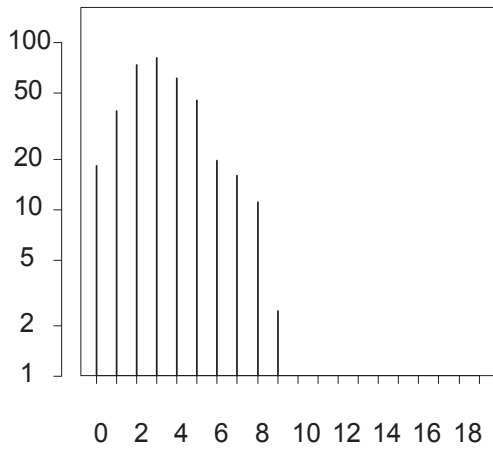
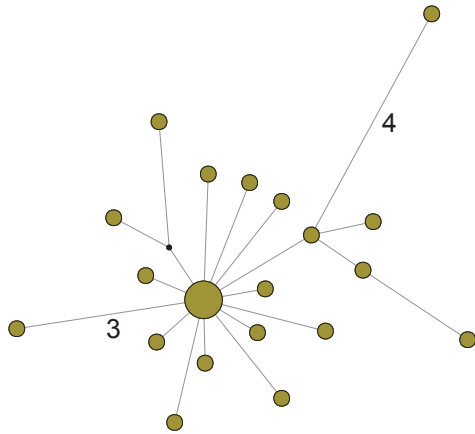
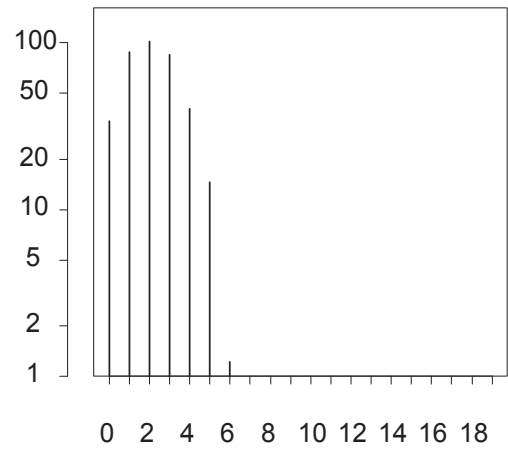
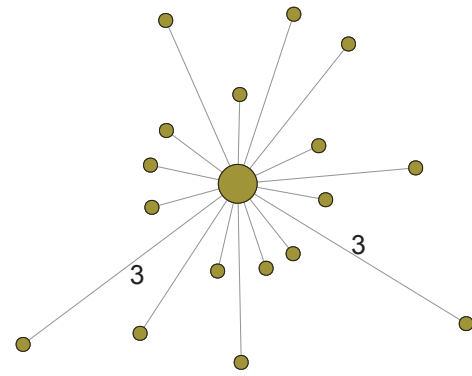


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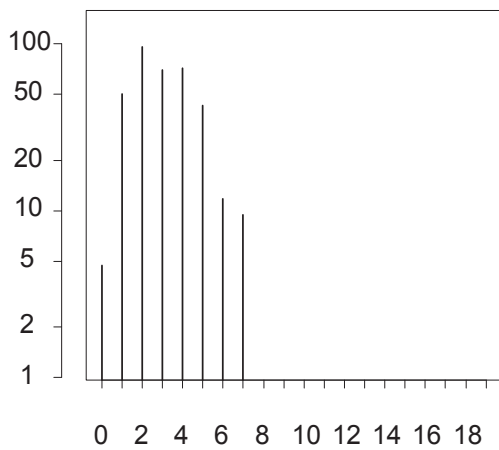
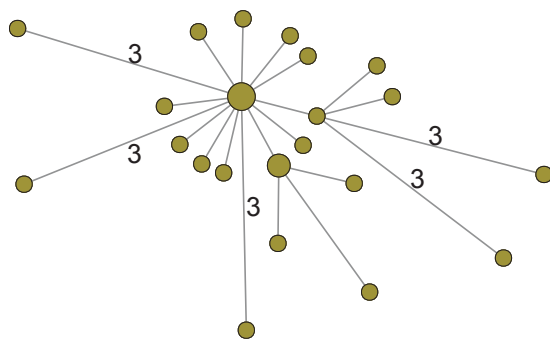
Caramel, 3y



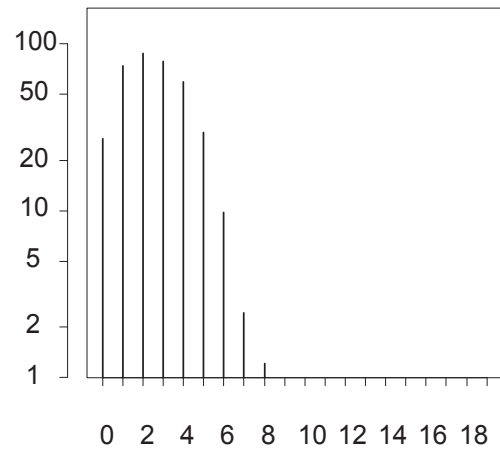
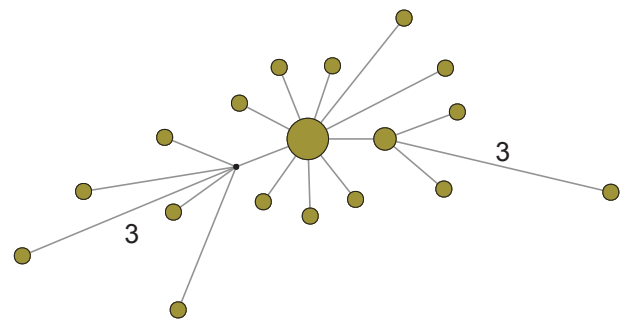
Gogol, 10y



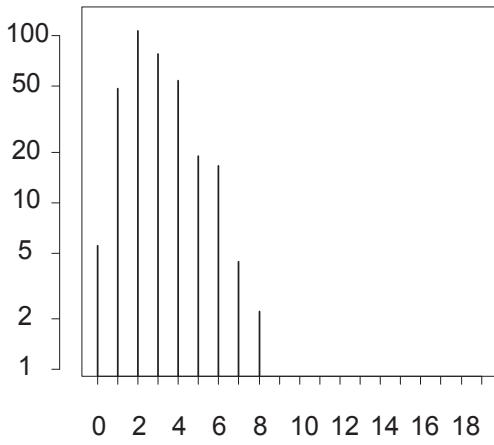
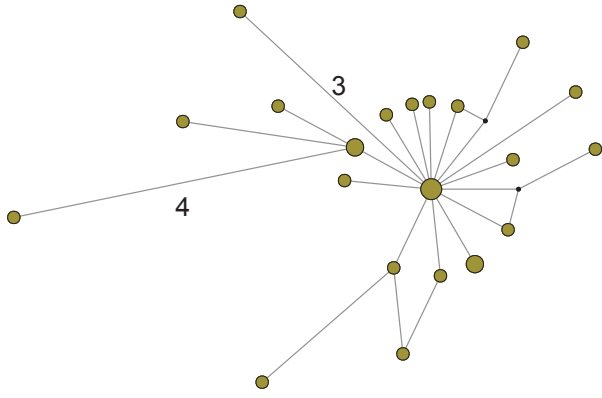
Gogol, 17y



