

# Protein Interactions Extrapolated from Feline Protein Complexes

S. Martin\*, Z. Mao†, L. S. Chan†, S. Rasheed†

10/21/2006

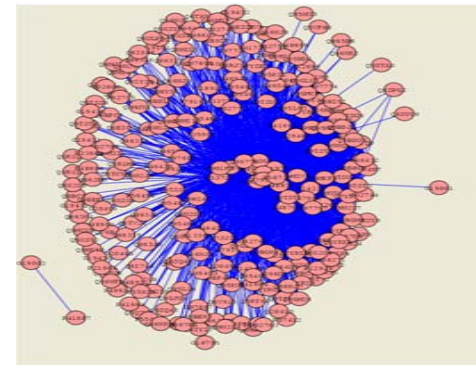
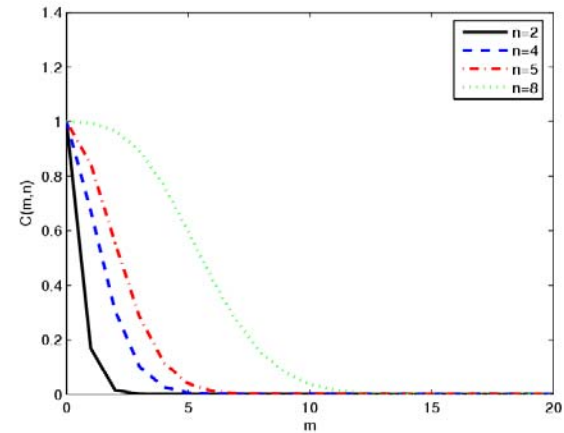
\*Sandia National Laboratories  
Albuquerque, NM

