#### Gaussian Processes: A method for automatic QSAR and ADME modelling

Olga Obrezanova, Joelle M.R. Gola, Matthew D. Segall

22 August 2007



Copyright © 2007 Galapagos NV



- Gaussian Processes
  - > A powerful computational modelling technique
- Application predictive ADME and QSAR modelling (ADME absorption, distribution, metabolism and excretion)
  - > New techniques for finding method parameters
  - > Examples and comparison with other methods
- Automatic modelling process







- Machine learning method based on Bayesian approach.
   Not widely used in QSAR and ADME field yet.
- Advantages:
  - Does not require a priori determination of model parameters.
  - Nonlinear relationship modelling.
  - > Built-in tool to prevent overtraining, no need for cross-validation.
  - Inherent ability to select important descriptors.
  - Provides uncertainty estimate for each prediction.
- Sufficiently robust to enable automatic model generation







•  $D = \{Y, X\} - given data.$ We want to find function *f*:

*Y=f(X)*+noise.

• Bayesian rule

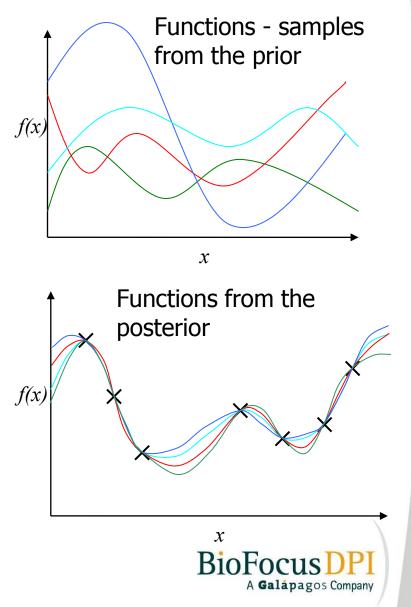
$$P(f \mid D) \propto P(D \mid f) P(f)$$

posterior

prior

4

- Prediction is a mean of posterior distribution.
- Gaussian Process defines a distribution over functions.



# Gaussian Processes: Practical steps

Structure of functions determined by covariance (kernel) function:

 $\operatorname{cov}(f(\boldsymbol{x}), f(\boldsymbol{x}')) = C(\boldsymbol{x}, \boldsymbol{x}')$ 

 Distribution of functions (property values) is multivariate Gaussian with zero mean and covariance matrix

 $\boldsymbol{K} = \boldsymbol{C} + \boldsymbol{\theta}_3 \boldsymbol{I}$ 

> Hyperparameter  $\theta_3$  is a variance of noise present in the observed values.



### Gaussian Processes: Hyperparameters

ARD covariance function

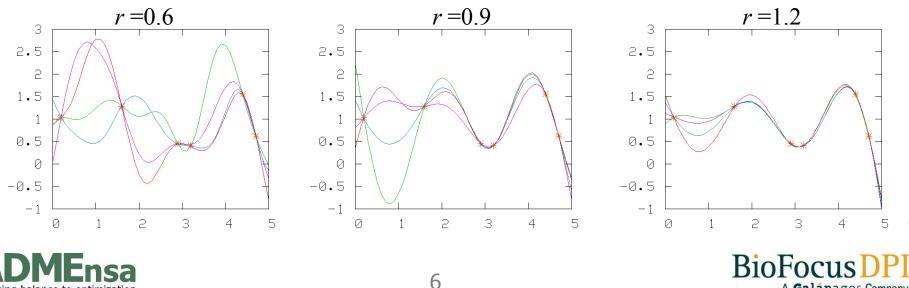
$$C(\mathbf{x}, \mathbf{x}') = \theta_1 \exp\left[-\frac{1}{2} \sum_{i} (x_i - x'_i)^2 / r_i^2\right] + \theta_2$$

automatic relevance determination

Control fit and smoothness via hyperparameters

 $\succ$   $\theta_3$  is a variance of noise in the observed values. Too small value leads to overfitting.

 $\succ$  { $r_i$ } are length scale parameters.