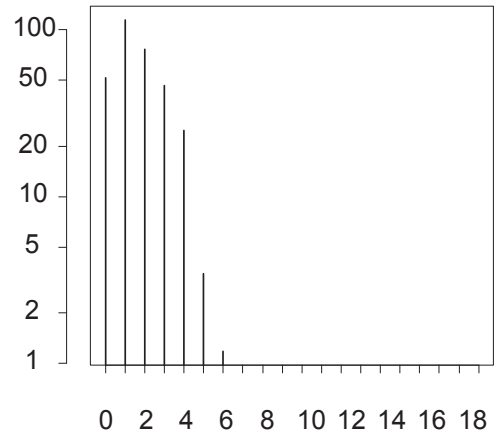
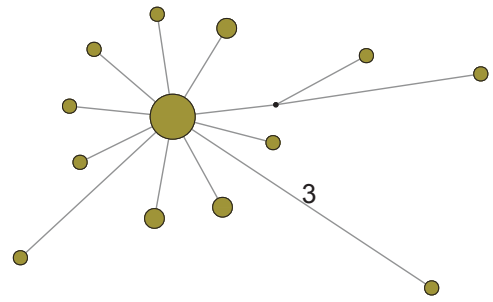
Jacobo, 6y



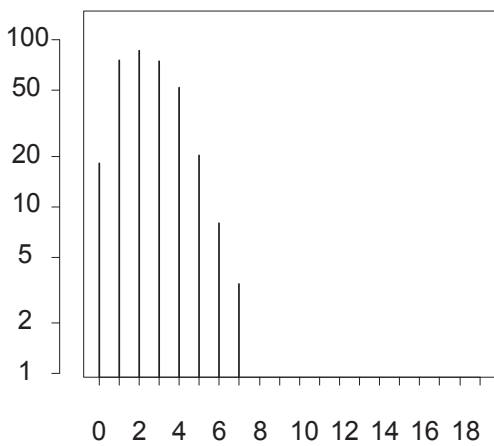
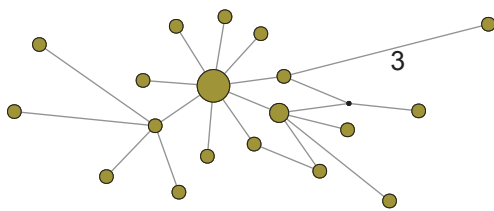
Kinshasa, 17y



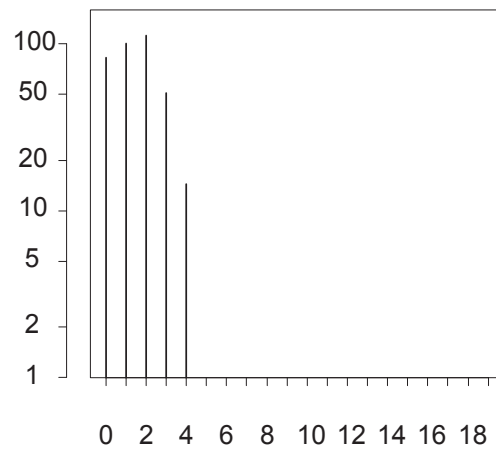
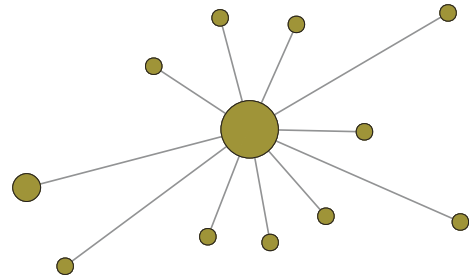
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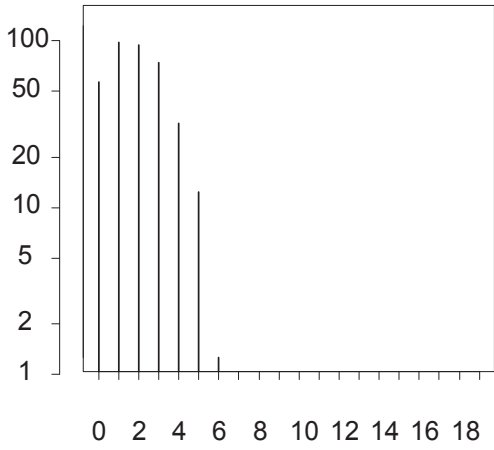
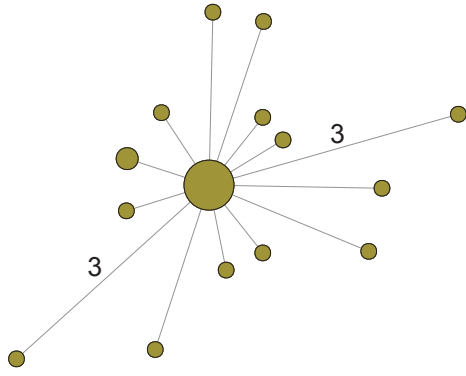
Kiriku, 3y



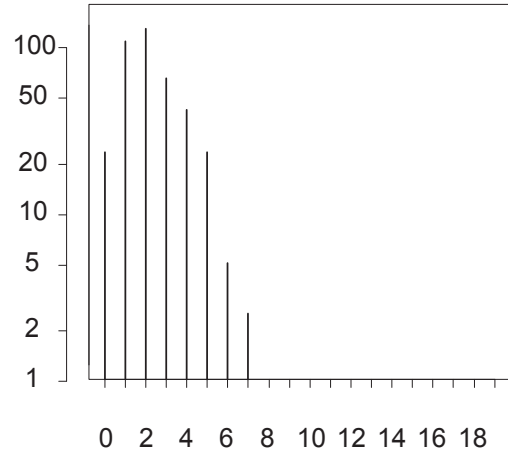
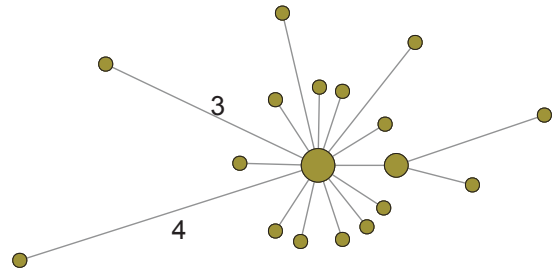
Romario, 9y



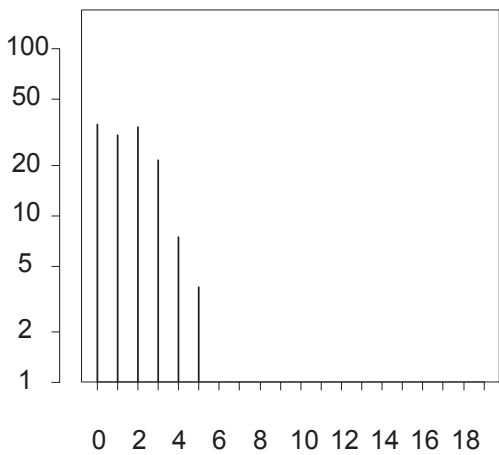
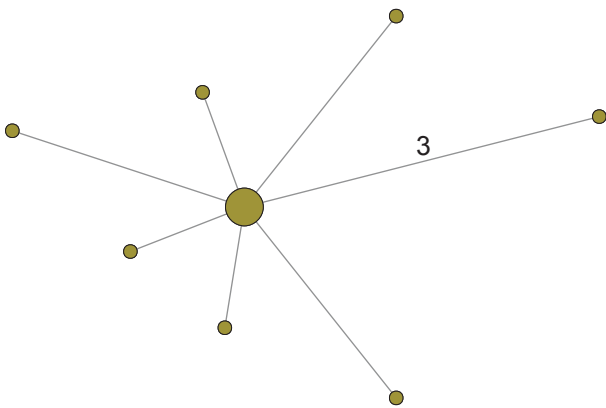
Rubra, 31y



