

# Notebook: Community Genetics

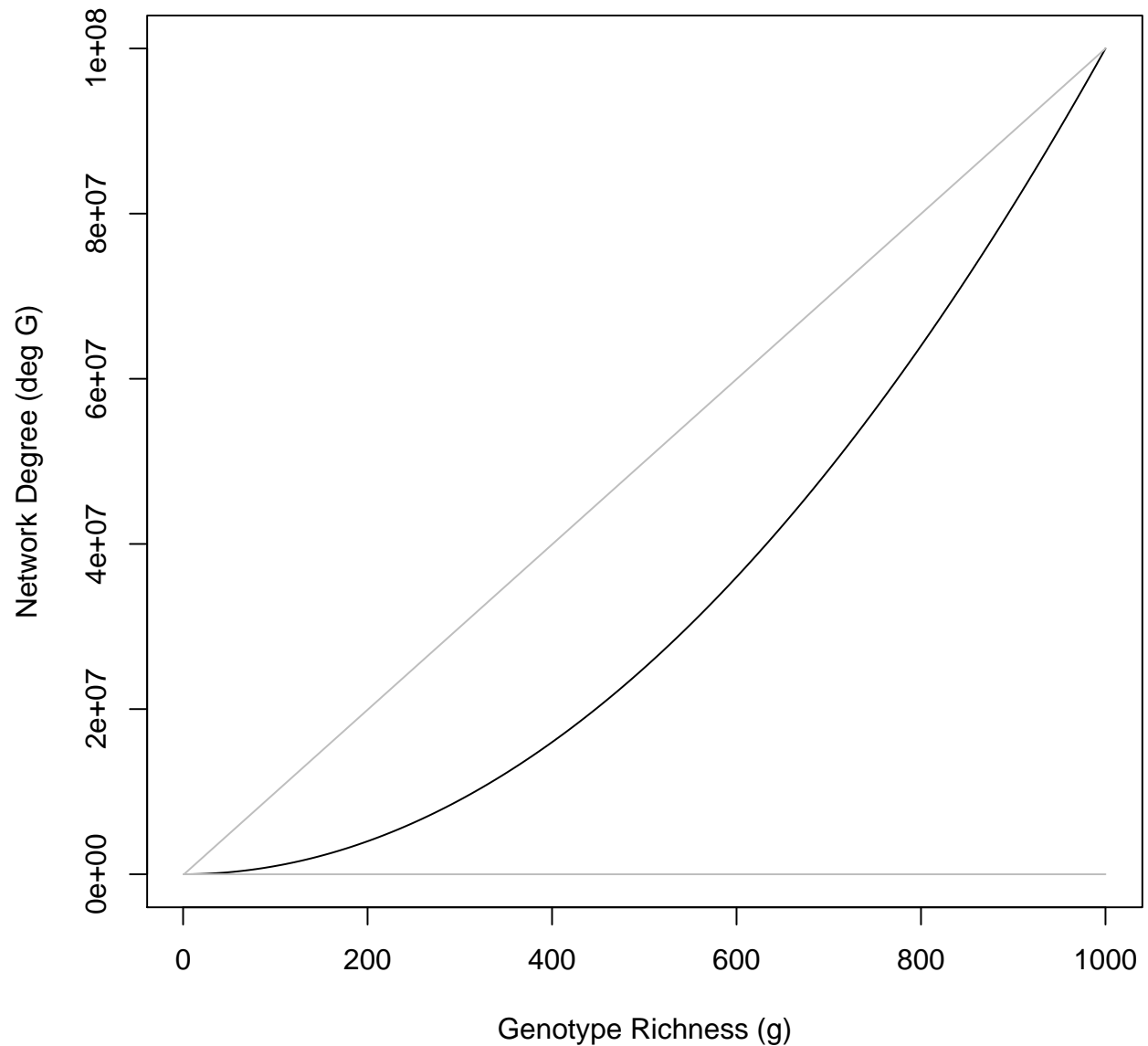
## Summary

## Notebook

Fri 30 Oct 2020 02:28:22 PM EDT

- Given a network of species ( $n$ ) with uniform genotypic richness ( $g$ ) we would calculate the number of individuals ( $m$ ) to be equal to  $ng$ .
- If the graph is regular, the number of vertices ( $v$ ), then the degree of the graph  $\deg(G)$  can be calculated as  $m(k-1)$ , where  $k$  is the degree of each node.
- Using these assumptions, we can calculate the scaling of the graph degree in response to variation in the genotypic richness, assuming each node is the maximum degree.

