

# Structured feature selection

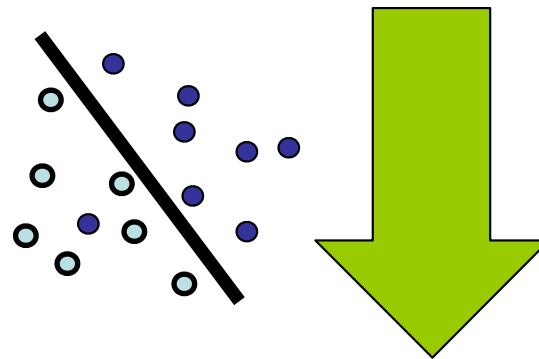
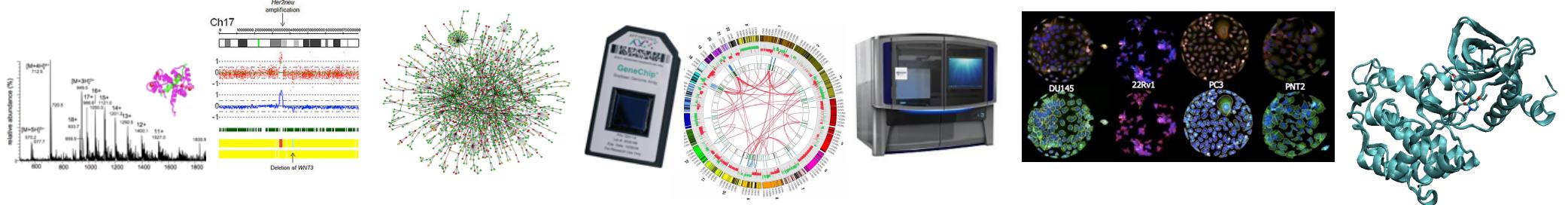
Jean-Philippe Vert

Jan 27, 2015

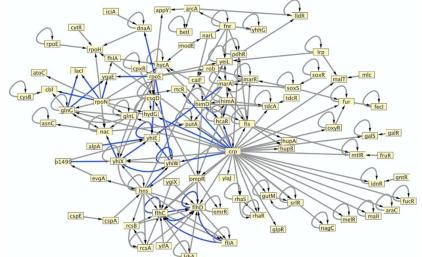
# CBIO at work



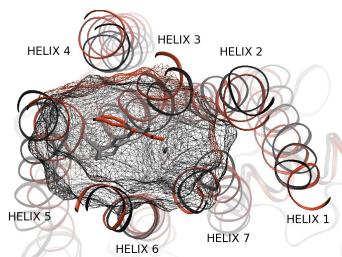
# Rationale of the team



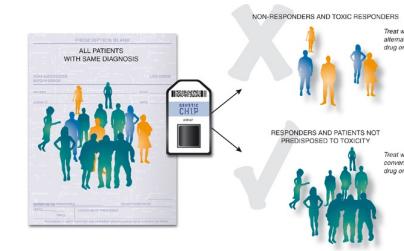
Machine learning



Mecanisms,  
drug targets



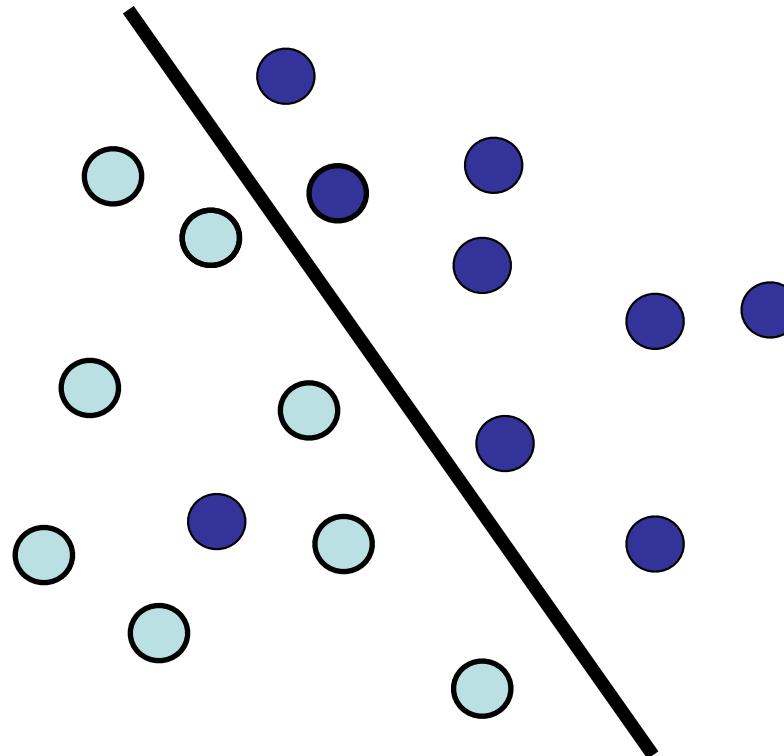
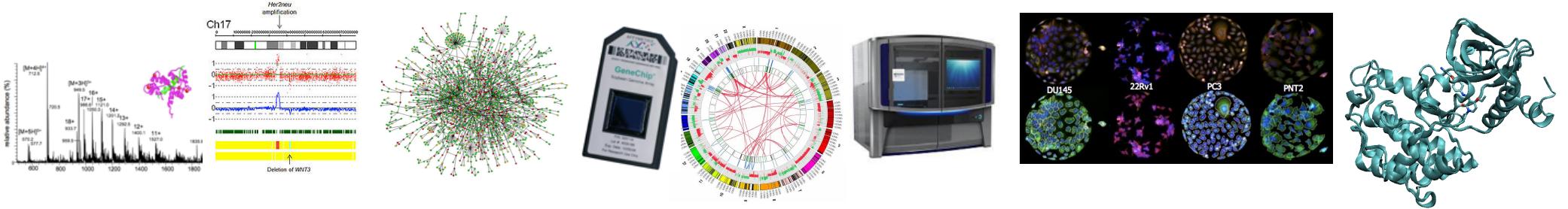
Drug design