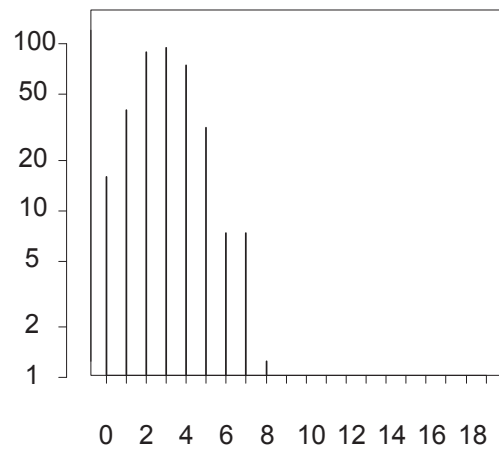
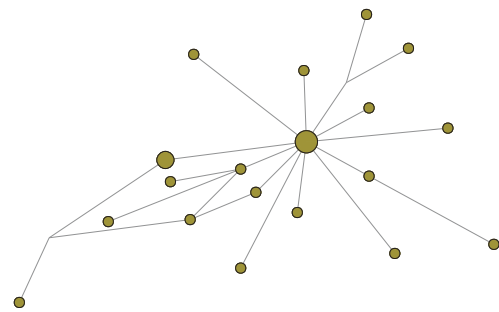
Sagu, 13y



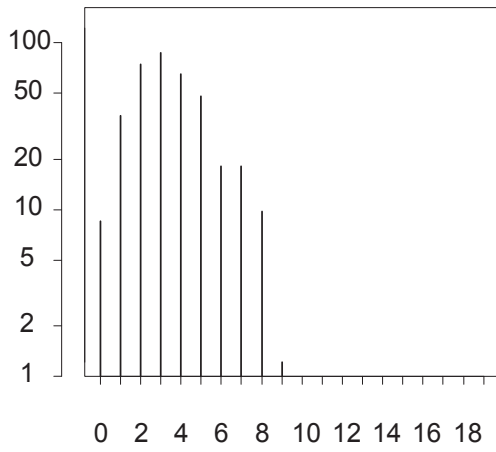
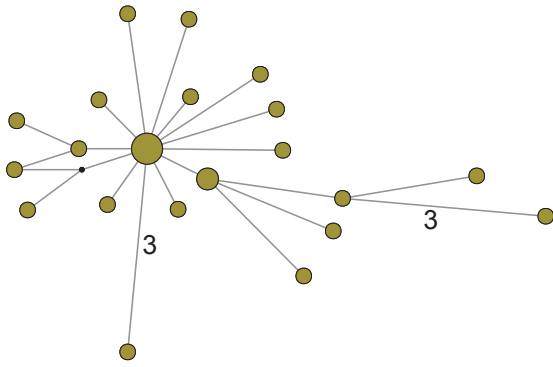
Sumatra, 38y



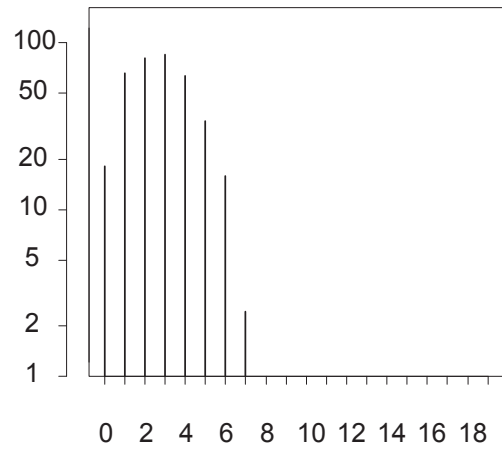
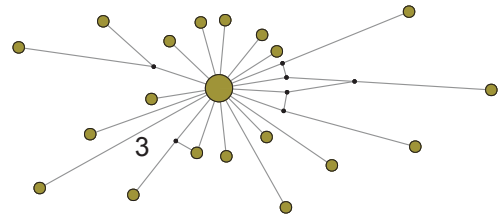
Utan, 7y



Utan, 11y

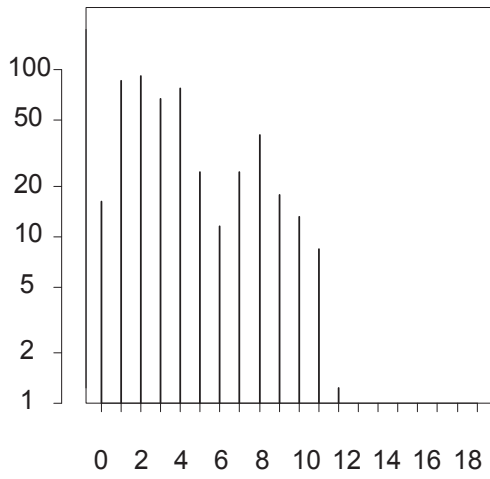
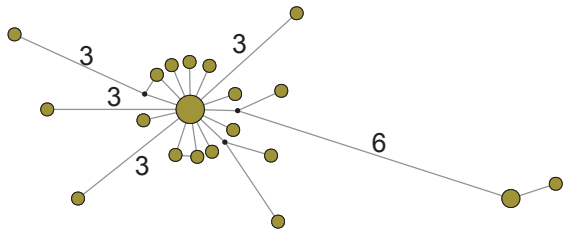


Yao, 8y

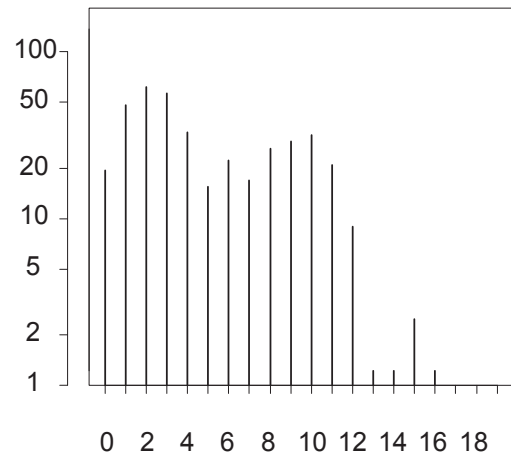
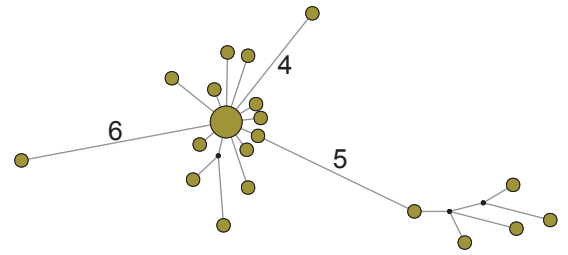