†University of Southern California  
Los Angeles, CA



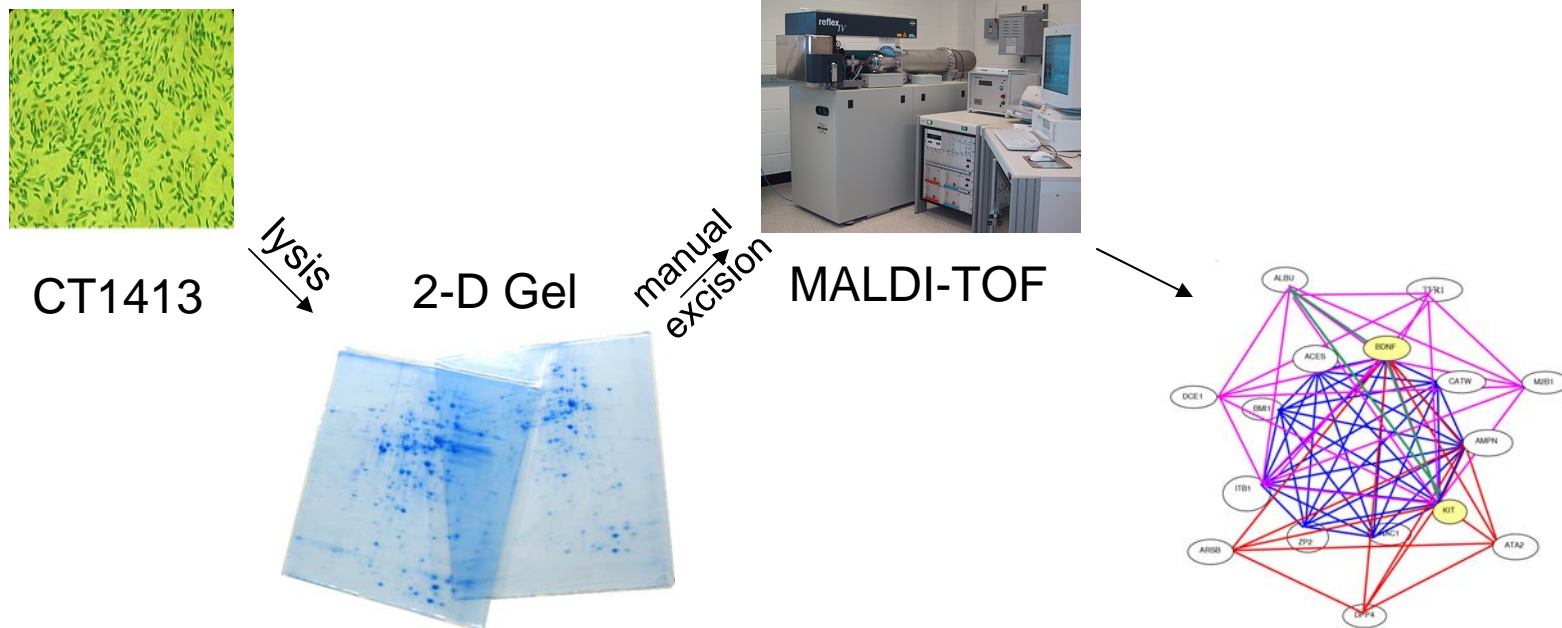
# Outline of Talk

- Feline Protein Complexes
  - Experimental Data
  - Inferring Protein Interactions
- Extrapolating Protein Interactions
  - Relating Protein Interactions to Amino Acid Sequence
  - Application to Experimental Data
- Conclusion



# Protein Complexes

- Feline protein complexes were identified using cat melanoma cell line CT1413, 2-D gel electrophoresis, and MALDI-TOF mass spectrometry.



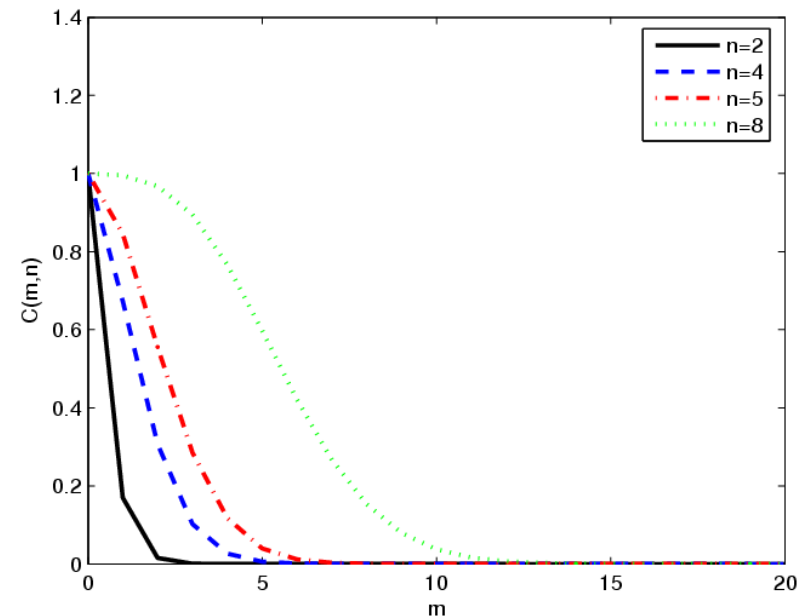
- The end result: groups of proteins assumed to be related by function/interaction potential.

# Inferring Interactions from Complexes

- Initial assumption: if two proteins occur in the same complex they may interact.
- Natural extension: if a protein pair occurs in multiple complexes it is more likely to interact.
  - We computed the probability  $C(m,n)$  that two proteins occur in  $m$  or more complexes of size  $n$ .

