**Download Data Set (to be done prior to module)**

For this module we will be using a Picea glauca (white spruce) dataset of 15 phenotypes, 1694 individual trees, and some 6000 SNP markers. The markers have no linkage map, nor does the data set include pedigree based information. Picea glauca like most conifers, has a very large estimated genome size of 16.15 pg or 2100cM (estimated genetic map size), and 12 autosomal chromosomes. This means that we have very low marker coverage - this is further detailed in the paper (Beaulieu et al. 2014). White spruce is widespread in the Boreal and used mostly in residential home construction in Canada and paper making.

We will use a slightly altered version of the original dataset for the sake of time; however, the original dataset and associated paper by Beaulieu et al. (2014) lives here if anyone is interested in taking a look.

<http://datadryad.org/resource/doi:10.5061/dryad.6rd6f>