Personalized  
medicine



# Machine Learning?



# Example: Toxicogenetics / Pharmacogenomics

## Toxicogenetics Challenge Data

Chemical  
descriptors

10K attributes

Genotypes	Not available	337 LCLs
	RNASeq	
	46K transcripts	

1.3M SNPs

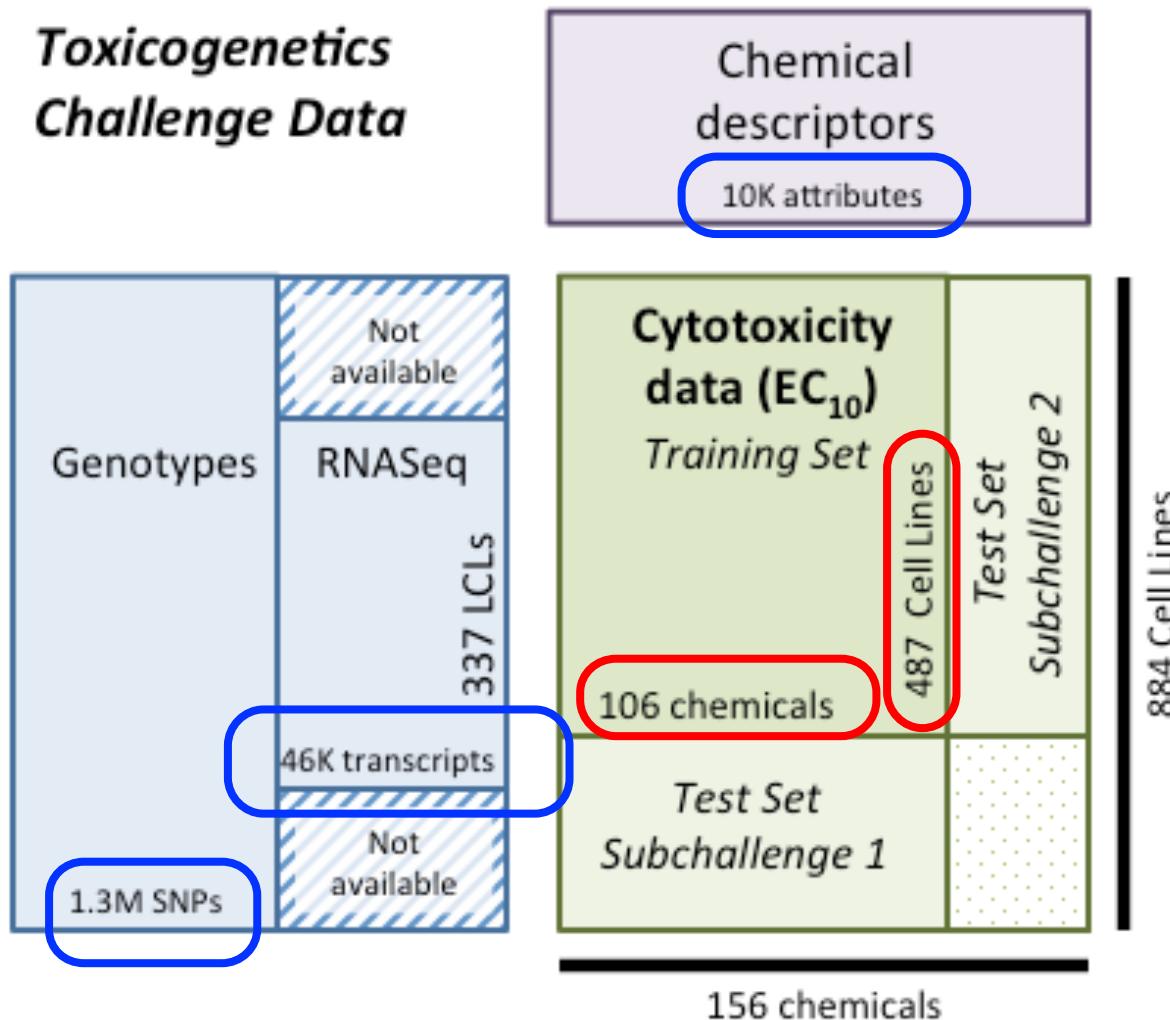
Cytotoxicity data ( $EC_{10}$ ) <i>Training Set</i>	487 Cell Lines	<i>Test Set</i> <i>Subchallenge 2</i>
	106 chemicals	

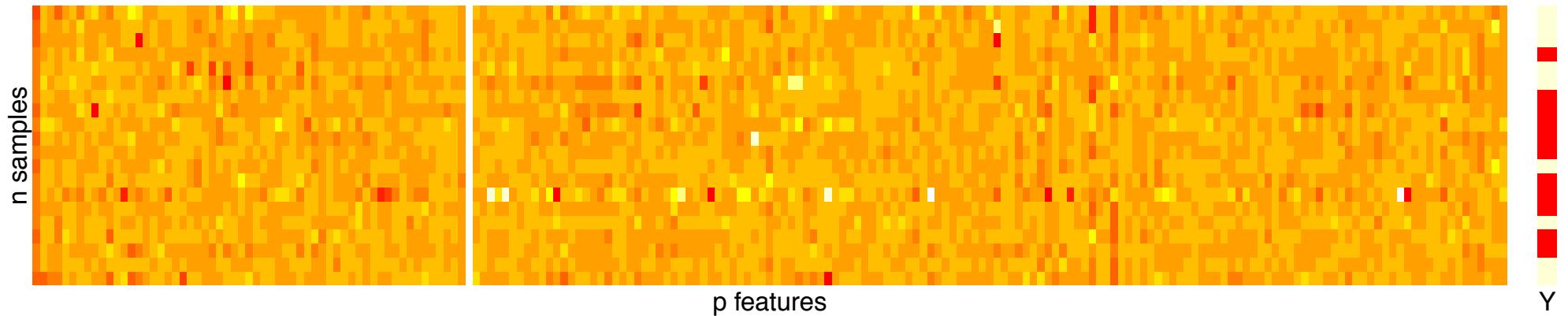
<i>Test Set</i> <i>Subchallenge 1</i>		884 Cell Lines
	156 chemicals	

# Problem: $n \ll p$

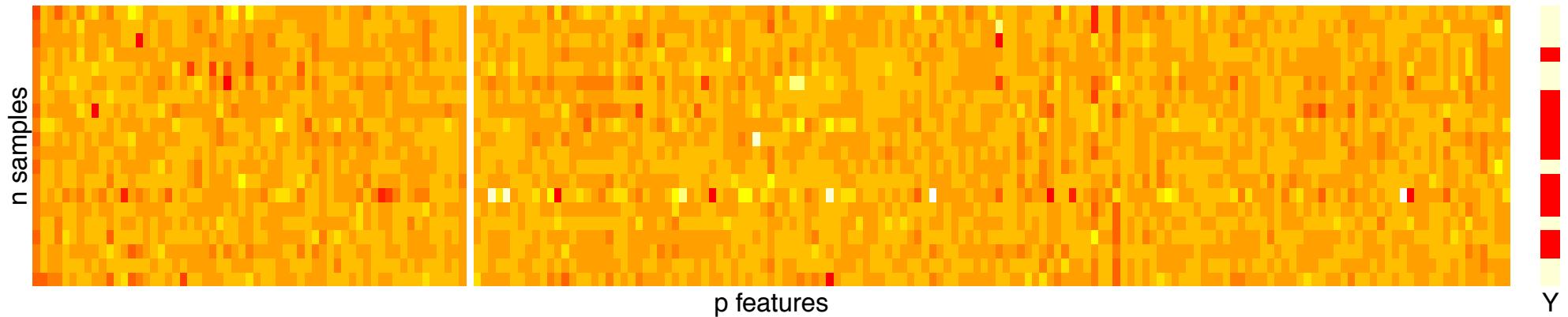
## Toxicogenetics Challenge Data



# Example: Patient stratification



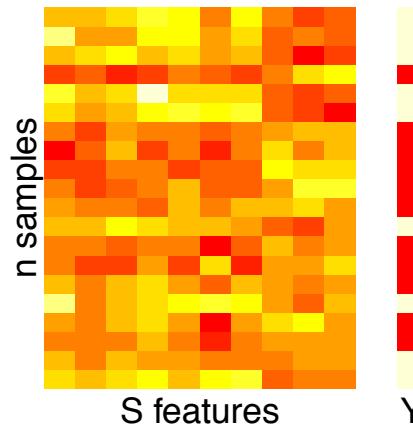
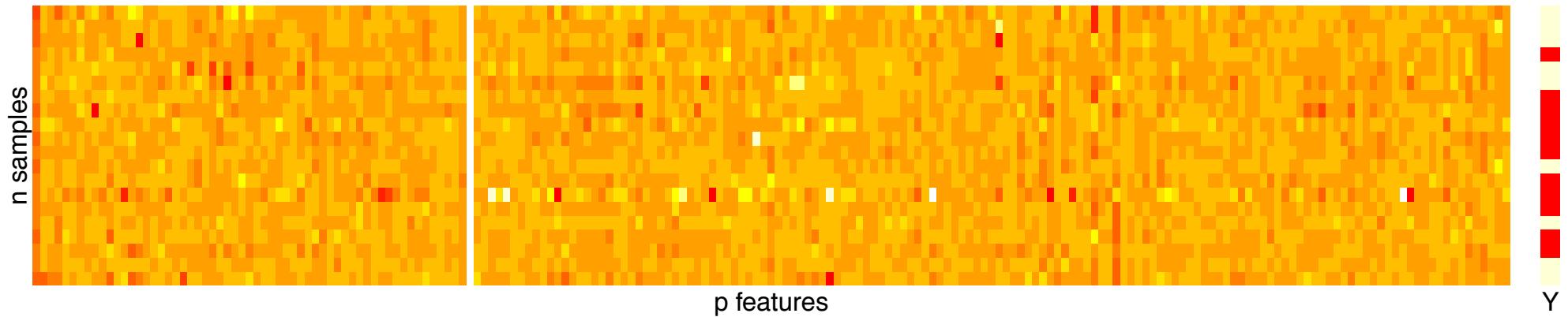
# Problem again: $n \ll p$



$n = 1E2 \sim 1E4$   
(patients)

$p = 1E4 \sim 1E7$   
(genes, mutations,  
copy numbers, ...)