$$C(m, n) = \sum_{i \geq m} \binom{c}{i} P_n^i (1 - P_n)^{c-i}$$

$$P_n = \frac{n(n-1)}{a(a-1)}$$



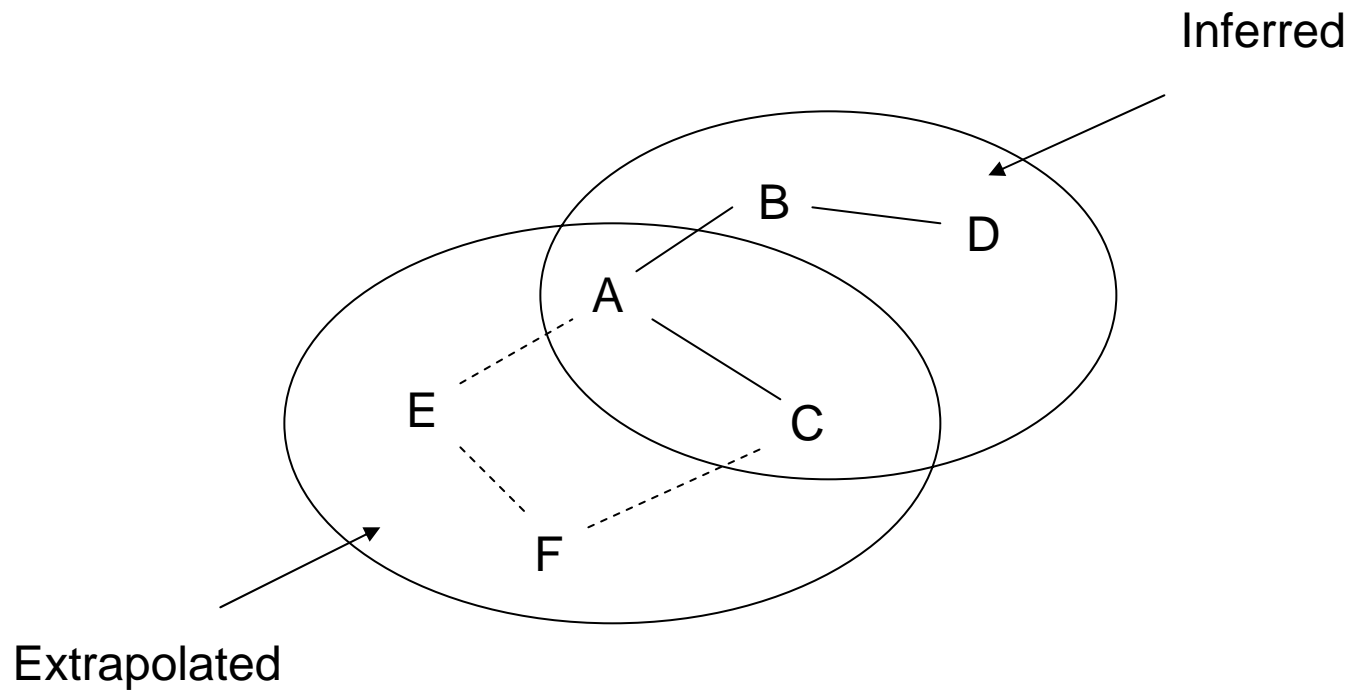
- We compared the actual counts to  $C(m,n)$  to find protein pairs that were likely to interact.

