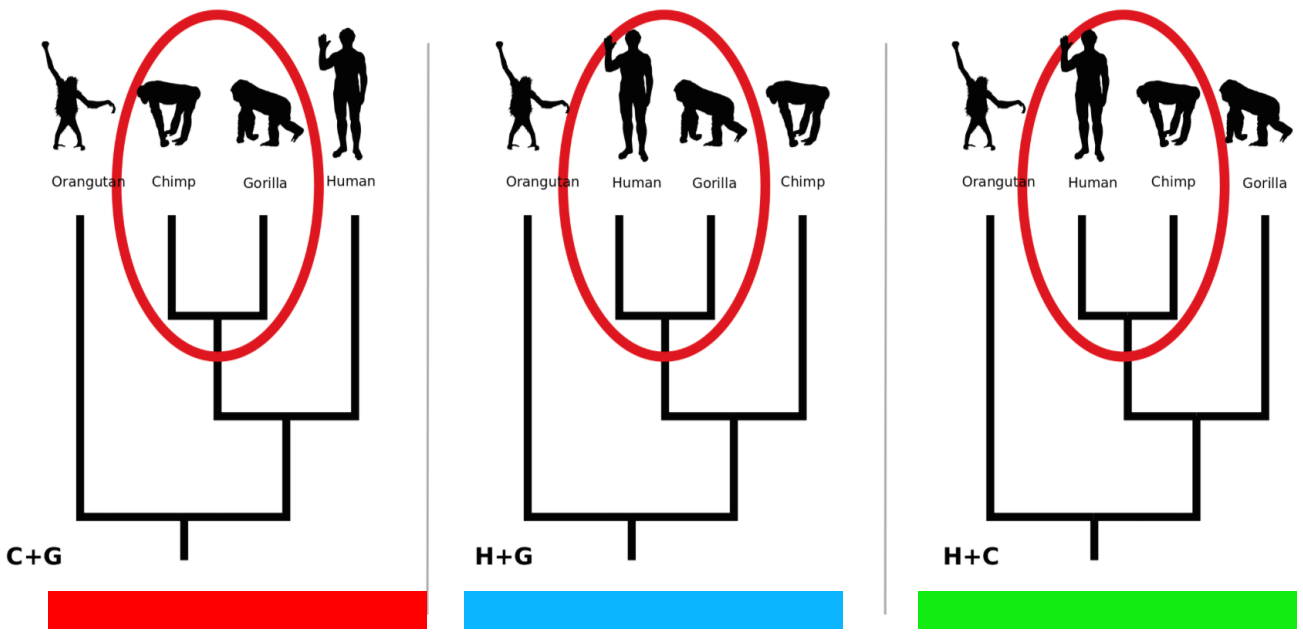
Bootstrapping phylogenies



from Mark Holder

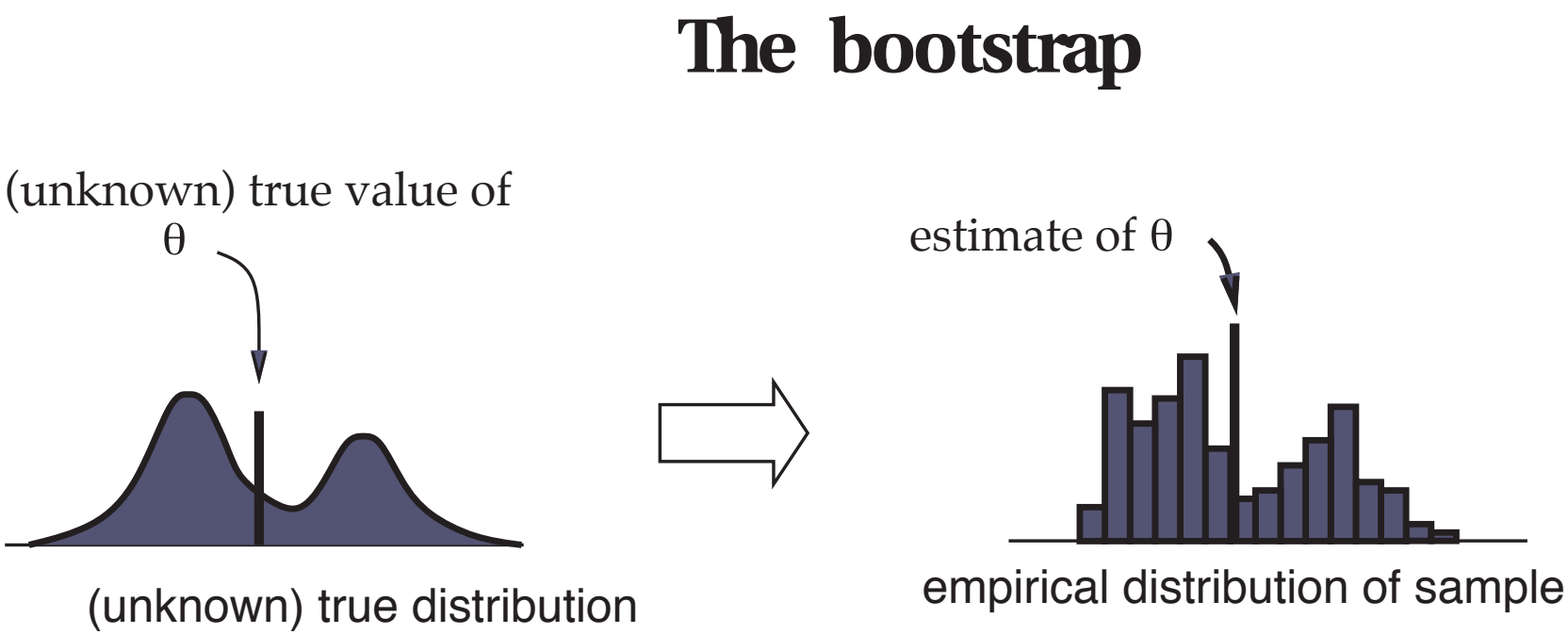
Bootstrapping phylogenies

Human	G	C	C	A	G	C	T	G	C	T
Chimp	G	C	C	G	G	G	T	A	T	T
Gorilla	G	T	C	A	A	C	T	A	T	G
Orang	C	T	C	A	A	G	T	G	C	G

