Kernel Methods Annotated Bibliography

References

[1] David Barber and Christopher K. I. Williams. Gaussian processes for bayesian classification via hybrid monte carlo. In Michael C. Mozer, Michael I. Jordan, and Thomas Petsche, editors, *Advances in Neural Information Processing Systems*, volume 9, page 340. The MIT Press, 1997.

[2] R. Gnanadesikan, J.R. Kettering, and S.L. Tsao. Weighting and selection of variables for custer analysis. *Journal of Classification*, 12:113–136, 1995.

[3] L.C. Kwee, D. Liu, X. Lin, D. Ghosh, and M. Epstein. A powerful and flexible multilocus association test for quantitative traits. *ASHG*, 82:386–397, 2008.

> Kernel based method that calculates similarity between genotypes as the weighted number of alleles shared identical by state. They fit the semi-parametric model by a method called least-squares kernel machines which they show is identical to analysis using a specific linear mixed model. Their model fixes the weights on the SNPs based on maf (SNPs with lower maf will be harder to match) or prior evidence of association between the SNPs and disease and force these weights to sum to one. Since these weights are fixed, marginal inference on the SNPs are not possible.

[4] Martin H. Law and James T. Kwok. Bayesian support vector regression. In *Proceedings of the Eighth International Workshop on Artificial Intelligence and Statistics (AISTATS)*, pages 239–244, Key west Florida, January 2001.

[5] Herbert K. H. Lee, Christopher H. Holloman, Catherine A. Calder, and Dave M. Higdon. Flexible gaussian processes via convolution.

[6] T. Muller, S. Selinski, and K. Ichstadt. Cluster analysis: a comparison of different similarity measures for snp data.

> Compares different similairty measures. All are some variant of the proportion of matches, some exclude the 0/0 (homozygous rare) match and others down weight this match. Idea behind weighting the 0/0 matches differently is that with SNPs with small maf the rare homozygous match will be in some way

[7] R. Neal. Monte carlo implementation of gaussian process models for bayesian regression and classification, 1997.

Place a Gaussian process prior on the function space by specifying the covariance function

[8] D.J. Schaid, S.K. McDonnell, S.J. Hebbring, J.M. Cunningham, and S.N. Thibodeau. Nonparametric tests of association of multiple genes with human disease. *ASHG*, 76:780–793, 2005.

Calculates a genetic score (similarity score) for each pair of individuals within the cases and each pair within the controls. Then takes the average of the genetic scores within each group and compares them based on a U statistic. Here the difference in the U stat for the cases and the U stat for the controls under the null hypothesis that there is no difference is calculated as multivariate normal with mean zero

[9] M. Smith and R. Kohn. Nonparametric regression using bayesian variable selection, 1994.

[10] Peter Sollich. Bayesian methods for support vector machines: Evidence and predictive class probabilities. *Machine Learning*, 46(1-3):21–52, 2002.

[11] Michael E. Tipping. Sparse bayesian learning and the relevance vector machine. *Journal of Machine Learning Research*, 1:211–244, 2001.

[12] Grace Wahba. Soft and hard classification by reproducing kernel hilbert space methods.

[13] J. Wessel and N.J. Schork. Generalized genomic distance-based regression methodology for multilocus association analysis. *ASHG*, 79:792–806, 2006.

Construct a dissimilarity/distance matrix on all pairs of N individuals based on the number alleles shared identical by state and weighted based on maf, functionality, or prior results from a single-locus-analysis of the SNPs. Then attempts to answer if the variation in the level of dissimlarity of the individuals can be explained by the phenotypic variation of interest based on an F statistic that is equivalent to a standard ANOVA F stat when we use Euclidean distance to construct the distance matrix on a single quantitative trait. Because the distribution prorperties of the F stat are complicated for non-Euclidean distance measures of discrete variables, the authors permutation tests to assess statistical significance.

[14] Christopher K. I. Williams and David Barber. Bayesian classification with gaussian processes. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 20(12):1342–1351, 1998.

Place a Gaussian process prior on the basis functions of the input vectors. The prior is given by specifying the covariance of the Gaussian process in a way so that points with nearby inputs will give way to similar predictions and assuming a zero mean. They use a Laplace approximation and Hybrid MC to find posterior samples of the hyperparameters of interest