# Interactions Inferred from Complexes

Pair	Prot. 1 Name	Abbr.	Acc. #	Prot. 2 Name	Abbr.	Acc. #	p-value
1	Integrin beta-1 precursor	ITGB1	P53713	Mast/stem cell growth factor recept	KIT	Q28889	<.001
2	Integrin beta-1 precursor	ITGB1	P53713	Sarcoplasmic/endoplasmic reticulum	SERCA2	Q00779	<.001
3	Integrin beta-1 precursor	ITGB1	P53713	Transferrin receptor protein 1	TFRC	Q9MYZ3	<.001
4	Sarcoplasmic/endoplasmic reticulum	SERCA2	Q00779	Mast/stem cell growth factor recept	KIT	Q28889	<.001
5	Zona pellucida sperm-binding protei	ZPB	P48834	Integrin beta-1 precursor	ITGB1	P53713	<.001
6	Serum albumin precursor	ALB	P49064	Integrin beta-1 precursor	ITGB1	P53713	<.001
7	Proto-oncogene tyrosine-protein kin	FES	P14238	Integrin beta-1 precursor	ITGB1	P53713	<.001
8	Sarcoplasmic/endoplasmic reticulum	SERCA2	Q00779	Transferrin receptor protein 1	TFRC	Q9MYZ3	<.001
9	Serum albumin precursor	ALB	P49064	Mast/stem cell growth factor recept	KIT	Q28889	<.001
10	Mast/stem cell growth factor recept	KIT	Q28889	Transferrin receptor protein 1	TFRC	Q9MYZ3	<.001
11	Pyruvate kinase, M1 isozyme	PKM2	P11979	Integrin beta-1 precursor	ITGB1	P53713	<.001
12	Integrin beta-1 precursor	ITGB1	P53713	Aminopeptidase N	APN	P79171	<.001
13	Serum albumin precursor	ALB	P49064	Sarcoplasmic/endoplasmic reticulum	SERCA2	Q00779	<.001
14	Proto-oncogene tyrosine-protein kin	FES	P14238	Mast/stem cell growth factor recept	KIT	Q28889	<.001
15	Sodium/calcium exchanger 1 precurso	NCX1	P48767	Integrin beta-1 precursor	ITGB1	P53713	<.001
16	Pyruvate kinase, M1 isozyme	PKM2	P11979	Mast/stem cell growth factor recept	KIT	Q28889	0.002
17	Sodium/calcium exchanger 1 precurso	NCX1	P48767	Mast/stem cell growth factor recept	KIT	Q28889	0.002
18	Proto-oncogene tyrosine-protein kin	FES	P14238	Sarcoplasmic/endoplasmic reticulum	SERCA2	Q00779	0.007
19	Zona pellucida sperm-binding protei	ZPB	P48834	Sarcoplasmic/endoplasmic reticulum	SERCA2	Q00779	0.007
20	Zona pellucida sperm-binding protei	ZPB	P48834	Mast/stem cell growth factor recept	KIT	Q28889	0.007
21	Integrin beta-1 precursor	ITGB1	P53713	Alkaline phosphatase, tissue-nonspe	ALPL	Q29486	0.007
22	Zona pellucida sperm-binding protei	ZPB	P48834	Serum albumin precursor	ALB	P49064	0.016
23	Beta-glucuronidase precursor	GUSB	O97524	Integrin beta-1 precursor	ITGB1	P53713	0.016
24	Glutamate decarboxylase, 67 kDa iso	GAD67	P14748	Integrin beta-1 precursor	ITGB1	P53713	0.016
25	Aminopeptidase N	APN	P79171	Mast/stem cell growth factor recept	KIT	Q28889	0.016
26	Zona pellucida sperm-binding protei	ZPB	P48834	Transferrin receptor protein 1	TFRC	Q9MYZ3	0.016
27	Mast/stem cell growth factor recept	KIT	Q28889	Interleukin-1 beta convertase precu	CASP1	Q9MZV6	0.016
28	Integrin beta-1 precursor	ITGB1	P53713	Cathepsin W precursor	CTSW	Q9TST1	0.016
29	Lysosomal alpha-mannosidase precurs	MANB	O46432	Integrin beta-1 precursor	ITGB1	P53713	0.038
30	Integrin beta-1 precursor	ITGB1	P53713	Toll-like receptor 4 precursor	TLR4	P58727	0.038
31	Serum albumin precursor	ALB	P49064	Transferrin receptor protein 1	TFRC	Q9MYZ3	0.038