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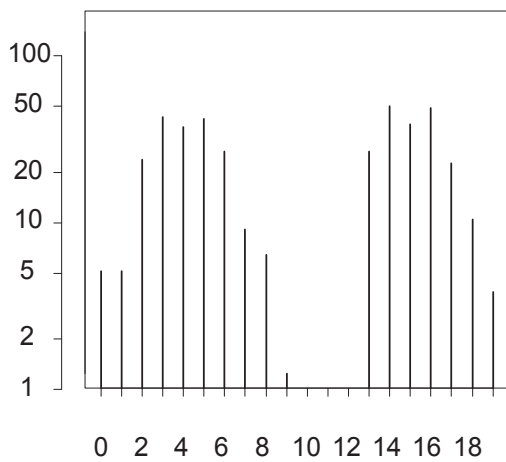
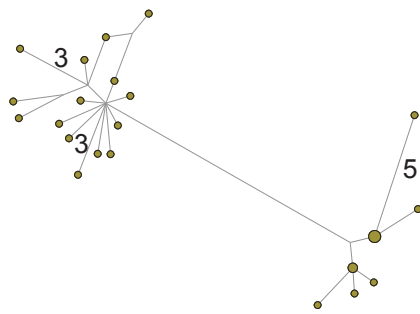
Celine, 10y



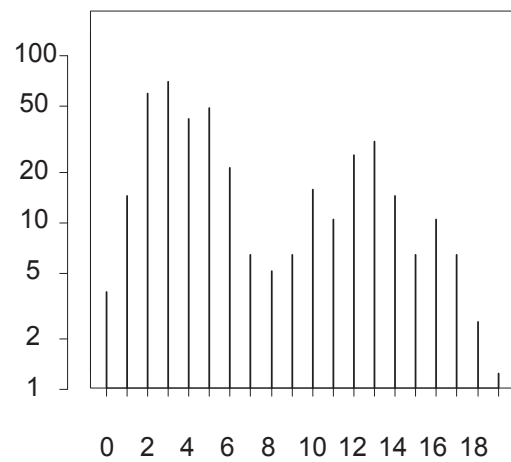
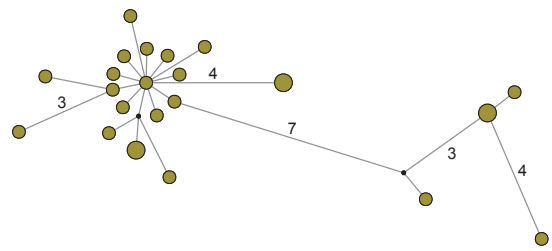
Coco, 24y



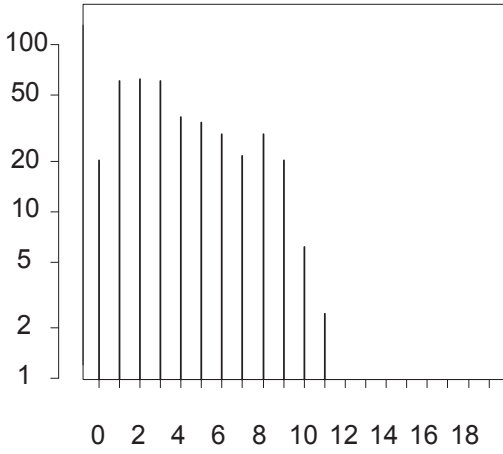
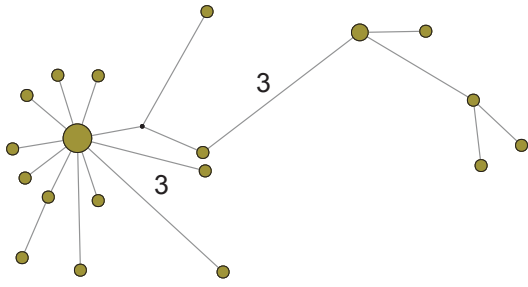
Kabisha, 24y



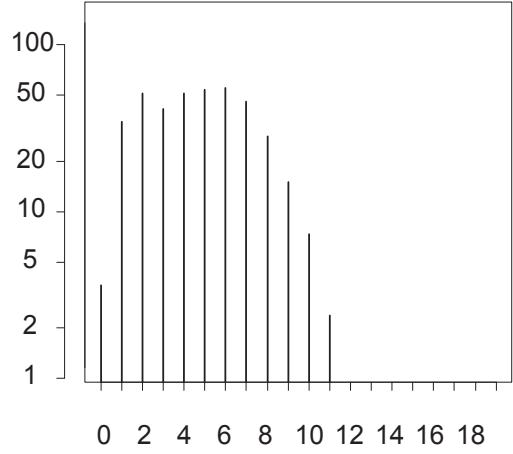
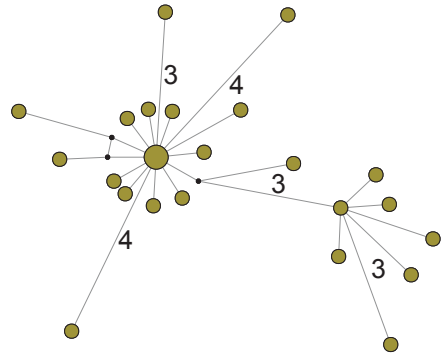
Kabisha, 25y



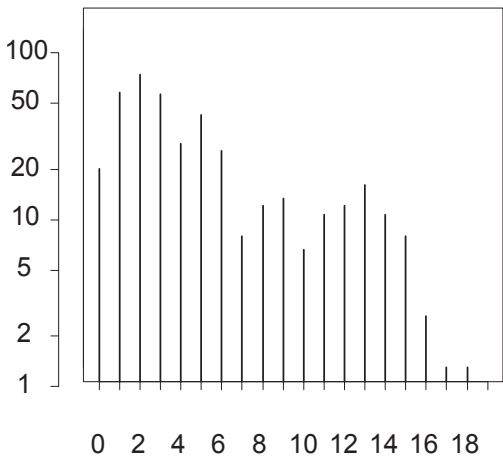
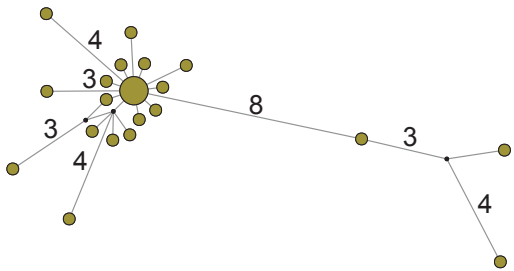
Kaos, 29y



