We often use the Lotka-Volterra (LV) model to understand the dynamics of simulated communities. What we often fail to check is if it is replicated known/observed macroecological patterns. The hollow-curve species abundance distribution (SAD) is widely recognized as a nearly universal pattern, being observed across a range of communities. Can the LV model be used to generate communities that follow this pattern? And how does the parameterization of the model affect the observed SAD?

**The model**

Rather than set the carrying capacity for each species individually, we set a community-wide carrying capacity (*K*). We further made the assumption that all species had equal access to resources such that each individual species had a carrying capacity *K/N* (where *N* is the number of extant species).