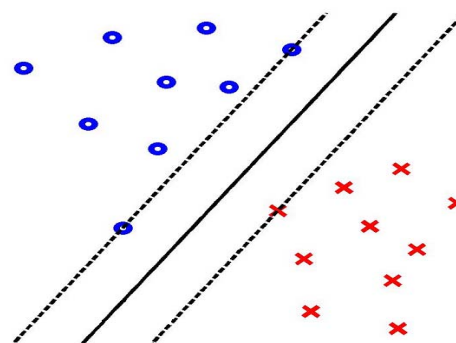
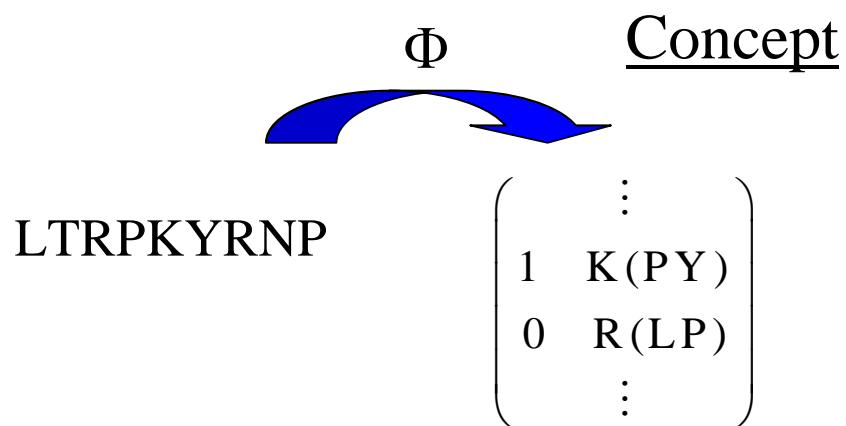
# Extrapolating Interactions to Cat Proteome

- Inferred Interactions involved 46 different proteins. We want to extrapolate to the 569 known proteins in the feline proteome.



- This can be done using the protein amino acid sequences.

# Amino Acid Tri-mer Kernel Support Vector Machine



## Implementation

maximize       $W(\alpha) = \sum_{i=1}^{\ell} \alpha_i - \frac{1}{2} \sum_{i,j=1}^{\ell} \alpha_i \alpha_j y_i y_j (\mathbf{x}_i \cdot \mathbf{x}_j)$

subject to       $0 \leq \alpha_i \leq C, \quad i = 1, \dots, \ell, \quad \text{and} \quad \sum_{i=1}^{\ell} \alpha_i y_i = 0.$

Replace inner product  
with *tri-mer kernel*

$$k(seq_1, seq_2) = (\Phi(seq_1), \Phi(seq_2))$$

and solve QP problem.

# Tri-mer Product

Tri-mers can be used to describe a single peptide, but in order to describe protein-protein *pairs* we use *tri-mer products*.

$$\Phi \otimes \Phi : X \times X \rightarrow F \otimes F \cong \mathfrak{R}^{N^2},$$

where  $\otimes$  is the tensor product, or all possible pairs.

## Example

$$\Phi(\text{LTRPKYRNP}) \otimes \Phi(\text{EYVEALYDFEAQQ...NKIGIFPANYVKPA}) =$$

$$\begin{pmatrix} \vdots \\ 1 \text{ K(PY)A(EL)} \\ 0 \text{ N(PL)A(EL)} \\ \vdots \end{pmatrix}$$



# Tri-mer Product

The tri-mer product results in an explosion of tri-mer pairs.

To avoid producing and analyzing the large number of pairs we use the following relation

$$\left( \Phi \otimes \Phi (A, B), \Phi \otimes \Phi (C, D) \right) = k(A, C)k(B, D)$$

This relation allows us to use tri-mer products while avoiding actual enumeration of products.