# Feature Selection



# Feature Selection techniques

- 1) **Filter methods**: test association between features and response one by one (eg: correlation, t-test, ...)
- 2) **Wrapper methods**: search a subset of features such that the classifier works well (best subset selection, forward search, recursive feature elimination...)
- 3) **Embedded methods**: directly optimize sparse models (eg: lasso, elastic net, ...)

# But...

.....

## Gene expression profiling predicts clinical outcome of breast cancer

Laura J. van 't Veer<sup>\*†</sup>, Hongyue Dai<sup>†‡</sup>, Marc J. van de Vijver<sup>\*†</sup>,  
Yudong D. He<sup>‡</sup>, Augustinus A. M. Hart<sup>\*</sup>, Mao Mao<sup>‡</sup>, Hans L. Peterse<sup>\*</sup>,  
Karin van der Kooy<sup>\*</sup>, Matthew J. Marton<sup>‡</sup>, Anke T. Witteveen<sup>\*</sup>,  
George J. Schreiber<sup>‡</sup>, Ron M. Kerkhoven<sup>\*</sup>, Chris Roberts<sup>‡</sup>,  
Peter S. Linsley<sup>‡</sup>, René Bernards<sup>\*</sup> & Stephen H. Friend<sup>‡</sup>

70 genes (Nature, 2002)

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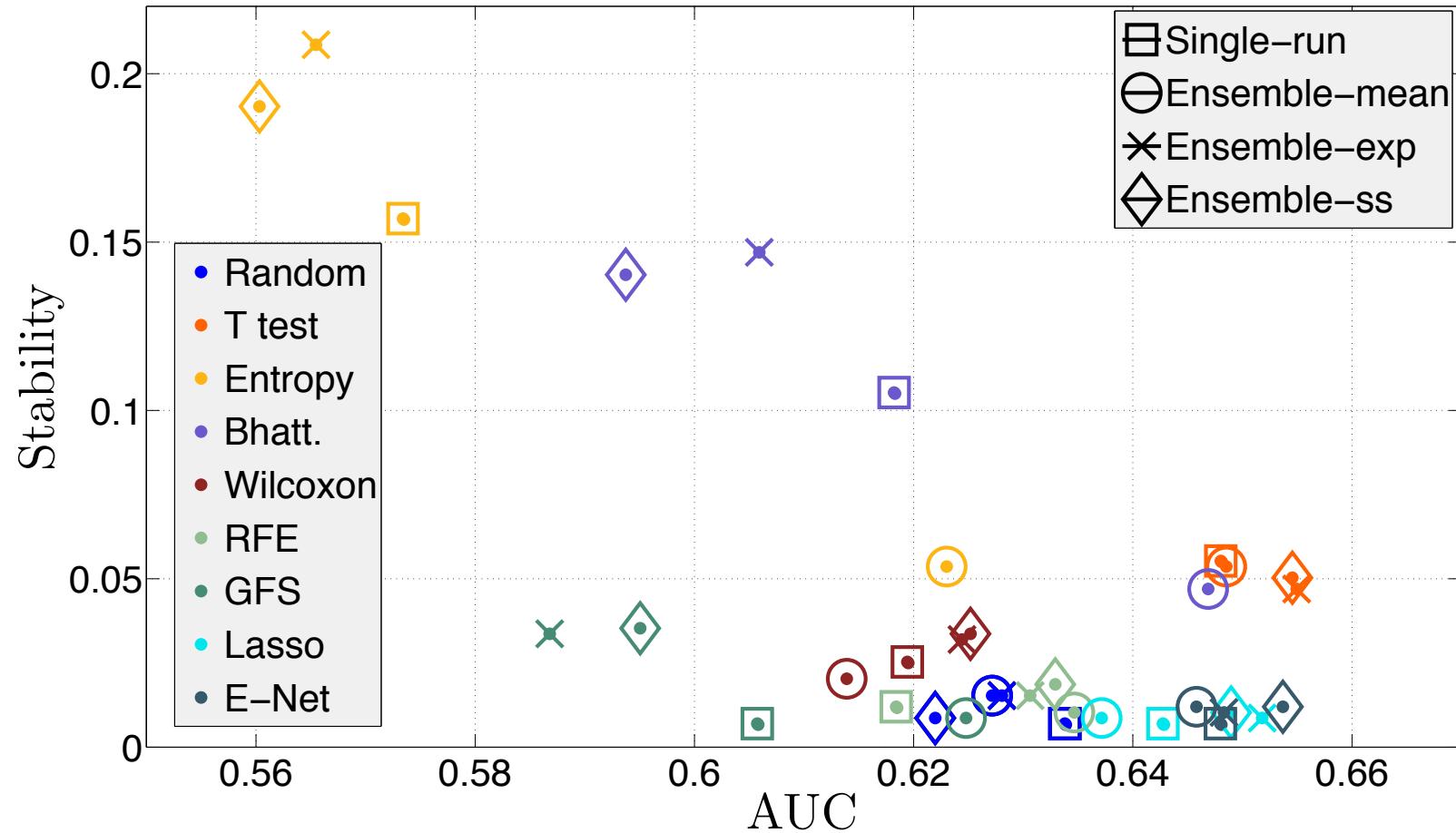
## Gene-expression profiles to predict distant metastasis of lymph-node-negative primary breast cancer

Yixin Wang, Jan G M Klijn, Yi Zhang, Anieta M Sieuwerts, Maxime P Look, Fei Yang, Dmitri Talantov, Mieke Timmermans,  
Marion E Meijer-van Gelder, Jack Yu, Tim Jatkoe, Els M JJ Berns, David Atkins, John A Foekens

76 genes (Lancet, 2005)

3 genes in common

# and nothing seems to work better



(Haury et al., 2011)

# Give up machine learning and go to Tahiti?



# Sparsity with the LASSO

- Linear model

$$f(x) = w_1 x_1 + w_2 x_2 + \dots + w_P x_P$$

- Sparse when  $w_K=0$  for many K's

- Learn a sparse model by

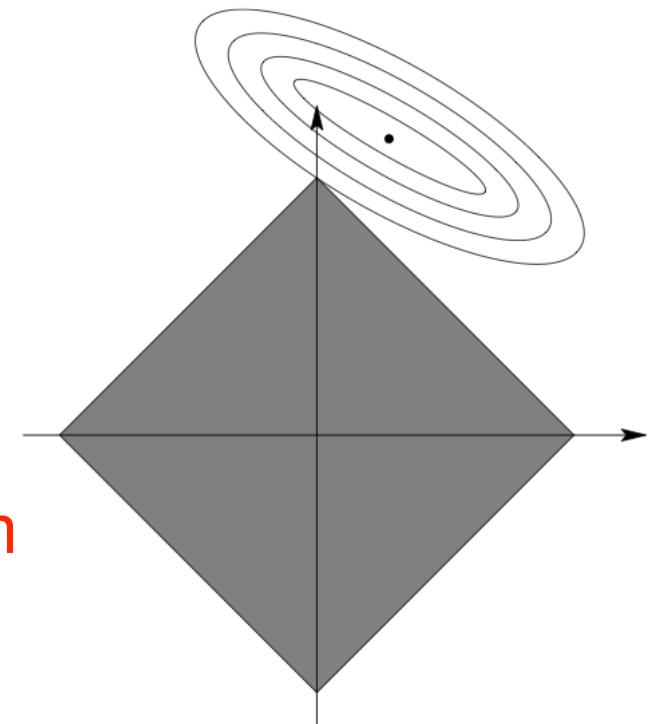
**minimize Error(w)**

*such that*

**w is in the grey box O**

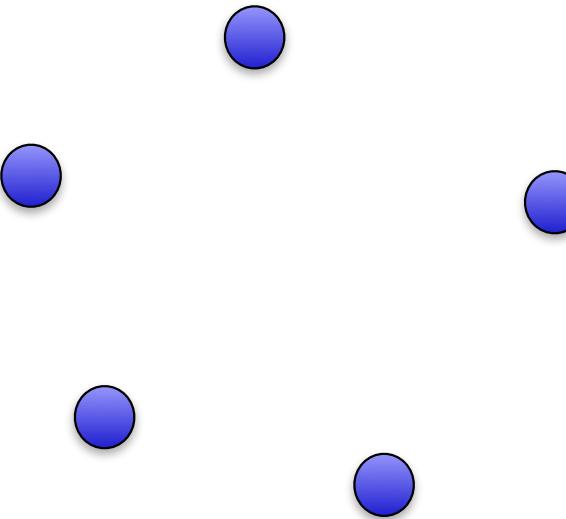
- O is convex -> **efficient algorithm**

