# *Lecture 1: Introduction* Isabelle Guyon guyoni@inf.ethz.ch

# **Class Organization**

http://clopinet.com/isabelle/Projects/ETH/





## Textbook

Feature Extraction: Foundations and Applications (I. Guyon et al Eds.) to be published in Springer.

http://clopinet.com/restricted/FSBook.pdf login: fextract password:ws0506



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## QSAR: Drug Screening



#### Binding to Thrombin (DuPont Pharmaceuticals)

- 2543 compounds tested for their ability to bind to a target site on thrombin, a key receptor in blood clotting; 192 "active" (bind well); the rest "inactive". Training set (1909 compounds) more depleted in active compounds.

- 139,351 binary features, which describe three-dimensional properties of the molecule.



#### Weston et al, Bioinformatics, 2002















































#### The Datasets

- Arcene: cancer vs. normal with massspectrometry analysis of blood serum.
- **Dexter**: filter texts about corporate acquisition from Reuters collection.
- **Dorothea**: predict which compounds bind to Thrombin from KDD cup 2001.
- **Gisette**: OCR digit "4" vs. digit "9" from NIST.
- Madelon: artificial data.

http://clopinet.com/isabelle/Projects/NIPS2003/Slides/NIPS2003-Datasets.pdf



Dataset	Size	Туре	Features	Training Examples	Validation Examples	Test Example
Arcene	8.7 MB	Dense	10000	100	100	700
Gisette	22.5 MB	Dense	5000	6000	1000	6500
Dexter	0.9 MB	Sparse integer	20000	300	300	2000
Dorothea	4.7 MB	Sparse binary	100000	800	350	800
Madelon	2.9 MB	Dense	500	2000	600	1800















	Best frac. feat	Actual frac	
ARCENE	5%	30%	
DEXTER	1.5%	50%	
DOROTHEA	0.3%	50%	
GISETTE	18%	50%	
MADELON	1.6%	96%	







#### Hyperparameters and Chains

A model often has hyperparameters:

```
> default(kridge)
```

```
> hyper = { 'degree=3', 'shrinkage=0.1' };
```

```
> model = kridge(hyper);
```

Models can be chained:

```
> model = chain({standardize,kridge(hyper)});
```

```
> [resu, model] = train(model, D);
```

```
> tresu = test(model, testD);
```

```
balanced_errate(tresu.X, tresu.Y)
```

