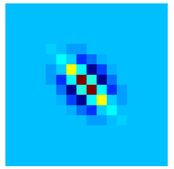
Maximally Informative Dimensions Using an Approximate Mutual Information Measure and Wavelets

Micah Richert[1,2], Bart Krekelberg[3], Thomas D. Albright[2]
[1]Dept Biol., UCSD, La Jollla, CA [2]Salk Inst., La Jolla, CA [3]Rutgers Univ., Newark, NJ

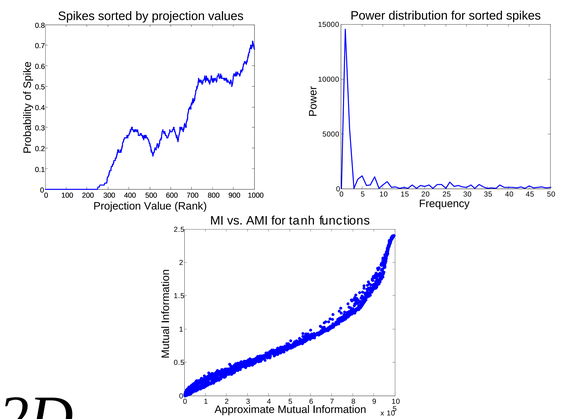


Introduction

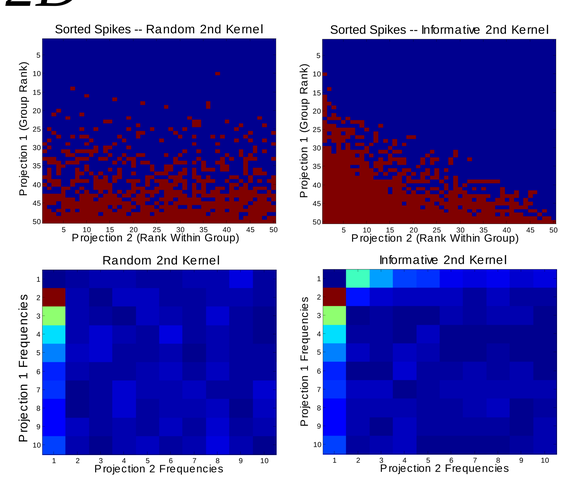
Reverse correlation is the process of estimating 1 or more linear kernels that predict the response of the cell given a stimulus. The spike triggered average (STA) is the simplest example, however, STA and STC do not perform well for highly non-gaussian stimuli. For this reason, Sharpee et. al. developed Maximally Informative Dimensions (MID). The basic idea is to find a linear kernel that maximizes the mutual information between the output of the linear model and the spike train of a cell. There are several issues with MID: binning is required to calculate mutual information, there are many local maxima, and no obvious stopping criteria. We propose a heuristic approach to address these issues.

Approximate Mutual Information

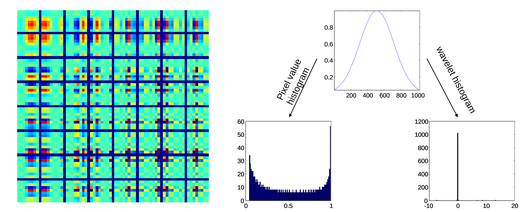
1D



2D



Wavelets



Hybrid Nelder-Mead Simplex Optimization

1. Sort Simplex Values
2. Reflection (around Centroid)
   1 in N*2 times, perform line maximization using gradient.
   N is the length of the kernel
3. Expansion
4. Contraction
5. Shrink

Stop when AMI for the test set is significantly worse over the 30 most recent iterations (over fit).

Speed and Accuracy

Mean Correlation Coefficient

Nonlinearity	MID	Hybrid
Mild	0.959	0.949
Even	0.056	0.822
Sigmoid	0.988	0.991

Mean Execution Time (sec)

Nonlinearity	MID	Hybrid
Mild	299	179
Even	341	171
Sigmoid	255	100

Conclusions

Uses justifiable stopping criteria
  Faster than ad hoc criteria used for MID

Imposes pseudo-smoothness constraint
  Simplex optimization in wavelet domain enhances low spatial frequencies

Benefits of new Information measure:
  No bins
    no parameter to tweak
    fewer local maxima
  Ideal for 2 or more dimensions

Often better accuracy than MID

micah@salk.edu