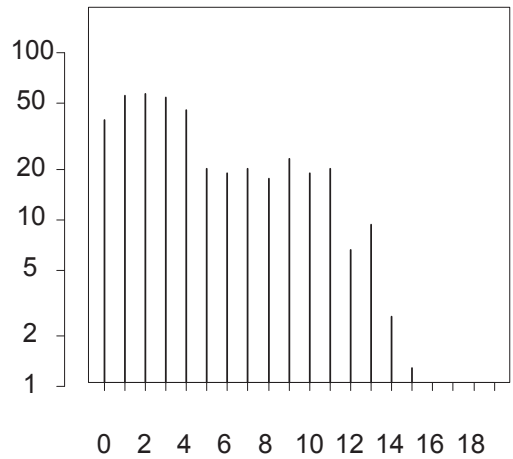
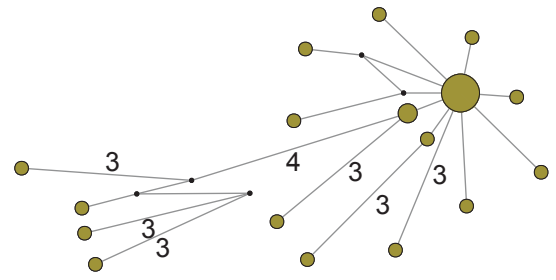
Louise, 25y



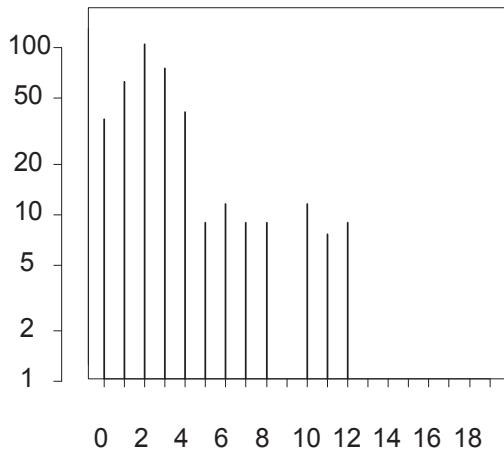
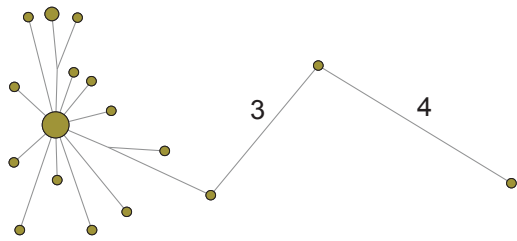
Rebecca, 7y



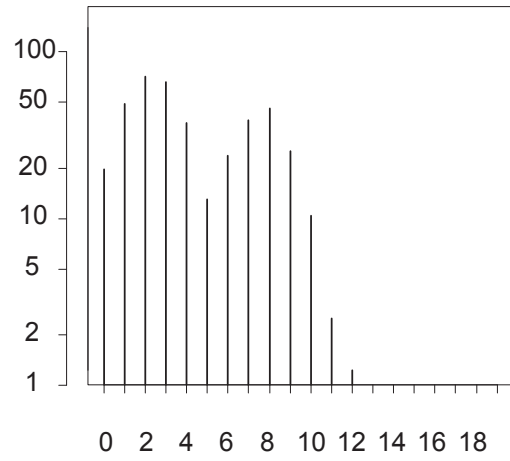
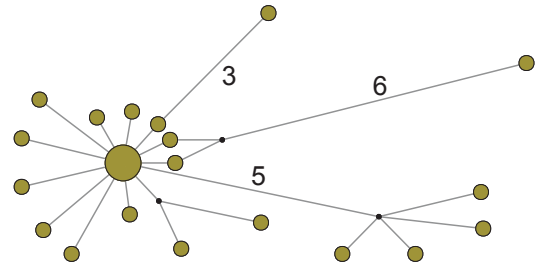
Rubra, 35y



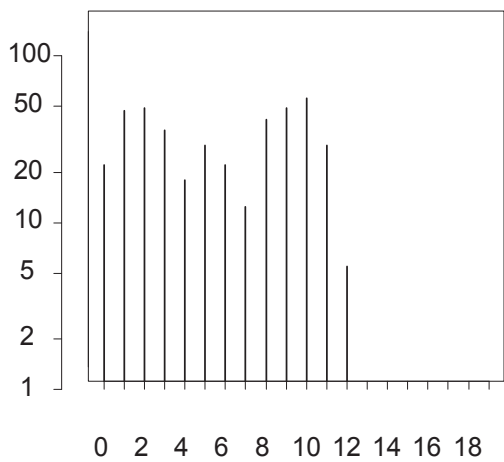
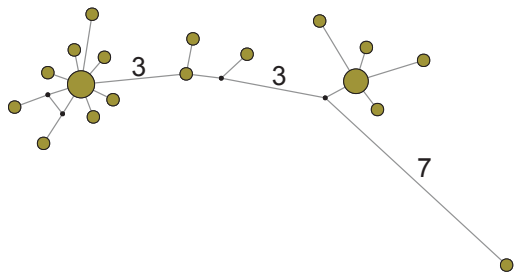
Rubra, 38y



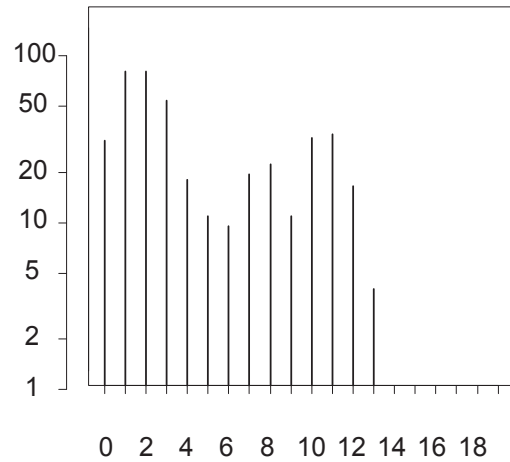
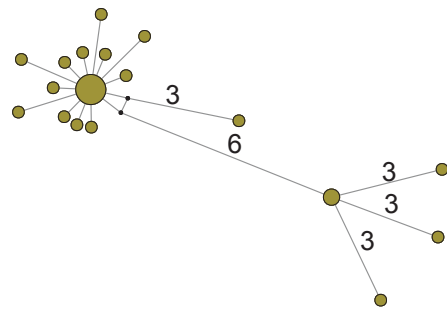
Sagu, 17y



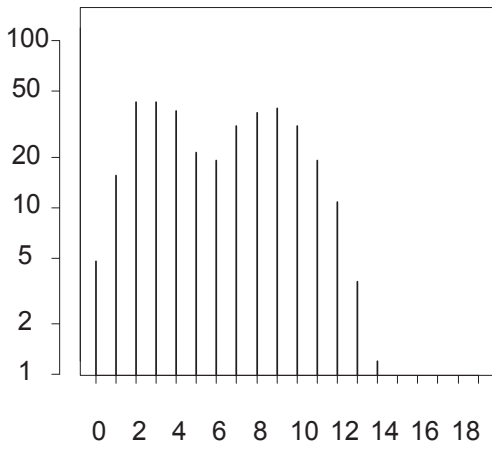
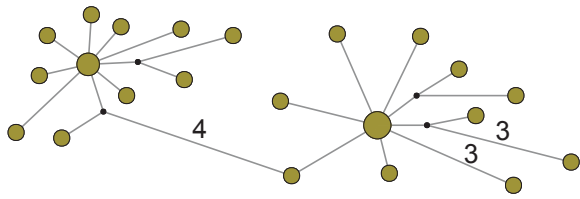
Sagu, 19y