- O has edges -> **sparsity**



# Structured sparsity with atomic norms

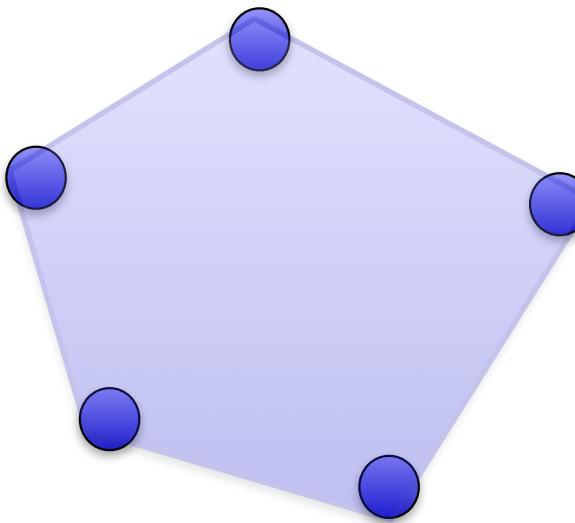
1) Choose a set of ATOMS



# Structured sparsity with atomic norms

1) Choose a set of ATOMS

2) Take the convex hull  $O$



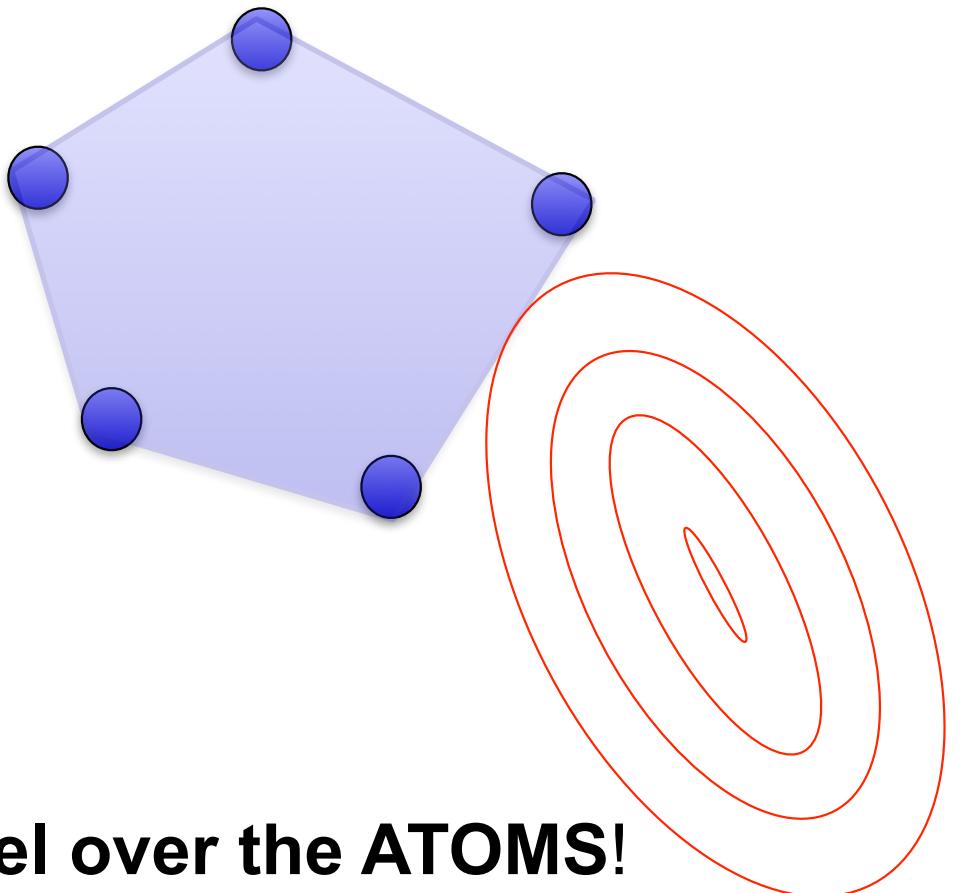
# Structured sparsity with atomic norms

1) Choose a set of ATOMS

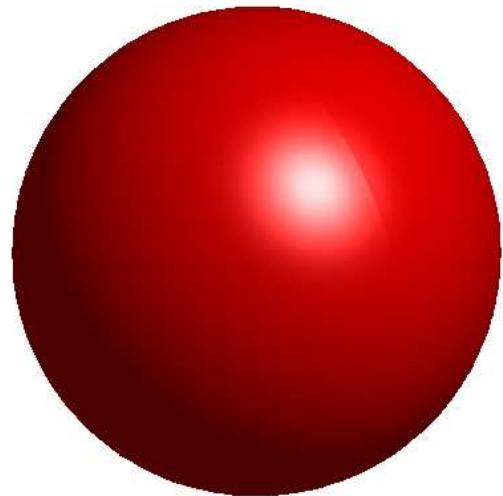
2) Take the convex hull

3) Minimize  $\text{Error}(w)$   
such that  
 $w$  is in the convex hull