In fact we use a symmetric tri-mer product kernel

$$k(A, C)k(B, D) + k(A, D)k(B, C).$$

# Accuracy Assessment of Tri-mer SVMs

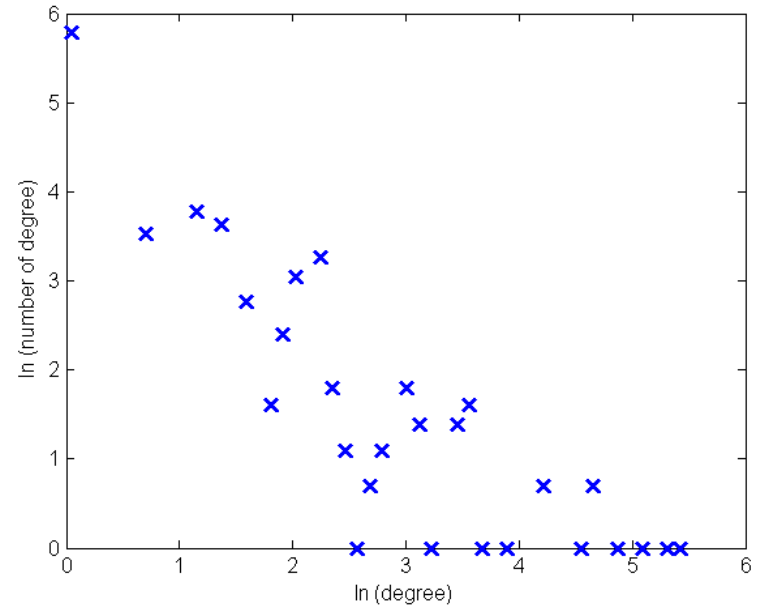
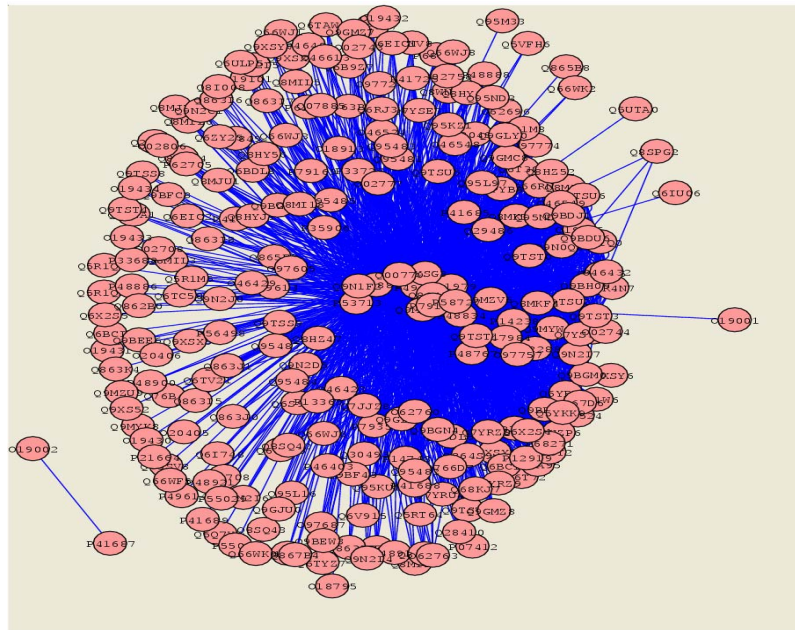
- To assess the accuracy of the extrapolation method we used 10-fold cross validation on the inferred protein interactions.

Num. Pairs	Num. Comps.	Comp. Size	Acc.	Spec.	<u>Sens.</u>
300	1		83.5	84.7	81.6
142	3	2	89.9	92.2	89.4
98	4	3	92.8	91.8	92.8
77	5	4	94.1	92.4	96.0
69	6	5	95.7	95.6	96.3
48	8	6	96.8	95.5	98.3
40	9	7	96.3	95.0	96.7
31	11	8	96.7	97.5	97.5

- The confidence levels were varied to obtain more or less inferred protein pairs, and the negatives (non-interactions) were taken at random.

# Extrapolated Network

- Using the SVM trained on 69 protein pairs (inferred interactions from at least 6 complexes at .05) we extrapolated to the entire cat proteome.



- As a check we plotted the degree distribution of the network to see that it was scale-free.

# Conclusions

- We performed a computational analysis of an experimental technique which produced protein complexes.
  - Suggested a new way to infer protein interactions from complexes
  - Added evidence to validity of experimental technique.
  - Extrapolated from limited set of proteins to entire proteome.
  - Produced hypothetical feline protein network.

**Questions?**