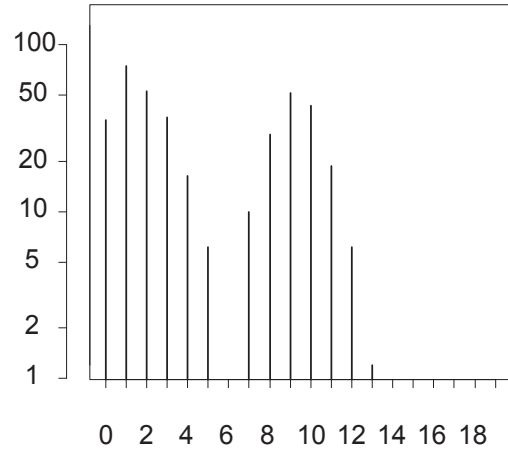
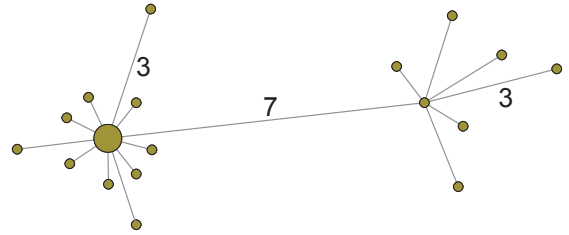
Shogun, 7y



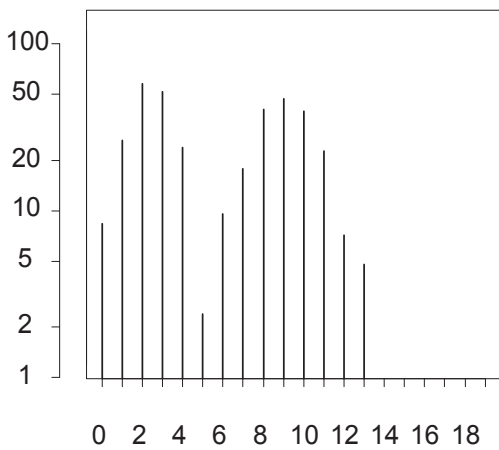
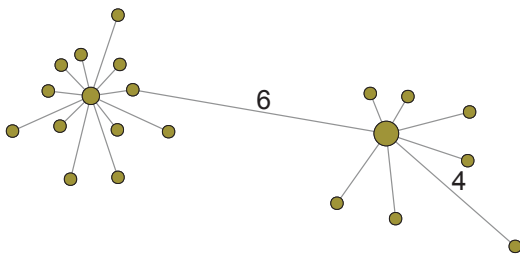
Sumatra, 40y



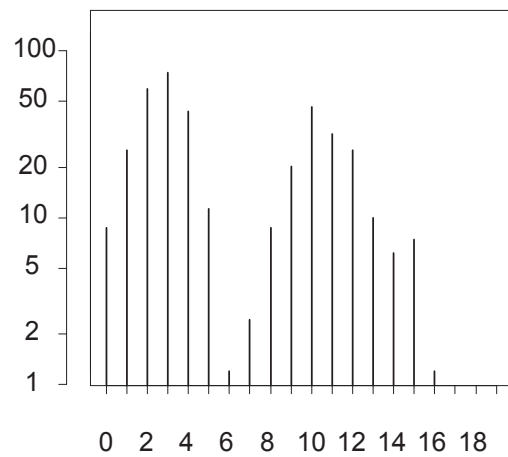
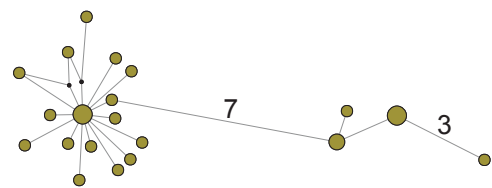
Yucca, 32y