A Galapagos Company

#### Gaussian Processes: How to find hyperparameters?

- Use Bayesian inference in hyperparameters space.
  - Posterior for hyperparameters

 $P(\boldsymbol{\theta} \mid D) \propto P(\boldsymbol{Y} \mid \boldsymbol{X}, \boldsymbol{\theta}) P(\boldsymbol{\theta})$ 

- > Full integration over all hyperparameters
- > Or choose most probable value  $\theta$  that optimizes the marginal log-likelihood

$$\log P(\boldsymbol{Y} | \boldsymbol{X}, \boldsymbol{\theta}) = -\frac{1}{2} \log(\det \boldsymbol{K}) - \frac{1}{2} \boldsymbol{Y}^{t} \boldsymbol{K}^{-1} \boldsymbol{Y} - \frac{N}{2} \log 2\pi$$

Complexity penalty fit

• No need for cross-validation or validation set! Also prevents overtraining.



# Gaussian Processes: Make predictions

- Want to make prediction y\* at unseen (test) point x\*.
- Predictive distribution is Gaussian with mean and variance:

$$\langle y^* \rangle = k^t K^{-1} Y$$
  
prediction
 $\sigma^{*2} = C(x^*, x^*) - k^t K^{-1} k$ 
Confidence in prediction

> k describes covariance of training and new points,  $k_n = C(\mathbf{x}^*, \mathbf{x}^{(n)})$ .

For test set points need to add noise variance to GP variance.





#### ADME and QSAR modelling:

#### Techniques for determining hyperparameters





# Finding hyperparameters

• Optimize the marginal log-likelihood

$$\log P(\boldsymbol{Y} | \boldsymbol{X}, \boldsymbol{\theta}) = -\frac{1}{2} \log(\det \boldsymbol{K}) - \frac{1}{2} \boldsymbol{Y}^{t} \boldsymbol{K}^{-1} \boldsymbol{Y} - \frac{N}{2} \log 2\pi$$

- Conjugate gradient methods
  - Computationally demanding. Inversion of matrix NxN at each step, N is a number of compounds in the training set. Comp. cost O(N<sup>3</sup>).
  - The function has multiple maxima. Search can get trapped in a local maximum.
- Need to find simplified approaches.



# Techniques for finding hyperparameters

"Fixed" values.

$$r_i = 4\sqrt{M}\,\sigma(\mathbf{x}_i), \quad \theta_2 = \sqrt{N}\sigma_{\mathbf{y}},$$

*M* is a number of descriptors. Search for  $\theta_1$ ,  $\theta_3$ .

- Forward variable selection provides feature selection.
- Optimization by conjugate gradient methods (only length scales).
  - Length scales show which descriptors are most relevant.
- Nested sampling.
  - Search in the full hyperparameter space.
  - Search does not get trapped in local maxima.





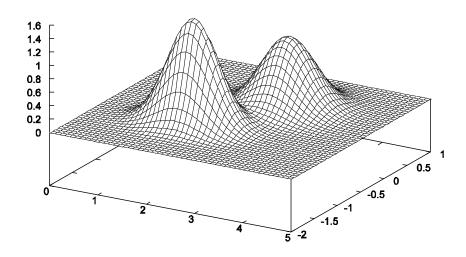
- Method by John Skilling to estimate evidence and generate posterior samples. (http://www.inference.phy.cam.ac.uk/bayesys/Valencia.pdf)
- We want to find most probable hyperparameter values, i.e that give the maximum of the likelihood.
- Key idea:
  - > Sample uniformly from wide prior space of all hyperparameters.
  - Iteratively replace samples with low likelihood by new samples with high likelihood.
  - At the end of the process we have points corresponding to high likelihood values.

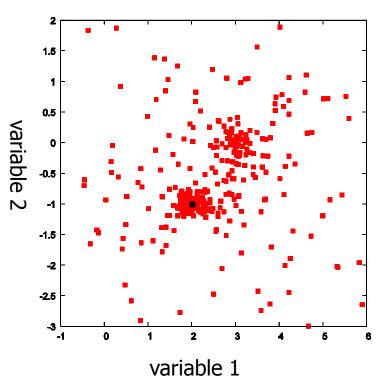






- 2 variables.
- Find maximum of likelihood:





**BioFocus** 

A Galápagos Company





# ADME and QSAR modelling:

#### Examples and comparison







- F. Burden, JCICS 2001, 41, 830-835.
- 245 ligands for the benzodiazepine receptor (in vitro binding affinities as pIC<sub>50</sub>).
- 59 descriptors:
  - Randic and Kier-Hall indices (E-Dragon: www.vcclab.org),
  - > counts of atoms, rings and functional groups.
- Test set 15%.
  - > Burden's set split is not known to us.
  - Used set split based on uniform sample of Y values.