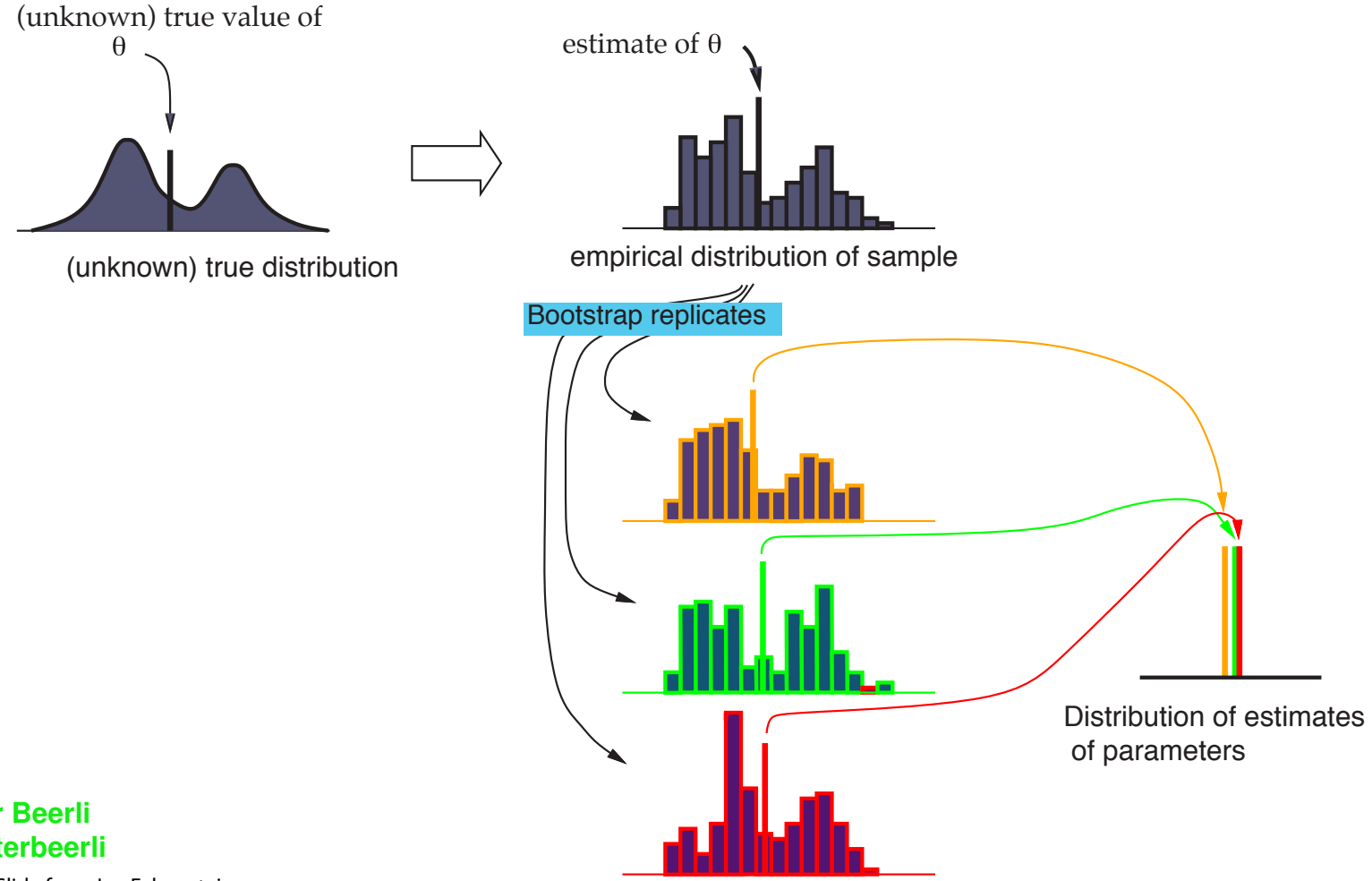


http://phylo.bio.ku.edu/mephytis/boot-sample.html

Bootstrapping phylogenies

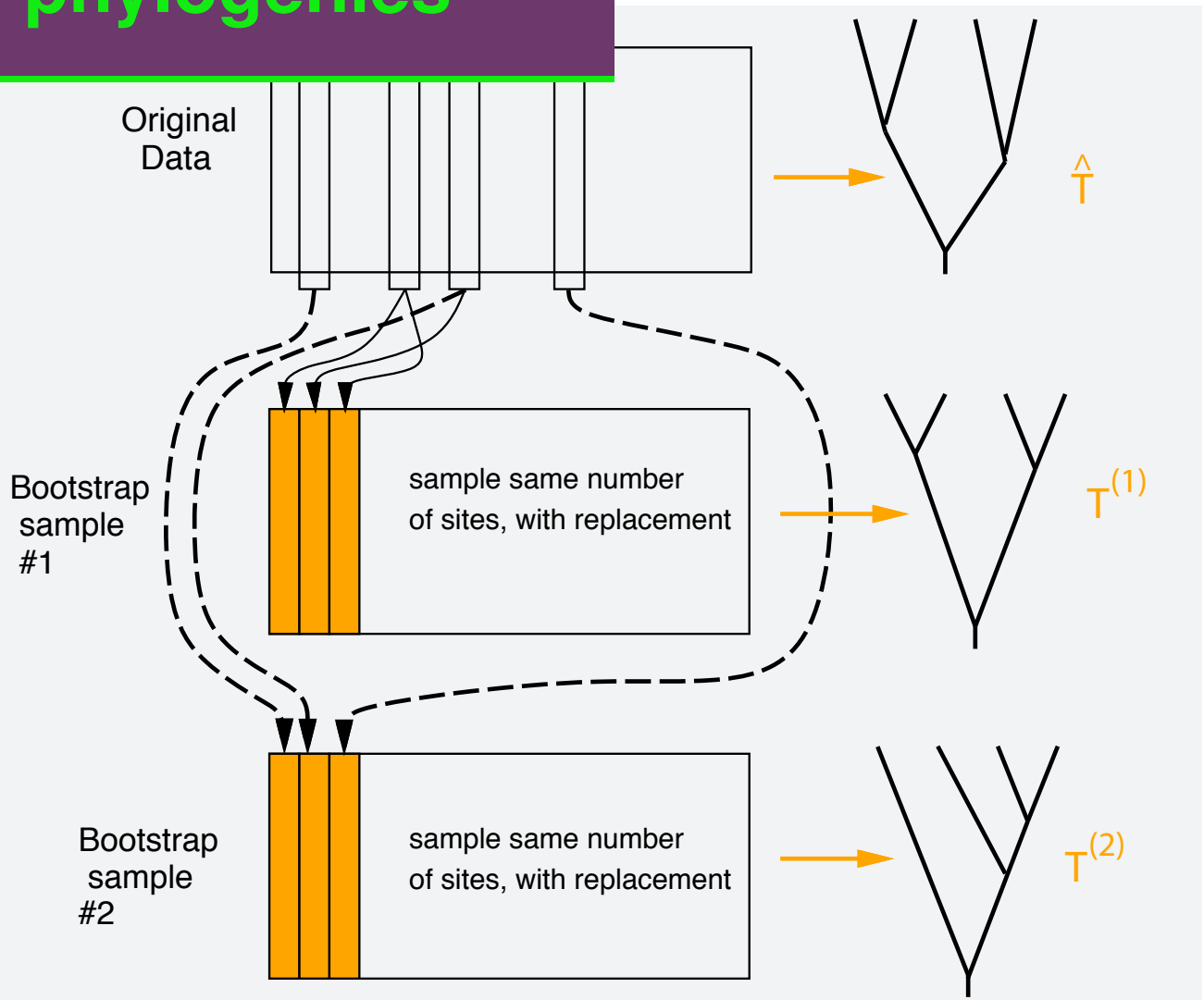


Bootstrapping phylogenies



Slide from Joe Felsenstein

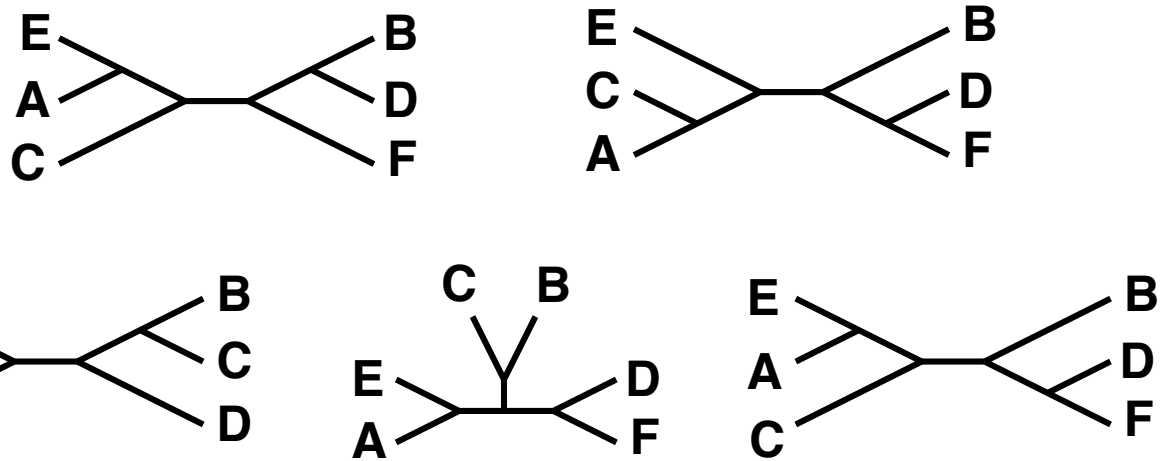