The solution is a **sparse model over the ATOMS!**

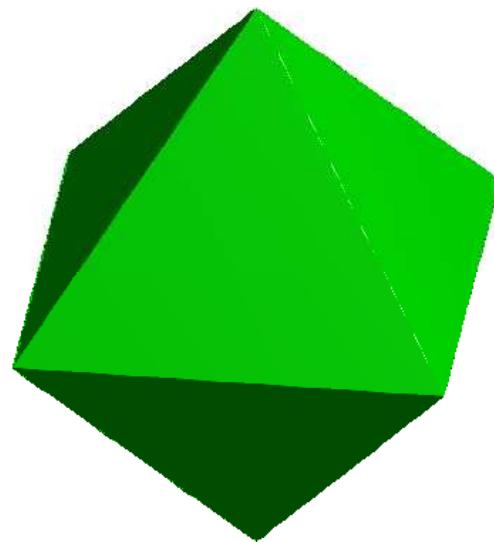


# Quizz: where are the atoms?



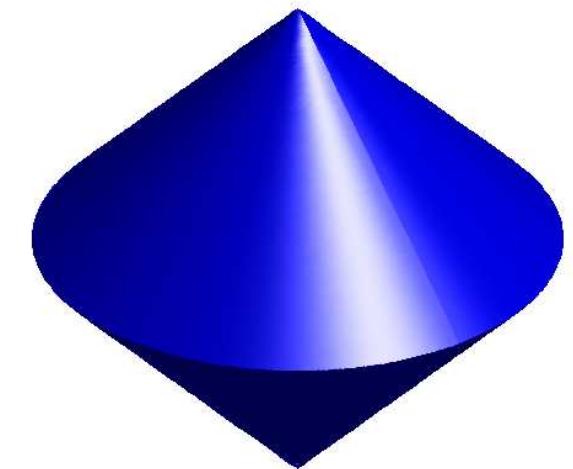
$$\|w\|_2$$

Ridge



$$\|w\|_1$$

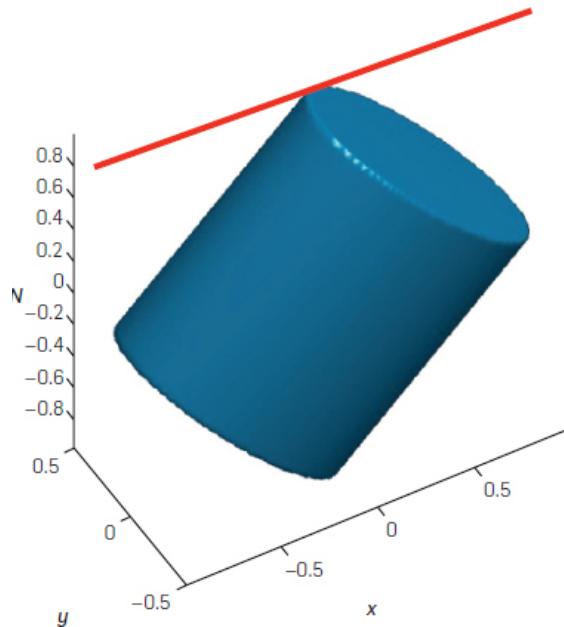
Lasso



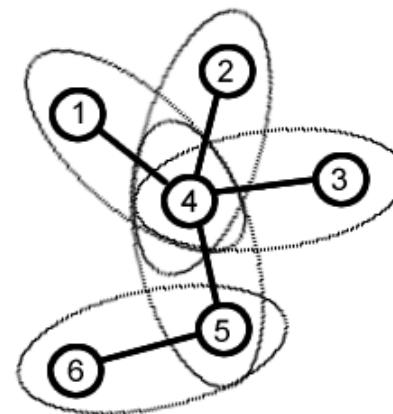
$$\sqrt{w_1^2 + w_2^2} + |w_3|$$

Group Lasso

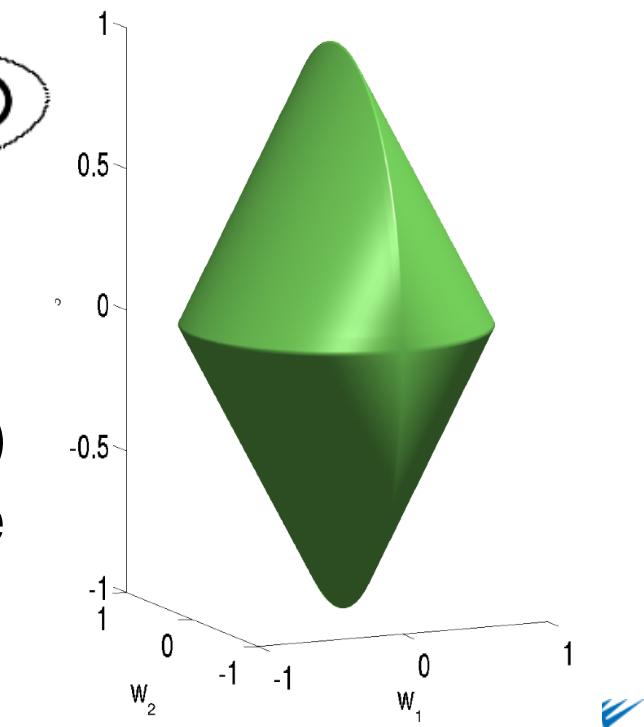
# Quizz (cont.)



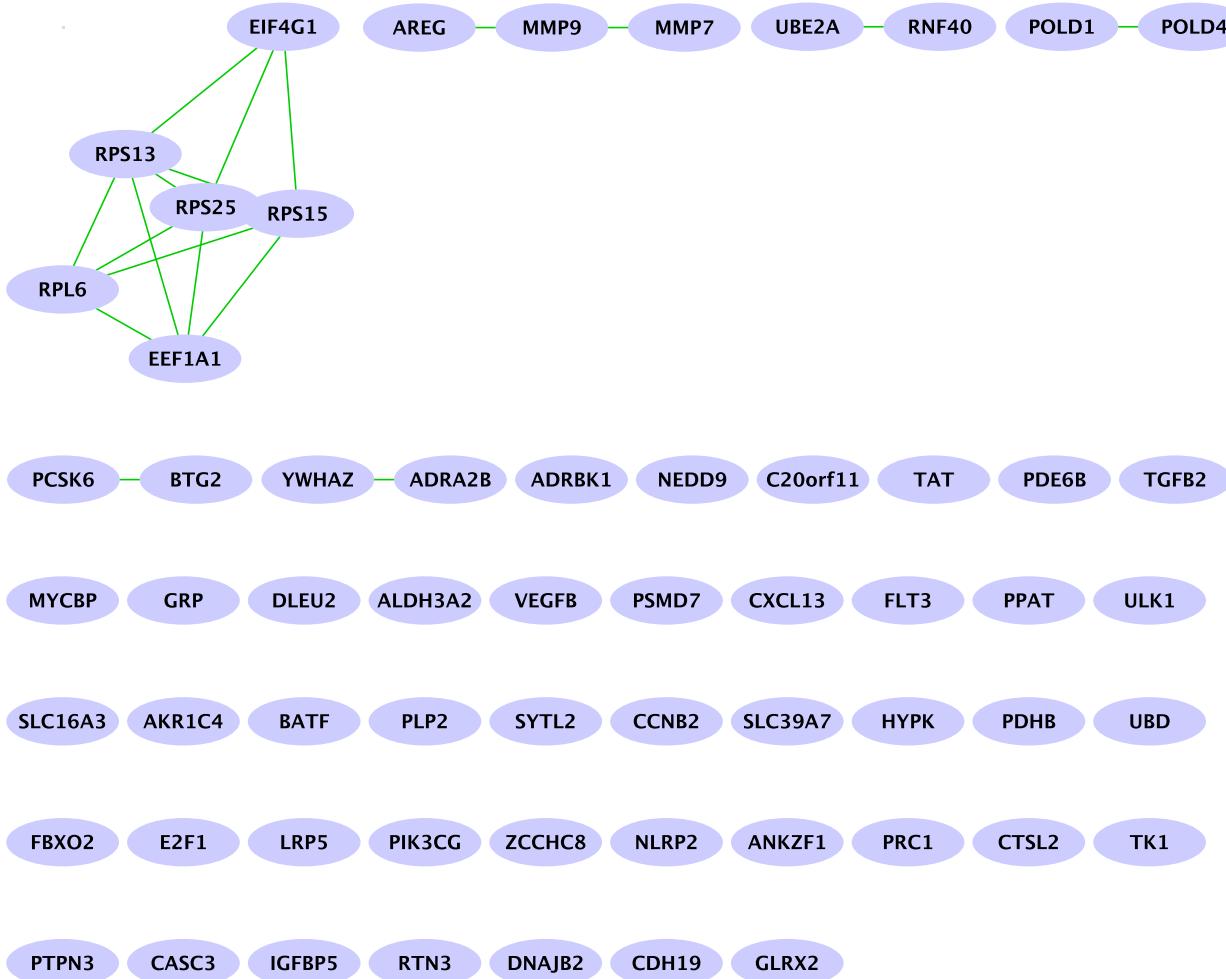
Trace norm  
to learn matrices with small rank



