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.

```r
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")
```
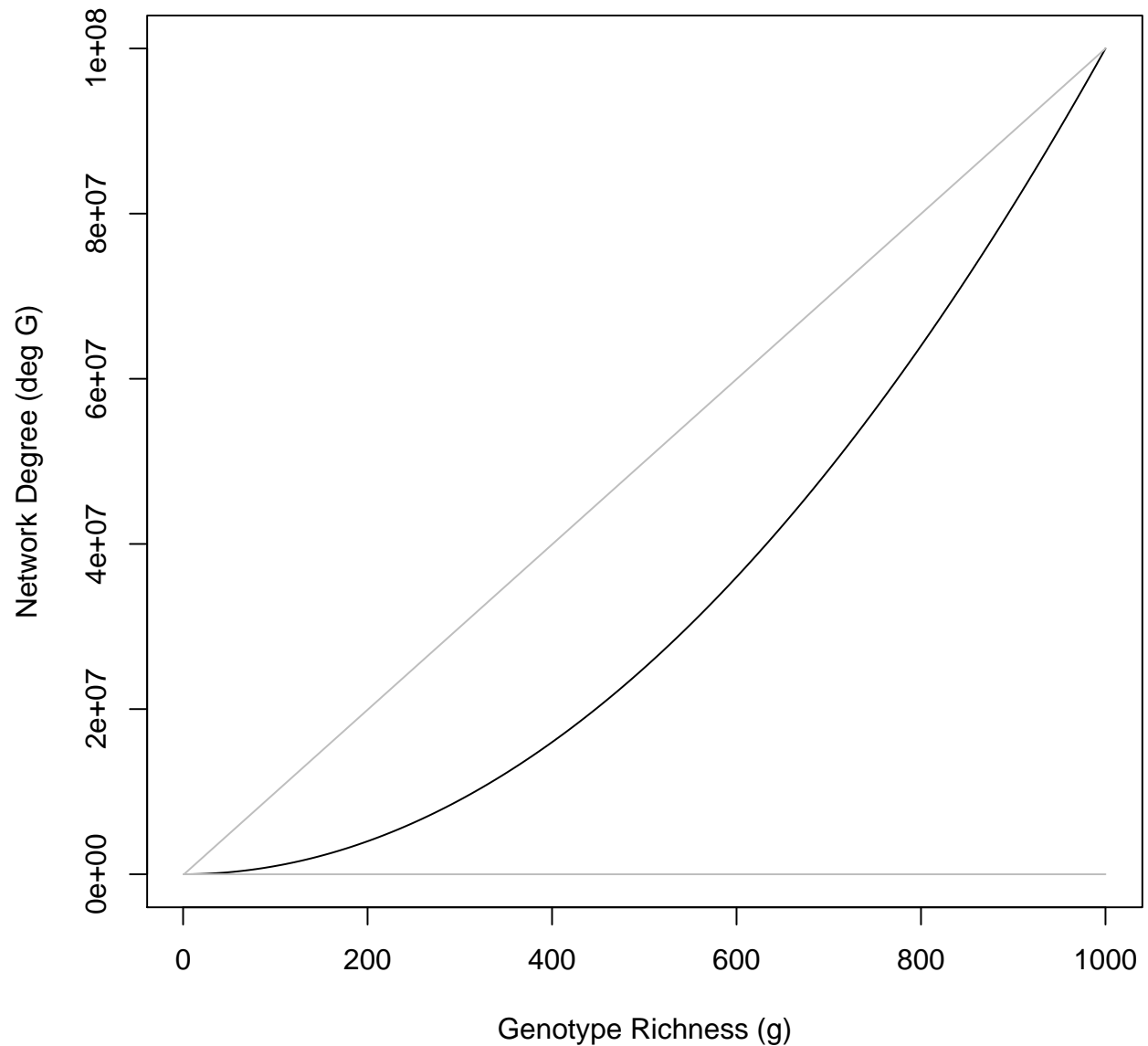
We can expand this to variation in the node degree mainting a regular graph.

