# S.M.3 - RDPG reconstructed networks have diverse structures

In this appendix, we check that the networks reconstructed from the RDPG do keep a variety of structural components, especially when selecting small species pools from within them. In order to do so, we induced 400 random subgraphs containing within 30 and 70 species, both from the Canadian and European metaweb. For each of these subgraphs, we measured eight variables: the mean and standard deviation of trophic levels, the standard deviation of degree (total, in, and out), and the proportion of top, intermediate, and basal species. We selected a random subset of 300 rows from the network-property matrix to fit a Principal Component Analysis projection matrix (W), which we then used to project all networks into the space formed by the first two principal components.
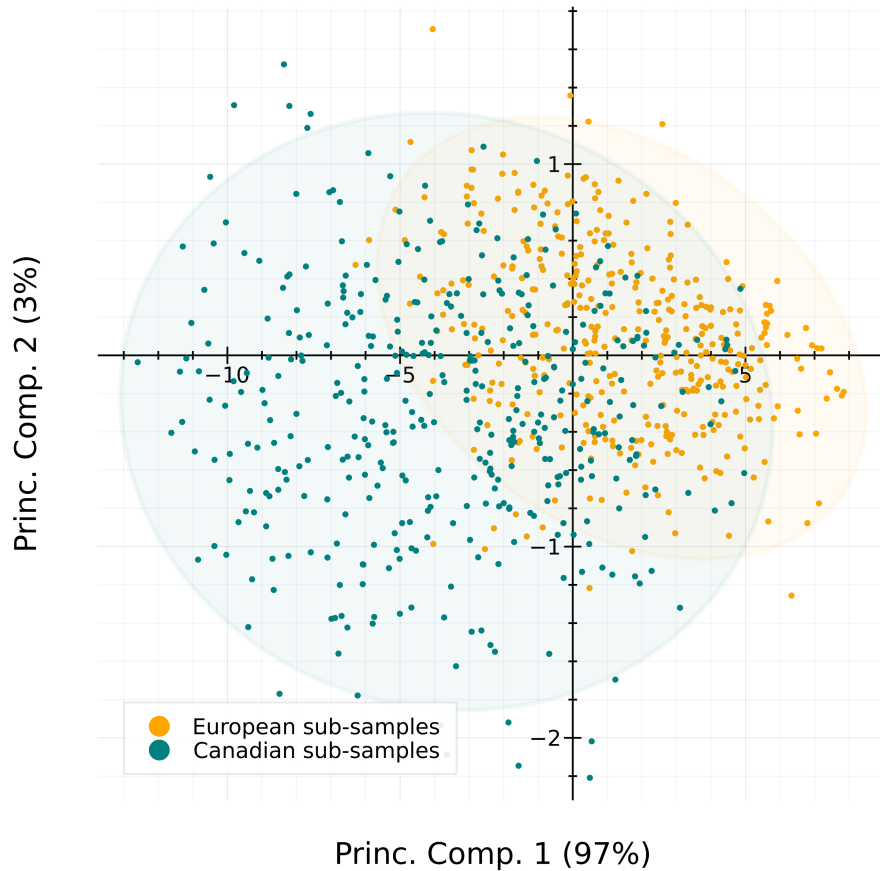
The first axis (explaining most variance) was strongly correlated to the standard deviation of the number of preys (-0.71), and the second axis to the standard

deviation in the number of predators (-0.95). These results match the conclusions in main text, namely that the first dimensions of network embedding capture the degree distribution.

Two things are important to note on this representation; each point is an induced sub-graph, and the ellipses are the 95% confidence interval around the points. First, there is some variations *within* a group (Europe *v.* Canada); second, the two groups do not fully overlap. This suggests that not only the sub-samples of the Canadian metaweb are not equivalent to the sub-samples of the European metaweb (*i.e.* the two networks have structural differences), realizations (here in the form of random local species pools) of the Canadian metaweb also show some variability; in short, reconstructing a metaweb using a RDPG will not result in homogeneous local networks, and may therefore be suitable for lower-scale predictions.