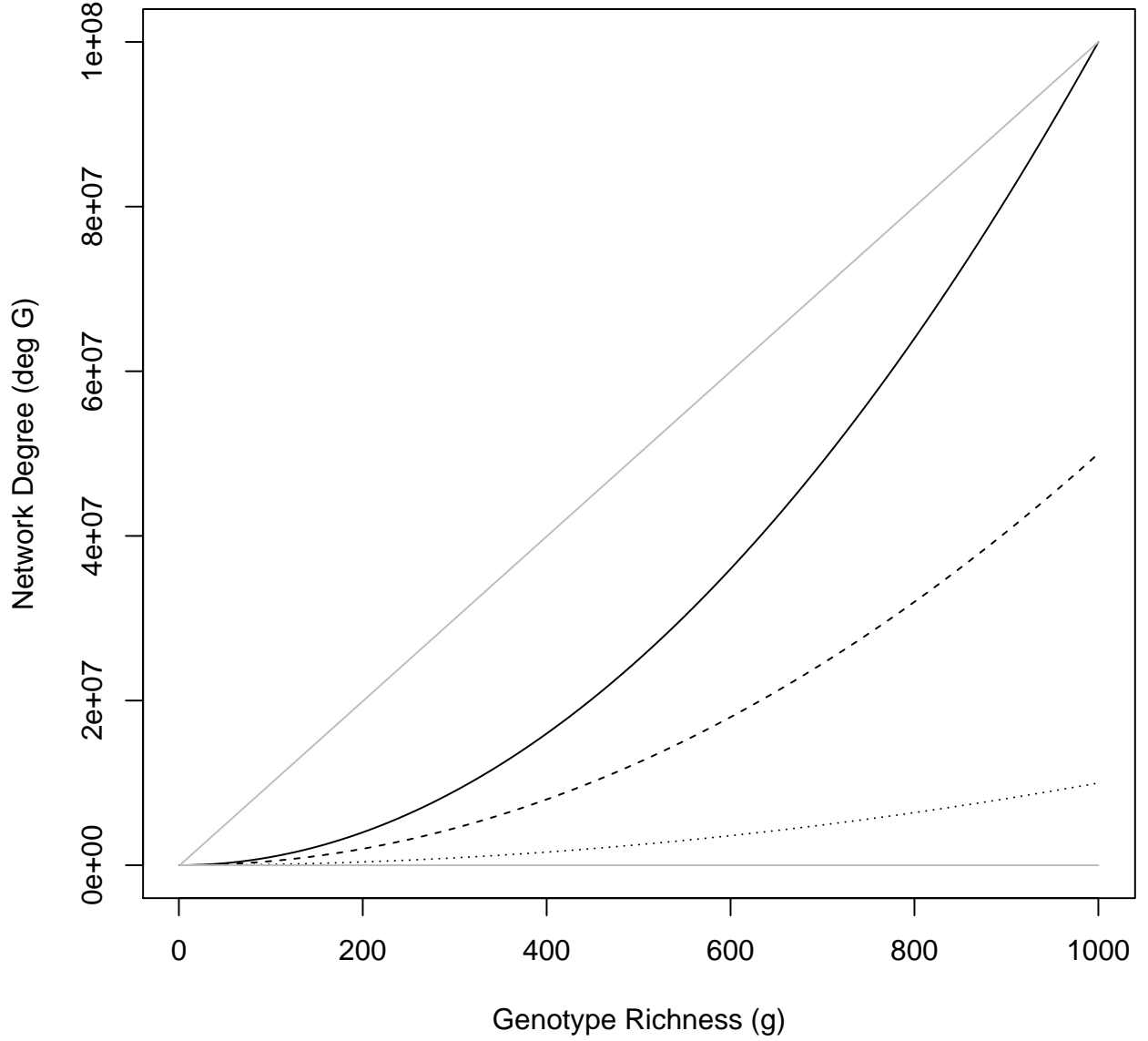
```
n <- 10
g <- seq(1, 1000)
dG <- n * g * (n * g - 1)
plot(dG~g, type = "l",
     xlab = "Genotype Richness (g)",
     ylab = "Network Degree (deg G)")
lines(range(g), range(dG), col = "grey")
lines(range(g), range(g), col = "grey")
```



