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Principle Component Analysis and its application to the Biological Sciences

Principle Component Analysis seeks to conceptualize underlying patterns or structures of observed variables y_{ib}, \dots, y_{ip} on p attributes at each of n sites s_i . PCA can be viewed as a rotation between data spaces of y_{ib}, \dots, y_{ip} and u_{il}, \dots, u_{ip} , where in effect, one is trying to reduce the dimensionality of the data to summarize the most important (i.e. defining) parts whilst simultaneously filtering out noise. I seek to impose this on various datasets to capture the cluster structure and potential underlying intricacies of that particular data set, while at the same time demonstrating its potential correlation with Graph Theory.