**Some further steps and material to be used in Discussion**

Even for regions with the same amount of Darwinian shortfall we still can have differences regarding how to fill out the shortfall. For example, one region can host species that present available information regarding genetic markers (for example in genebank), while the other one present little genetic information for the species. Even with the same amount of Darwinian shortfall we can distinguish different situations to fill the gap. A possible solution to better understand this would be mapping both information, the darwinian shortfall (accordingly our measure) and the genetic information. This component of Darwinian Shortfall is proposed by Rudbeck et al 2022 (<https://onlinelibrary.wiley.com/doi/full/10.1111/ecog.06142>). To me this is a complementary way to access the shortfalls. It is worth to note that our measure of Darwinian shortfall has more concordance with the definition by Diniz-Filho et al 2013 and Hortal et al 2015, that comprises species that have never been included in a phylogenetic analysis.