Bootstrapping phylogenies



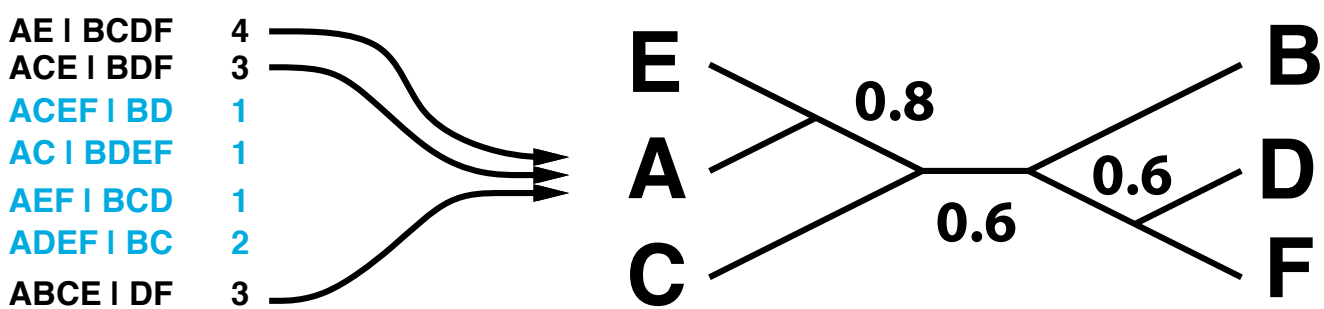
Bootstrapping

The majority-rule consensus tree

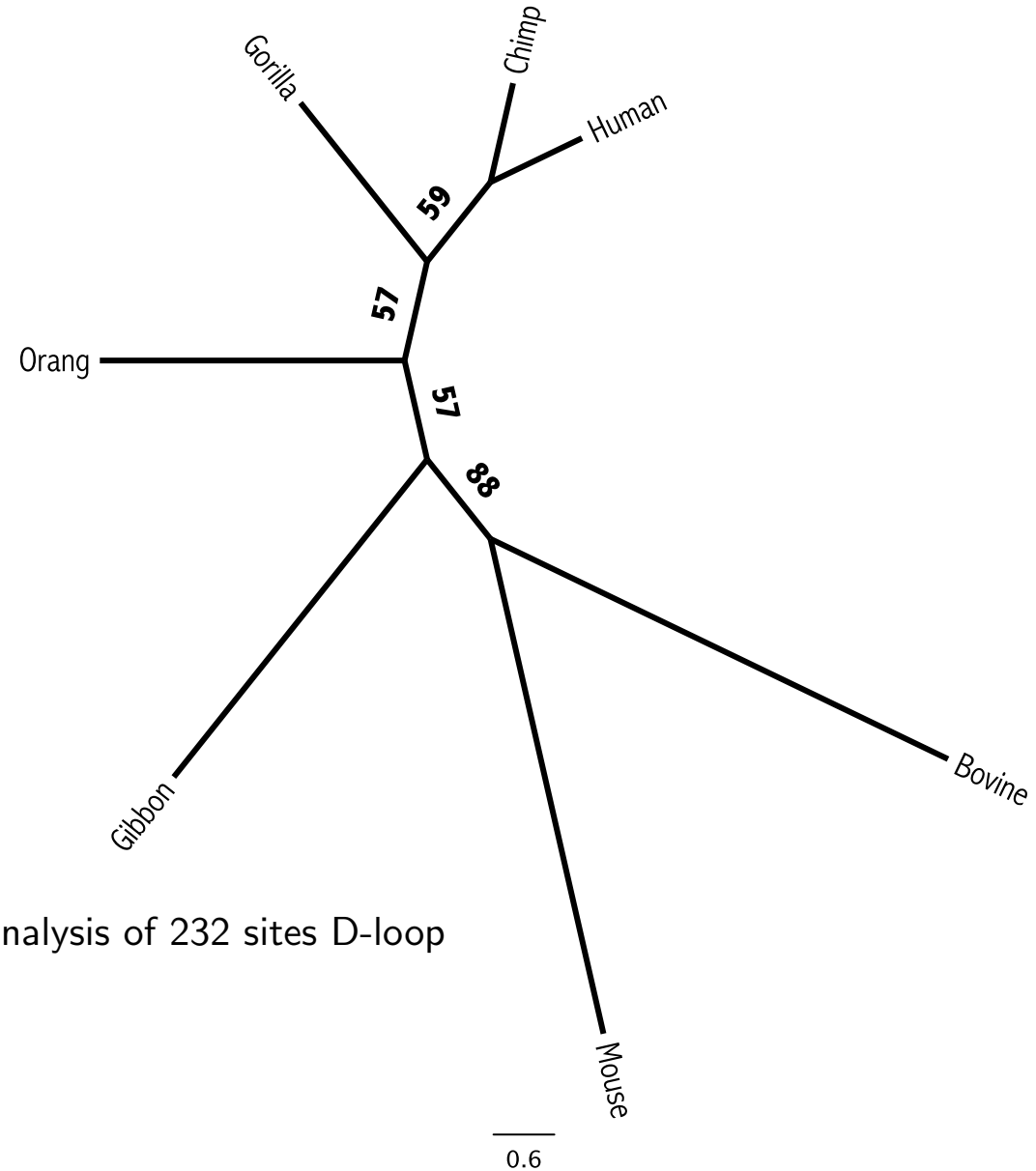
Trees:



How many times each partition of species is found:



Bootstrapping



From Hasegawa's analysis of 232 sites D-loop

Summary

- The bootstrap allows you to generate a distribution based on your sample. This allows to take into account unknown correlation structure among the data entries.
- The bootstrap has also problem in that we many need to block sample to consider correlations among sampling entries (for example sites in DNA sequences are correlated, any scheme that draws bootstrap samples independently for each site may be flawed.)
- A great tool to handle sampling that deviates from normal distributions.