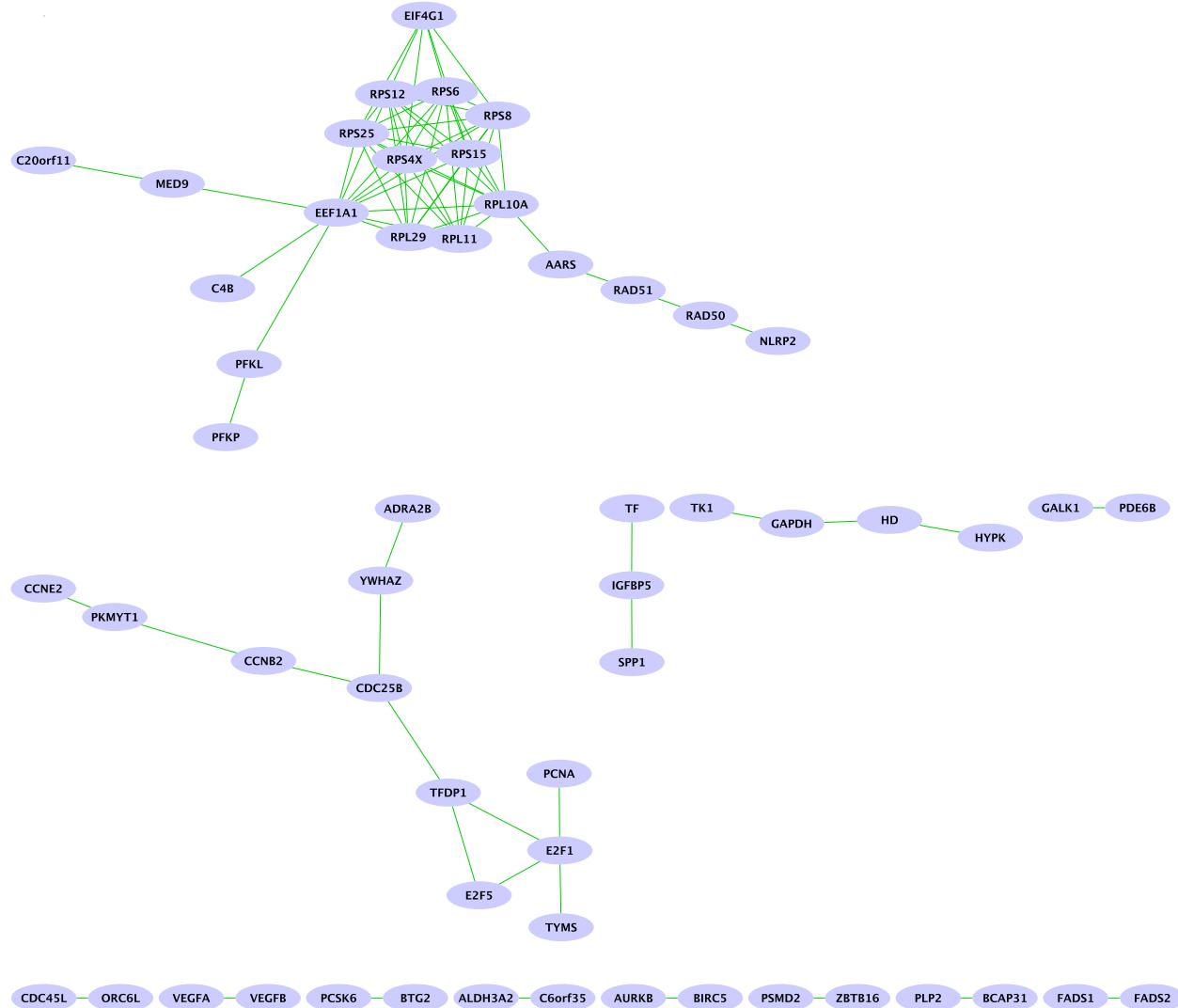
Graph Lasso (Jacob et al. 2009)  
to select features that tend to be  
connected over a given network



# Breast cancer prognosis signature with Lasso (accuracy=61%)



# Breast cancer prognosis signature with Graph Lasso (accuracy=64%)

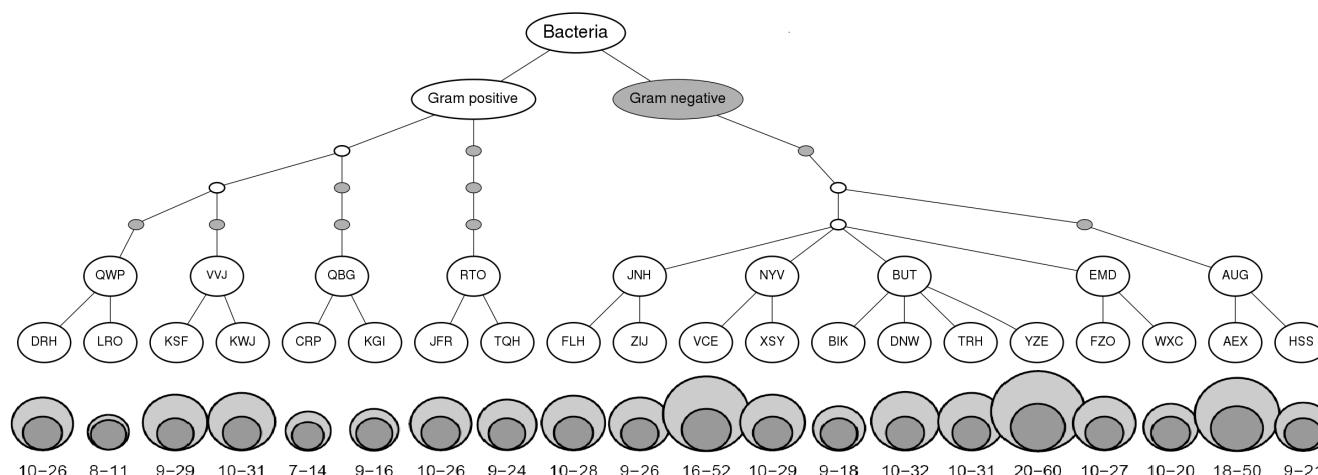
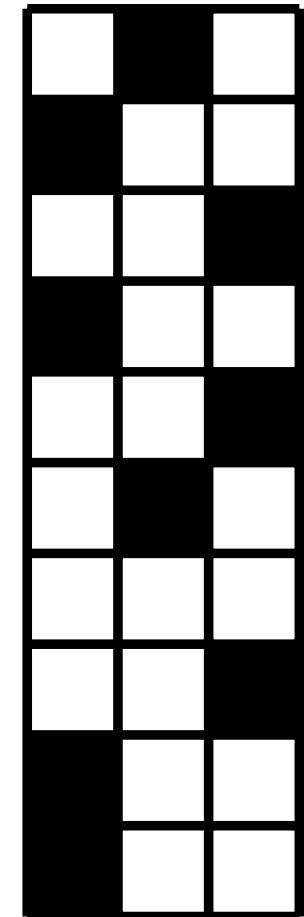


# Learning sparse models with disjoint support ?

## Motivation

- Multiclass or multi-task classification problems
- Eg: predict identity and emotion from a face
- Eg: cascade of classifiers

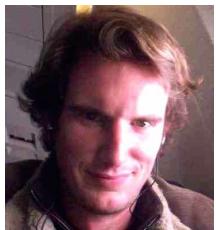
$X =$



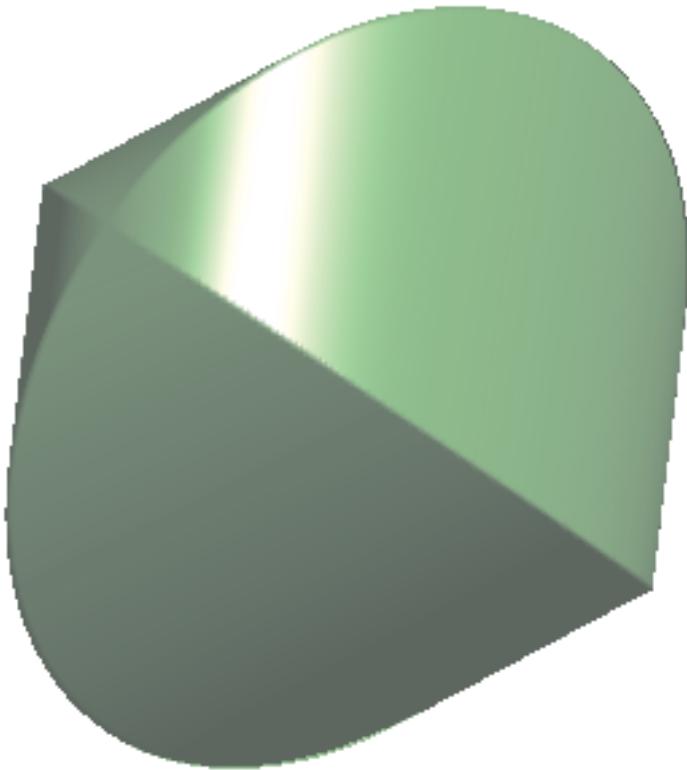
# An atomic norm (ECML 2014)



