Prediction of MHC Class I and II binding peptides incorporating bayesian transfer hierarchies

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So far...

- Increased feature set for Elastic Net (baseline) by incorporating interaction features, i.e, Protein (a,b) at Pos (x,y). There are 80100 features now compared to 300 earlier
- Using Matlab's Elastic Net implementation (Lasso) and SVM (symtrain and symclassify), I classified the binding and non-binding peptides. The accuracies between the two methods are now comparable and it varies from 70-75%, the state of the art reports 80% for real data. The accuracy of Elastic Net earlier was mediocre at 53% and there is a drastic improvement with the addition of these features.
- Question: How many training samples and testing samples needs to be there in each set for an acceptable result?

Model:

The optimization problem for two related MHC-Class II alleles classifier is given by

$$\underset{\mathbf{w}^{1},\mathbf{w}^{2},\mathbf{w}}{\text{minimize}} \qquad \frac{1}{2} \|\mathbf{y}^{1} - \mathbf{x}^{1}\|_{2}^{2} + \frac{1}{2} \|\mathbf{y}^{2} - \mathbf{x}^{2}\|_{2}^{2} + \lambda_{1} \|\mathbf{w}^{1}\|_{1} + \lambda_{2} \|\mathbf{w}^{2}\|_{1} + \alpha \|\mathbf{D}\mathbf{w}\|_{1}.$$

where,

$$\mathbf{D} = \begin{bmatrix} 1000 & \dots & -1000 \\ 1000 & \dots & 0 & -100 \\ 1000 & \dots & 00 & -10 \\ 1000 & \dots & 000 & -1 \end{bmatrix} \quad \mathbf{w} = \begin{bmatrix} \mathbf{w}^1 \\ \mathbf{w}^2 \end{bmatrix}.$$

We are going to introduce new variables $\mathbf{z}^1, \mathbf{z}^2, \mathbf{z}^3, \mathbf{z}^4, \mathbf{z}^5$ and reformulate the problem

Writing out the augmented lagrangian for the above problem,

$$\begin{split} \text{AL}(\mathbf{w}, \mathbf{z}^{0}, \mathbf{z}^{1}, \mathbf{z}^{2}, \mathbf{z}^{3}, \mathbf{z}^{4}, \mathbf{z}^{5}, \mathbf{u}^{1}, \mathbf{u}^{2}, \mathbf{u}^{3}, \mathbf{u}^{4}, \mathbf{u}^{5}) &= & \frac{1}{2} \left\| \mathbf{y}^{1} - \mathbf{z}^{1} \right\|_{2}^{2} + \frac{1}{2} \left\| \mathbf{y}^{2} - \mathbf{z}^{2} \right\|_{2}^{2} + \lambda_{1} \left\| \mathbf{z}^{3} \right\|_{1} + \lambda_{2} \left\| \mathbf{z}^{4} \right\|_{1} + \alpha \left\| \mathbf{z}^{5} \right\|_{1} \\ &+ \mathbf{u}^{1} (\mathbf{z}^{1} - \mathbf{x}^{1}) + \mathbf{u}^{2} (\mathbf{z}^{2} - \mathbf{x}^{2}) \\ &+ \mathbf{u}^{3} (\mathbf{z}^{3} - \mathbf{w}^{1}) + \mathbf{u}^{4} (\mathbf{z}^{4} - \mathbf{w}^{2}) + \mathbf{u}^{5} (\mathbf{z}^{5} - \mathbf{D} \mathbf{w}) \\ &+ \frac{\rho}{2} \left\| \mathbf{z}^{1} - \mathbf{x}^{1} \right\|_{2}^{2} + \frac{\rho}{2} \left\| \mathbf{z}^{2} - \mathbf{x}^{2} \right\|_{2}^{2} \\ &+ \frac{\rho}{2} \left\| \mathbf{z}^{3} - \mathbf{w}^{1} \right\|_{2}^{2} + \frac{\rho}{2} \left\| \mathbf{z}^{4} - \mathbf{w}^{2} \right\|_{2}^{2} + \frac{\rho}{2} \left\| \mathbf{z}^{5} - \mathbf{D} \mathbf{w} \right\|_{2}^{2} \end{split}$$

The derived updates are as below:-

```
w1 = [I] \setminus [z3 + ((1 / rho) * u3)]

w2 = [I] \setminus [z4 + ((1 / rho) * u4)]

w = [D] \setminus [z5 + ((1 / rho) * u5)]
```

Question: Is the above correct or should I stack all 3 rows to derive update for 'w' as 'w' is made up of 'w1' and 'w2'?

```
z1 = [eye(n1); sqrt(rho) * eye(n1)] \ [y1; (sqrt(rho) * x1) - ((1 / sqrt(rho)) * u1)]
z2 = [eye(n2); sqrt(rho) * eye(n2)] \ [y2; (sqrt(rho) * x2) - ((1 / sqrt(rho)) * u2)]
z3 = shrinkThreshold(w1 - 1/rho*u3, lambda1/rho)
z4 = shrinkThreshold(w2 - 1/rho*u4, lambda2/rho)
z5 = shrinkThreshold(D*w - 1/rho*u5, alpha/rho)
u1 = u1 + rho * (z1 - x1);
u2 = u2 + rho * (z2 - x2);
u3 = u3 + rho * (z3 - w1);
u4 = u4 + rho * (z4 - w2);
u5 = u5 + rho * (z5 - w);
```

Question: What is the order in which I should compute updates first? w1, w2, w, z1-z5? Is this order correct?

Question: How to initialize λ_1 , λ_2 , ρ and α ?

Question: We say $\mathbf{z}^1 = \mathbf{x}^1$, but \mathbf{x}^1 is a matrix of feature vector rows (80100 in length), unable to think of how to initialize \mathbf{z}^i