```r
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")
```
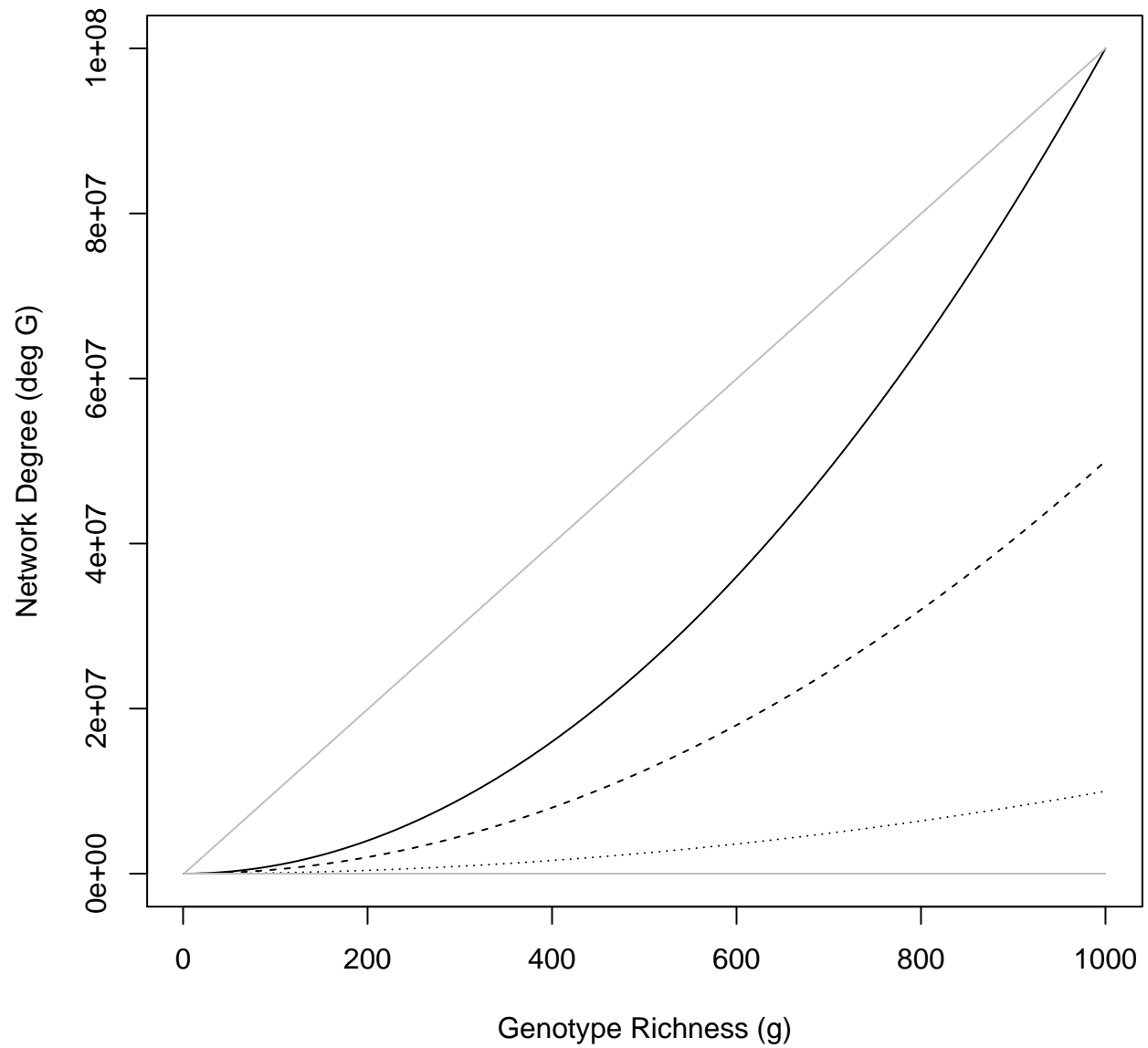
- This could be expanded to explore different network structures, such as centralized, modular, nested, etc.
- This could be done via formulations of the degree distribution, e.g. $P(k) = \frac{n_k}{n}$ for a regular network or Erdos-Renyi/Random, Scale-Free, Small-World, etc.
- Could also explore other metrics.