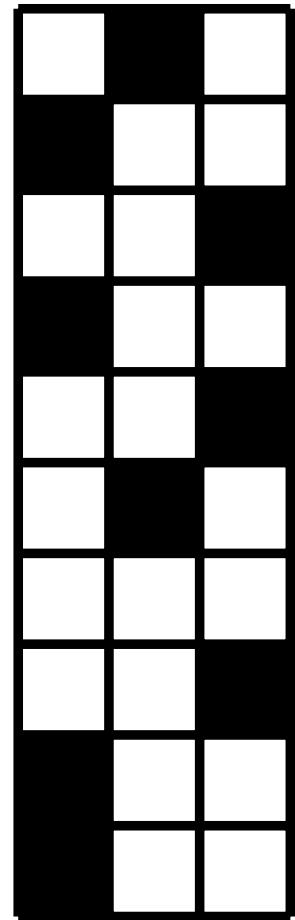
K. Vervier



A. d'Aspremont



$X =$

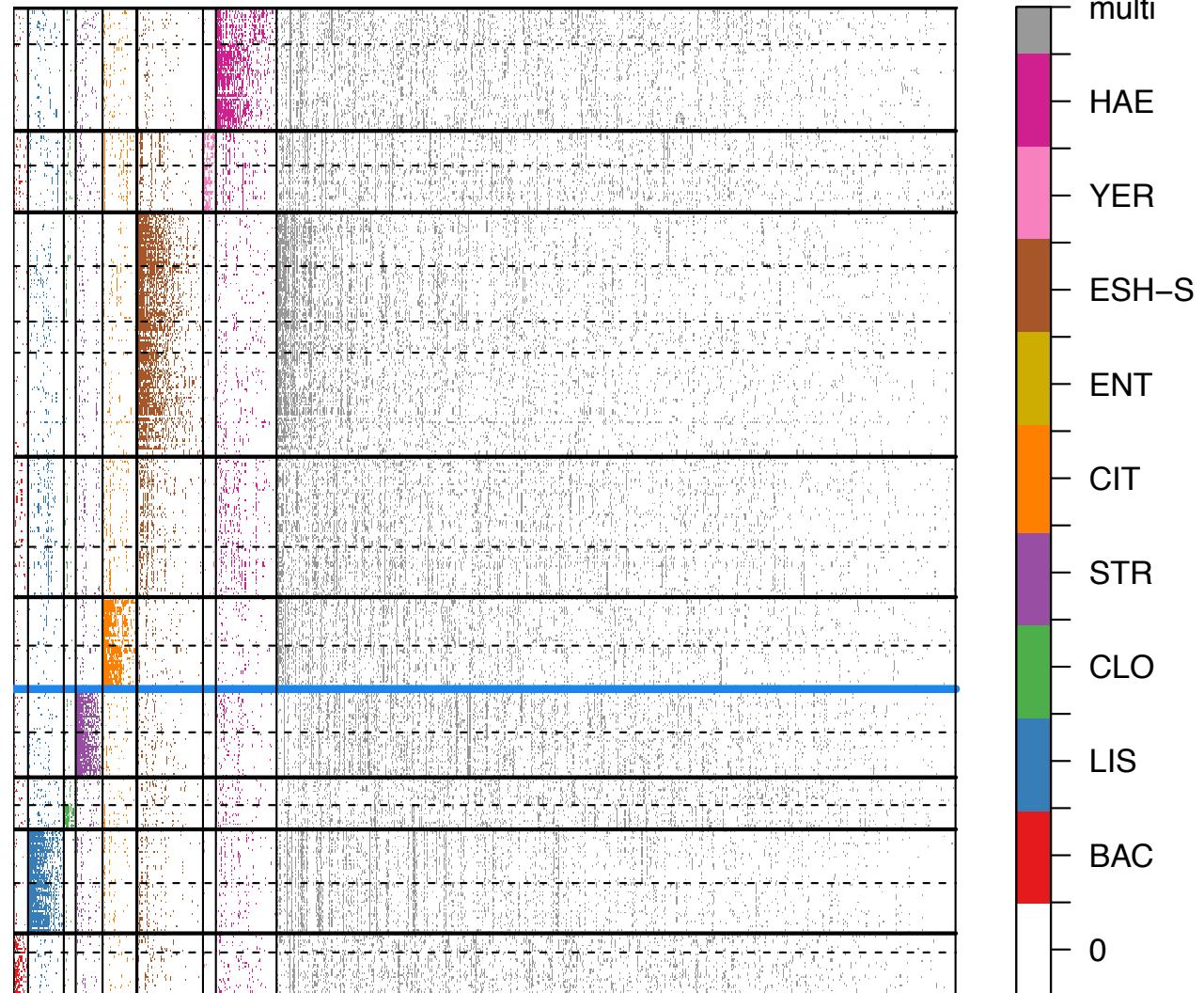


$$\Omega_K(X) = \sum_{i=1}^p K_{ii} \|x_i\|^2 + \sum_{i \neq j} K_{ij} |x_i^\top x_j|$$

# Application: Microbial identification from MALDI-TOF MS spectra



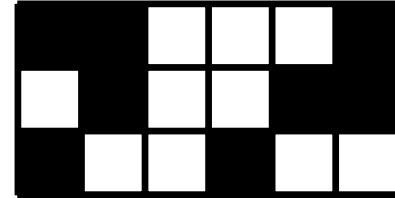
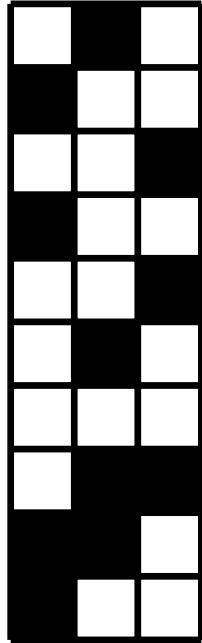
Spectra



# Learning **low-rank** matrices with **sparse** factors ?

$$X$$

=

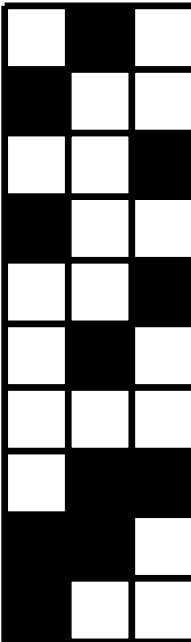


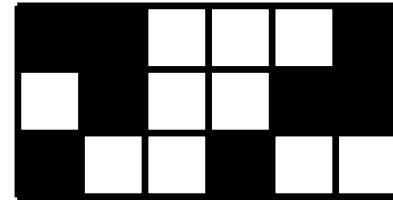
$$X = \sum_{i=1}^r u_i v_i^\top$$

- Bilinear regression with sparse latent factors
- Sparse PCA
- Sparse CCA
- Hidden clique problem
- Community detection in networks

# An atomic norm (NIPS 2014)

$$X$$

$$=$$
A 10x10 binary matrix X, shown as a sum of rank-1 matrices. It consists of several white rectangular blocks of varying sizes and positions on a black background. The blocks are arranged such that they overlap and cover the entire matrix.

A 10x10 binary matrix X, shown as a sum of rank-1 matrices. It consists of several white rectangular blocks of varying sizes and positions on a black background. The blocks are arranged such that they overlap and cover the entire matrix.

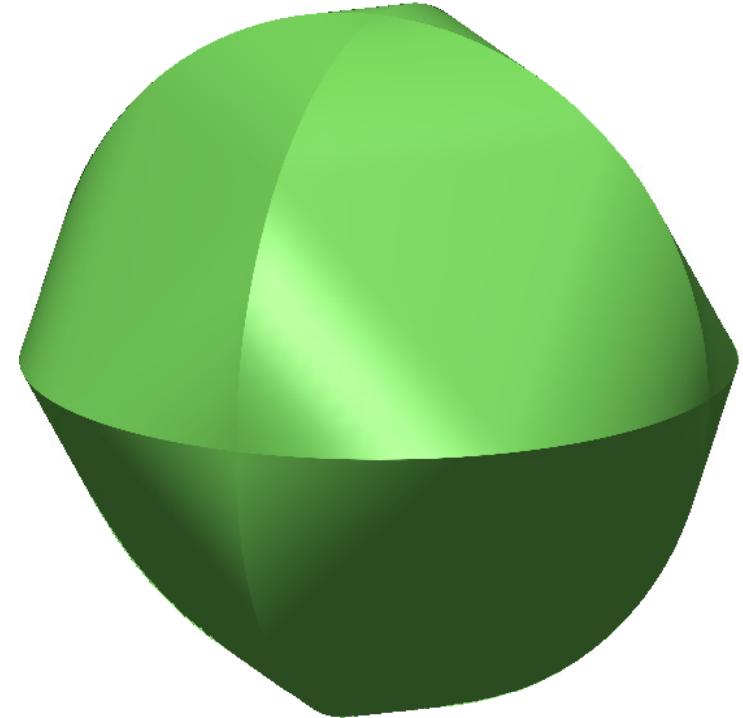


E. Richard



G. Obozinski

$$X = \sum_{i=1}^r u_i v_i^\top$$



# An atomic norm (NIPS 2014)

$$X = \begin{array}{|c|} \hline X \\ \hline \end{array} = \begin{array}{|c|} \hline \text{checkered} \\ \hline \end{array} \begin{array}{|c|} \hline \text{checkered} \\ \hline \end{array}$$