# Benzodiazepine set: Results

Method	Desc	r² <sub>corr</sub> (trn)	r <sup>2</sup> <sub>corr</sub> (test)	GP-Nest			
PLS	38(3)	0.32	0.53	on test set:			
GP-Basic	38	0.52	0.53	RMSE=0.46 R <sup>2</sup> =0.63			
GP-FVS	15	0.52	0.54	$r^{2}_{corr} = 0.65$			
GP-Opt	9	0.62	0.51	← VCCLAB (www.vcclab.org)			
GP-Nest	38	0.68	0.65				
ASNN+kNN	36	0.73	0.64				
BRANN	39	0.75	0.71	)			
GPmodel	39	0.76	0.66	Burden results			
GPlinear	39	0.78	0.71				

Training set - 208 compounds, test set - 37 compounds.





- Inhibition of human ether-a-go-go related gene by medication.
- 137 compounds with patch-clamp pIC<sub>50</sub> values.
- 166 descriptors:
  - > 2D SMARTS based + logP, PSA, charge, etc.
- Test set 20%.
  - > Set split based on clustering analysis (Tanimoto level = 0.7).





				GP-Opt
Method	Desc	R <sup>2</sup> (trn)	R <sup>2</sup> (test)	on test set:
PLS	166(2)	0.63	0.74	RMSE=0.6 R <sup>2</sup> =0.81
GP-Basic	166	0.79	0.76	$r_{corr}^{2}=0.81$
GP-FVS	17	0.76	0.80	
GP-Opt	26	0.82	0.81	
GP-Nest	166	0.81	0.77	
ASNN+kNN	166	0.94	0.77	VCCLAB (www.vcclab.org)

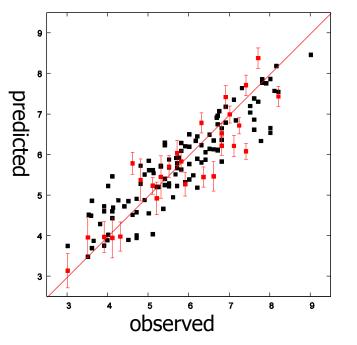
Training set - 110 compounds, test set - 27 compounds.





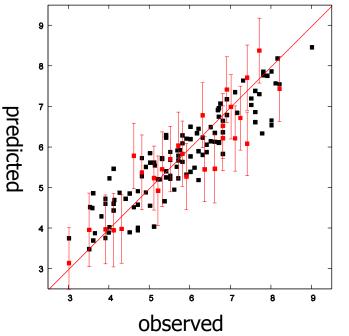


Predicted  $pIC_{50}$  values versus observed with error bars. Training set in black. Test set in red.



- Original GP error bars, do not include experimental noise variance
- Applicability of the model





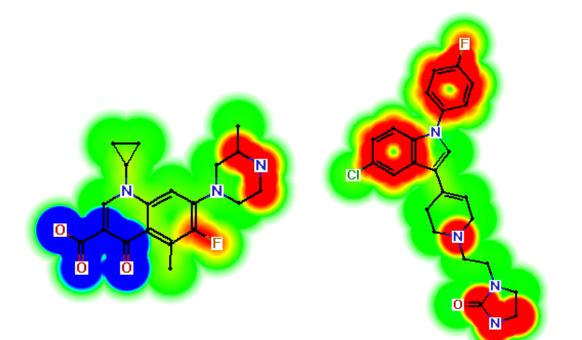
- Error bars include noise variance
- Confidence in prediction



# hERG inhibition model: Descriptors

#### • Important features:

- Lipophilicity
- Negative charge
- Positively charged nitrogen at pH 7.4
- > Aromaticity index
- HB donor acceptor pairs separated by 6 bonds
- > Ketone
- > Amide