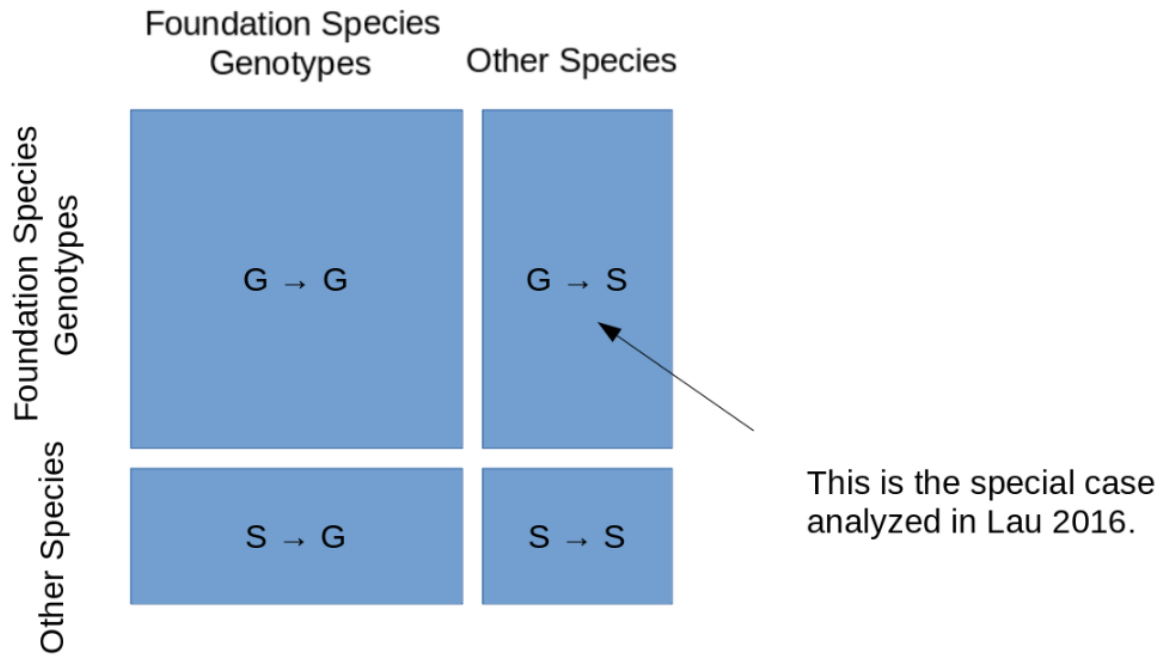
We can expand this to variation in the node degree maintaining a regular graph.

```
min.v <- n * g * 1/10
med.v <- n * g * 1/2
max.v <- n * g
dg.min <- n * g * (min.v - 1)
dg.med <- n * g * (med.v - 1)
dg.max <- n * g * (max.v - 1)

plot(dg.max ~ g, type = "l",
     xlab = "Genotype Richness (g)",
     ylab = "Network Degree (deg G)")
lines(g, dg.med, lty = 2)
lines(g, dg.min, lty = 3)
lines(range(g), range(dg), col = "grey")
lines(range(g), range(g), col = "grey")
```



- It would appear that for a regular graph, the scaling of the degree is super-linear, exponential as long as the graph is regular and the addition of genotypes results in the addition of a proportionate number of vertices (i.e. interactions).
- This could be expanded to explore different network structures, such as centralized, modular, nested, etc.
- The nested structure would be particularly interesting, as genotype communities are likely subsets of the larger community (Lau et al. 2016).
- This could be done via formulations of the degree distribution, e.g.  $P(k) = \frac{n_k}{n}$  for a regular network or Erdos-Renyi/Random, Scale-Free, Small-World, etc.
- Could also explore other metrics.



## References

Lau, Matthew K., Arthur R. Keith, Stuart R. Borrett, Stephen M. Shuster, and Thomas G. Whitham. 2016. "Genotypic variation in foundation species generates network structure that may drive community dynamics and evolution." *Ecology*. <https://doi.org/10.1890/15-0600.1>.