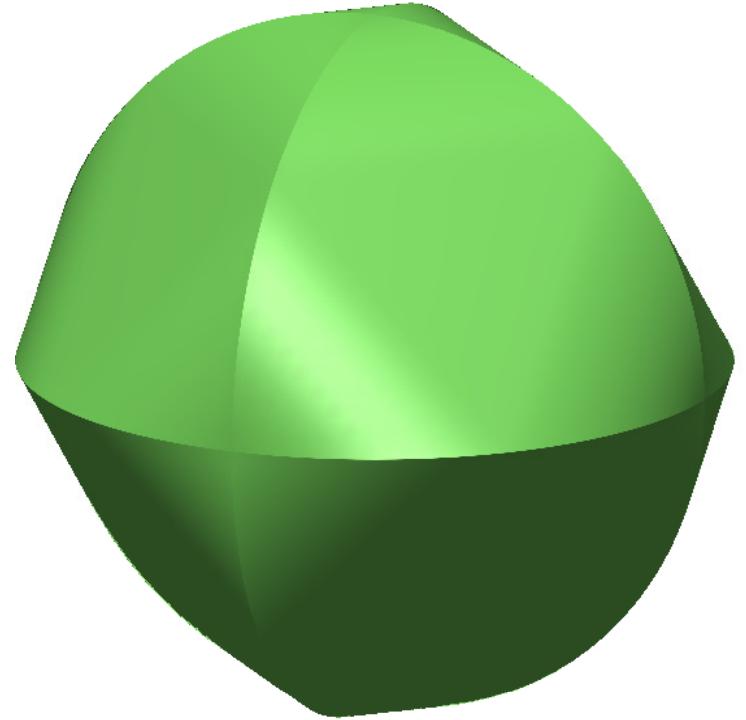
$$X = \sum_{i=1}^r u_i v_i^\top$$



E. Richard



G. Obozinski



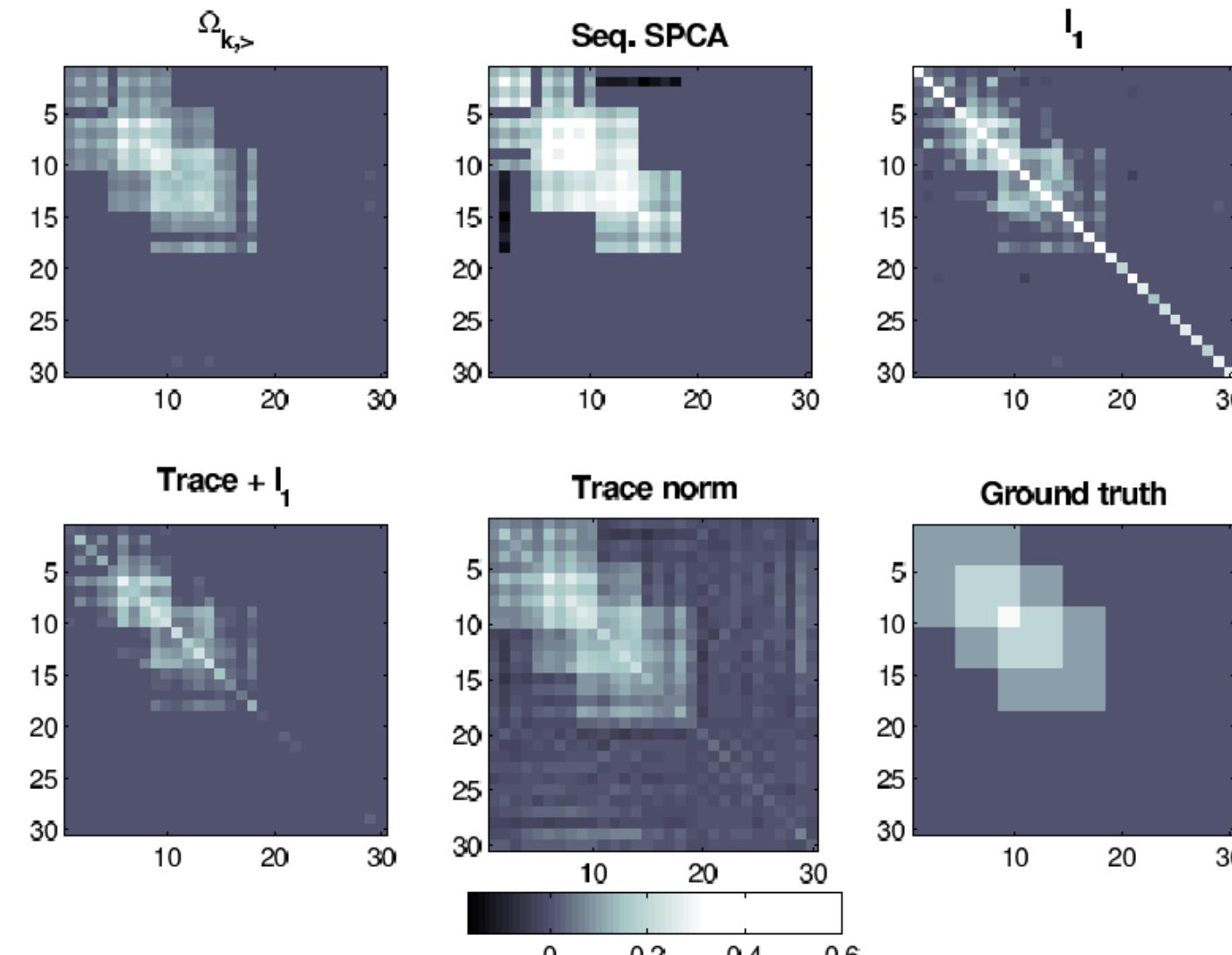
## Theorem

Learning with this norm is  
« statistically optimal » to infer  
sparse low-rank matrices

### **But**

Convex but NP-hard

# Preliminary results on sparse PCA



Sample covariance	Trace	$\ell_1$	Trace + $\ell_1$	Sequential	$\Omega_{k,\succeq}$
$4.20 \pm 0.02$	$0.98 \pm 0.01$	$2.07 \pm 0.01$	$0.96 \pm 0.01$	$0.93 \pm 0.08$	<b><math>0.59 \pm 0.03</math></b>

# Conclusion

## Make your Atomic norm !



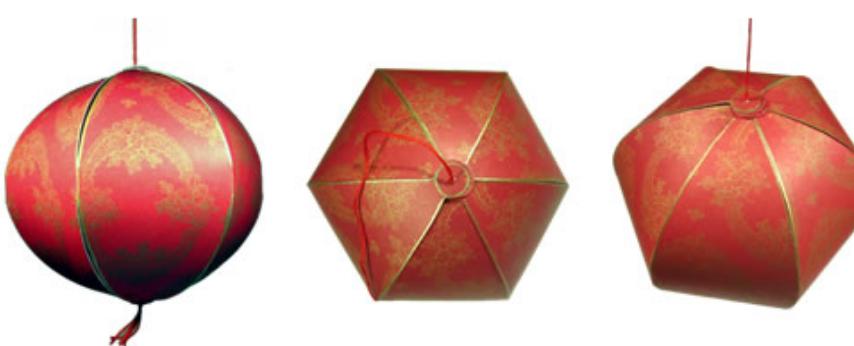
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 J'aime 1,7k 

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