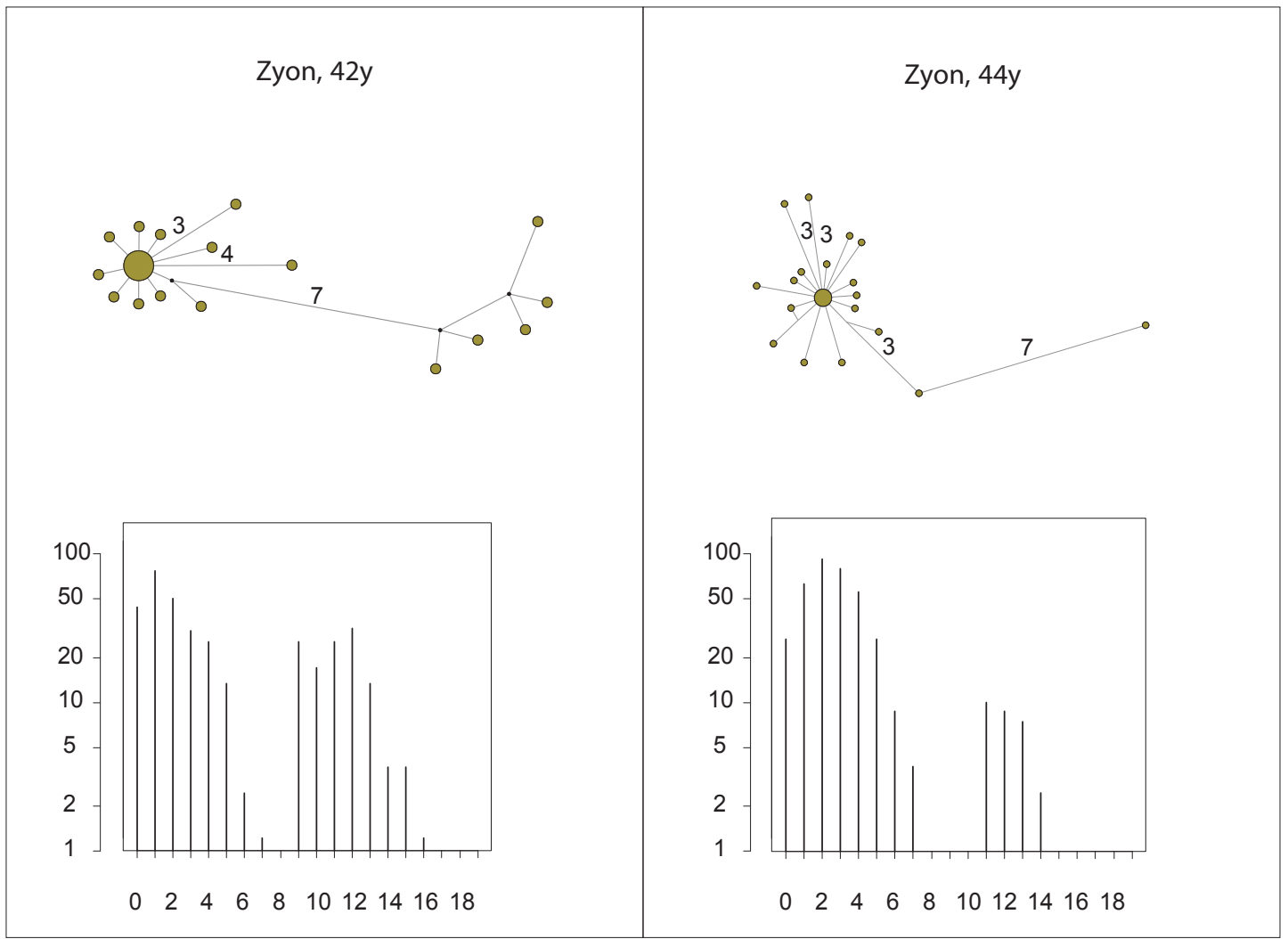


Yucca, 34y



Zyon, 37y

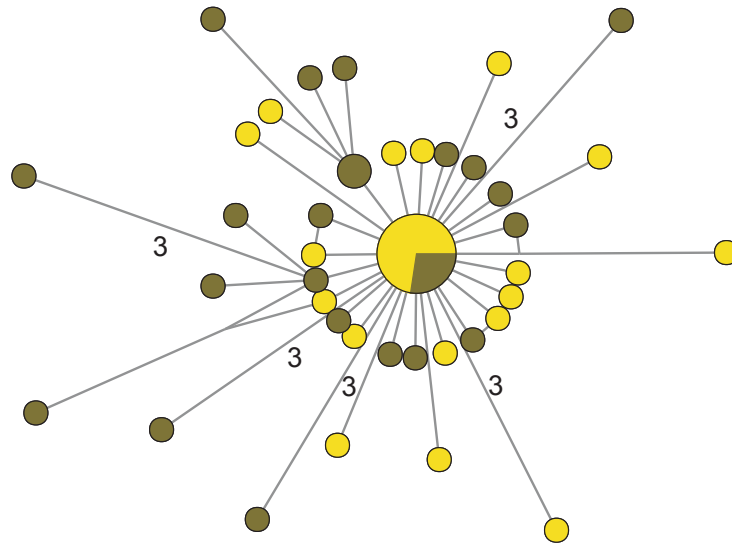




Supplementary Figure 1. Mismatch distributions and sequence networks for all individuals analyzed in this study. Plots are paired for each individual chimpanzee sample (y=years refers to individual age at time of sampling) with mismatch distribution on the left and network on the right. Mismatch distribution present the frequency of the number of mismatches (y-axis) according to the number of basepairs within the sequence alignment (x- axis). Within each network, node size is proportional to the frequency of the sequence occurrence (total n=15-25 for each individual). Branch lengths are directly related to the number of mutations between sequences, with values noted for differences greater than two base pairs.

