## Matching QSAR Sets SPE & Clustering and Weighted/Sampled Classification

Rajarshi Guha

Penn State University

## **Stochastic Proximity Embedding**

- Multidimensional scaling algorithm
- A stochastic form of a steepest descent algorithm
- Linear scaling (good for large datasets)
- In principle allows you to get the *intrinsic dimension* of the dataset

## **Stochastic Proximity Embedding**

- There are two main parameters that must be set:  $r_c$  and the final embedding dimension
- Quality of embedding is measured by the Sammon stress
- Ideally, in the *intrinsic dimensionality* the stress will be 0 or very close
- Currently the optimal parameters are obtained by an exhaustive search:  $.1 < r_c < 1$  and  $2 < D_{emb} < D_{inp}$

## **Stochastic Proximity Embedding**

- Strategy
  - . Find optimal  $r_c$  and  $D_{
    m emb}$
  - Cluster the dataset on the reduced coordinates
  - Badly predicted points should lie outside main clusters
- Problem
  - It assumes that the dataset can be clustered well

## Classification

- Unweighted LDA is very biased towards the good class
- Used the artemisinin dataset, with model descriptors (4)

**TSET Confusion Matrix** 

	b	g	$\checkmark$
b	0	50	0%
g	0	111	100%

**PSET Confusion Matrix** 

	b	g	$\checkmark$
b	0	4	0%
g	0	14	100%

- We can provide prior weights for the 2 classes
- First guess is to let  $W_{bad} = W_{good} = 0.5$
- The good class looses out and PSET is very poorly predicted

### **TSET Confusion Matrix**

### **PSET Confusion Matrix**

	b	g	$\checkmark$
b	32	18	64%
g	73	38	34%

	b	g	$\checkmark$
b	4	0	100%
g	11	3	21%

### What are we trying to optimize?

- True positives
- True negatives
- Overall correct
- How can we choose weights?
  - Look at overall correct vs.  $W_{good}$
  - . Look at how true positive and true negative rates vary with  $W_{good}$
  - Look at false positive vs true positive (ROC curve)

Plot of Weight for the Good Class vs. Overall Percentage Correct



 $W_{good}$ 

Plot of  $W_{good}$  vs. Percentage Of True Positives & True Negatives







**ROC Curve** 

- Use the PC's (i.e., rotated data) as feature vectors
- Not apparent how many to take, so trial & error!
- However for discrimination purposes kernel-PLS has been shown to be more useful <sup>a</sup>
- Strategy
  - Evaulate TSET PC's
  - Find minimum number (n) of PC's that give best classification
  - Evaluate PSET PC's
  - Use n PSET PC's to classify the PSET

<sup>&</sup>lt;sup>a</sup>Barker et al., J. Chemom., 2003, 17, 166-173

## **PC Classification (Artemisinin)**

**PC Classification (Artemisinin)** 

Results using 60 PC's

**TSET Confusion Matrix** 

	b	g	$\checkmark$
b	50	0	100%
g	0	111	100%

#### **PSET Confusion Matrix**

	b	g	$\checkmark$
b	3	1	75%
g	1	13	92%

### Jarvis Patrick Clustering And Classification of Residuals

# **JP - Overview**

- kNN based classification scheme
- Molecules are in the same class if
  - they are in each others J neighbor list
  - they have K neighbors in common
- Lots of scope for tweaking
- Fast algorithm

## **How Well Does JP Classify?**

- How do we determine the quality of classification?
  - Look at AP similarity values within a class
  - Compare average AP similarity value between classes
- However, since the algorithm is based on similarities in descriptor space this may not carry over to similarities in AP space

	Artemisinin, TSET
No. Class	Average In-Class AP Similarity
2	У
3	0.36, 0.37, 0.40
5	b

## JP - Varying J & K

Plot of Studentized Residuals Colored By JP Class Membership J = 20, K = 13



Plot of Studentized Residuals Colored By JP Class Membership (J = 20, K = 15)





- Artemisinin dataset
- Only the TSET is considered
- All reduced pool descriptors were used
- J = 20 chosen arbitrarily

Plot of Studentized Residuals Colored By JP Class Membership (J = 20, K = 14)