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Constructing a Classification Algorithm from Genome Wide Association Data

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Genome Wide Association (GWA) studies are large case control studies whose primary purpose is the identification and quantification of the effect that common genetic variants have on the inheritance of complex diseases. As these studies become larger and encompass more of the genome, the possibility of developing algorithms which attempt to predict whether or not a person will develop a disease based on their genetic profile becomes more realistic. Here, we show the results of the application of a simple classification algorithm, the Naïve Bayes classifier, to GWA data and discuss some of the statistical issues surrounding its implementation