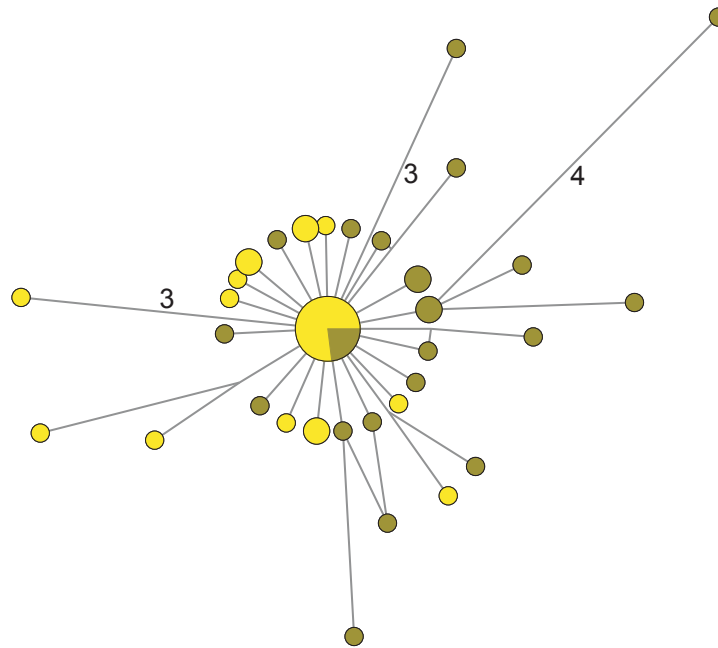
Gogol

- 10y
- 17y



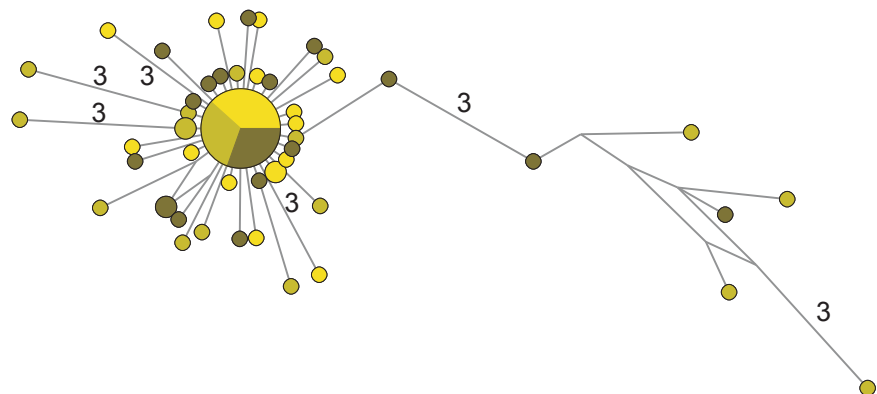
Kinshasa

- 11y
- 17y



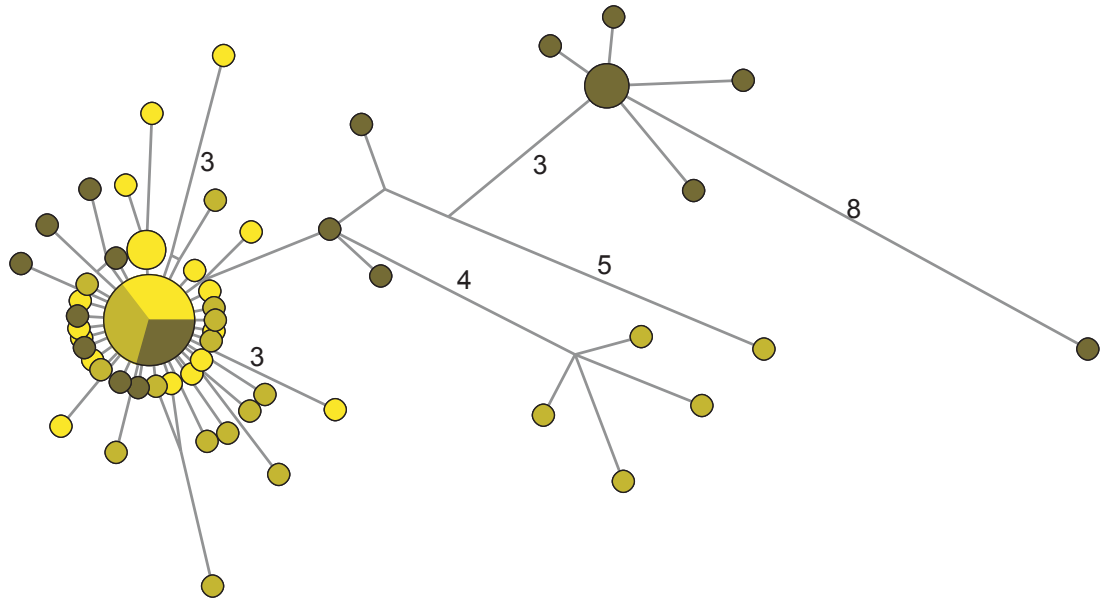
Rubra

- 31y
- 35y
- 38y



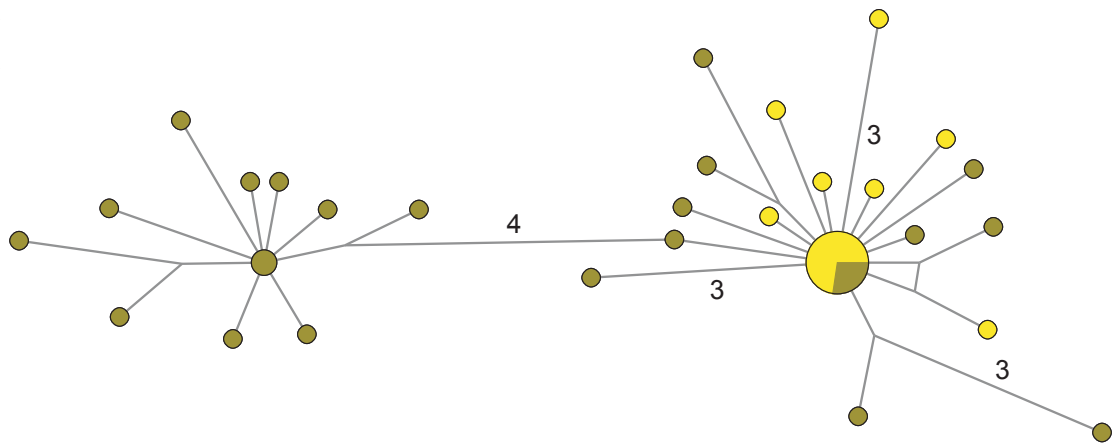
Sagu

- 13y
- 17y
- 19y



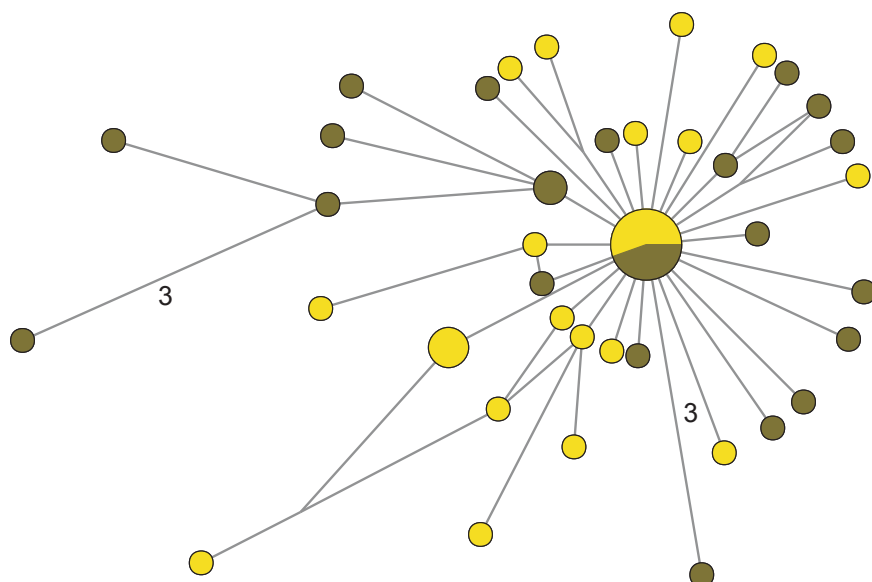
Sumatra

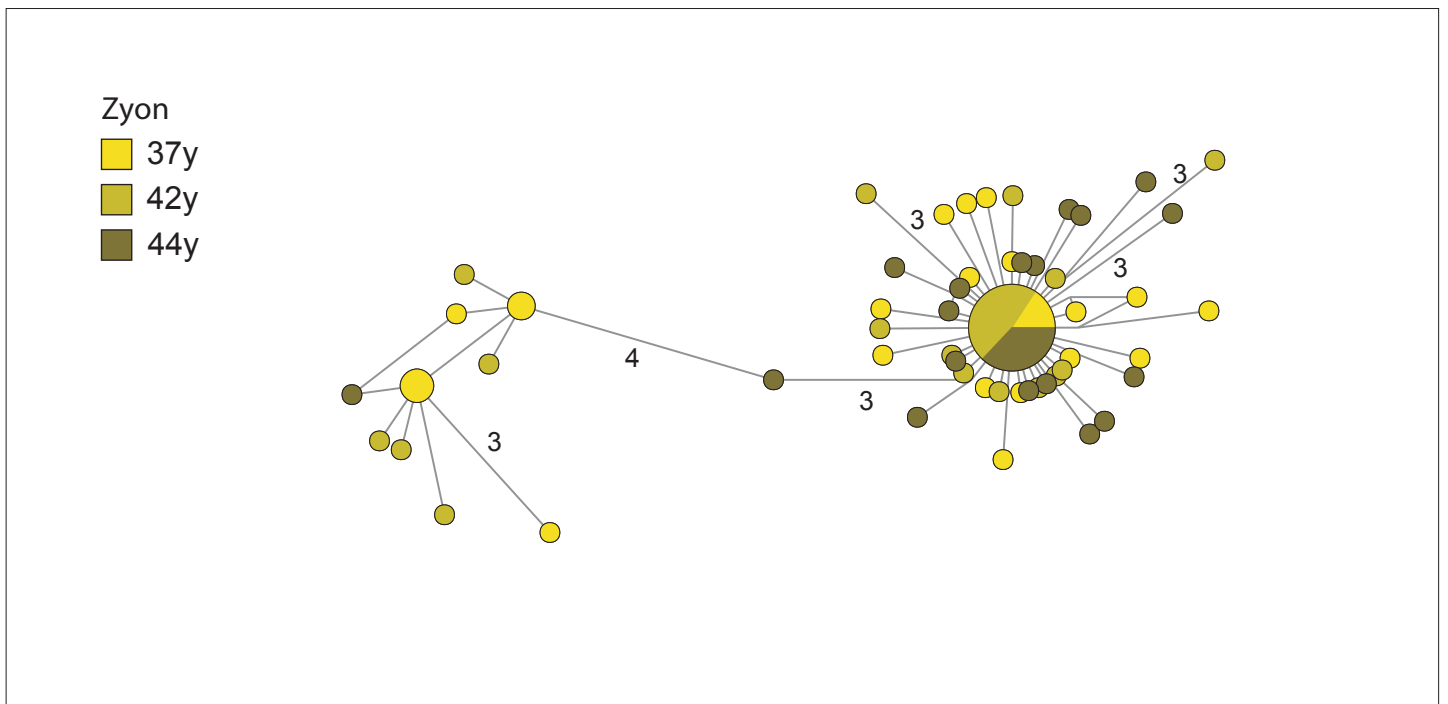
- 38y
- 40y



Utan

- 7y
- 11y





Supplementary Figure 2. Individual's networks from all serially sampled chimpanzees. y=years; refers to individual age at time of sampling. Within each network, node size is proportional to the frequency of the sequence occurrence. Branch lengths are directly related to the number of mutations between sequences, with values noted for differences greater than two base pairs.