hERG pIC<sub>50</sub> obs. = 4.3

predicted =  $3.99 \pm 0.84$ 

hERG pIC<sub>50</sub> obs. = 8 predicted =  $7.88 \pm 0.8$ 

BioFocus

A Galapagos Company



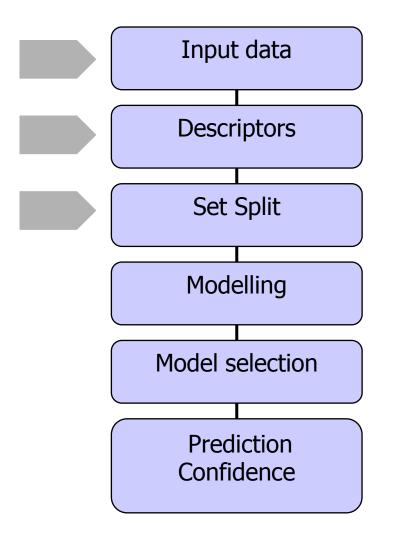


## Automatic modelling process





## Automatic Model Generation Process



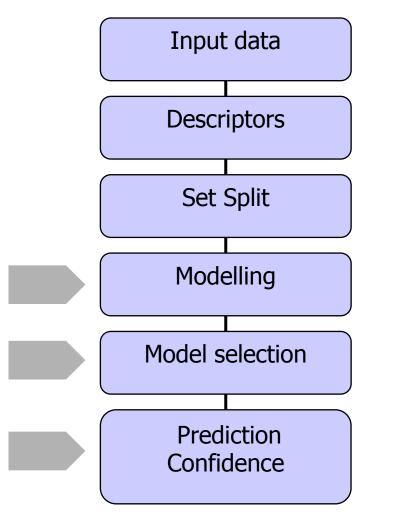
• User provides structures and property values.

• 2D SMARTS based descriptors and logP, flexibility, charge, PSA, etc. A user can import own descriptors.

- Split into 3 sets:
  - training (building a model),
  - validation (model selection),
  - test (independent).
- Clustering by structural similarity or Y based. Or user's own split.



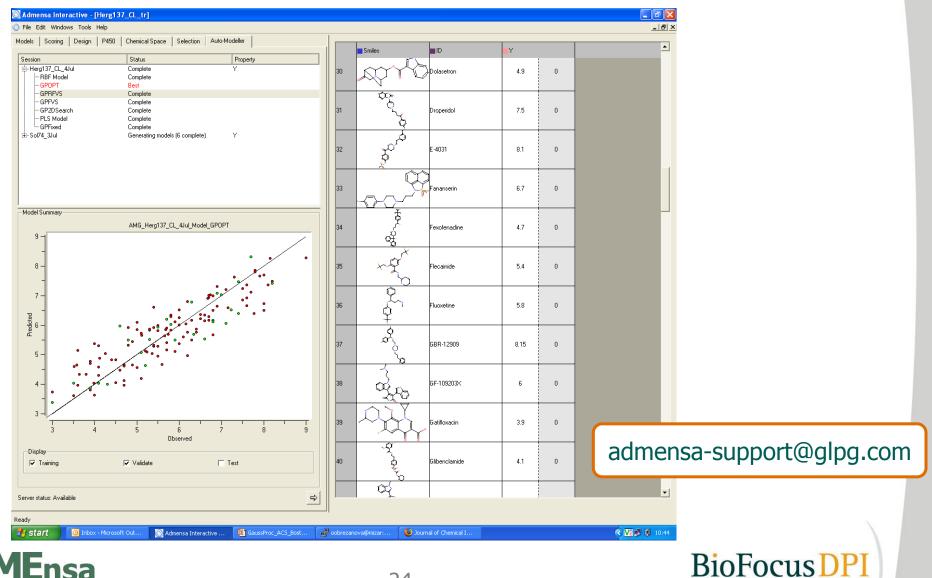
# Automatic Model Generation Process



- Modelling continuous data:
  - PLS
  - Gaussian Processes (5 techniques)
  - Radial Basis Functions + GA
  - categorical data:
    - Decision trees (C4.5)
- Best model selection is based on performance of validation set.
- Estimation of uncertainty for each prediction.



#### ADMEnsa Interactive. Auto-Modeler.



A Galápagos Company

Bringing balance to optimization



- Gaussian Processes is a powerful nonlinear modelling technique:
  - > No *a priori* determination of model parameters.
  - > Built-in tool to prevent overtraining, no need for cross-validation.
  - > Works well for a big pool of descriptors.
  - Identifies relevant descriptors.
  - Uncertainty with each prediction.
- Application to building QSAR and ADME models. New techniques for determining model parameters.
- Automatic model generation process accessible through an intuitive desktop environment.







- The Gaussian Processes Website. www.gaussianprocess.org
- D. MacKay. Information Theory, Inference, and Learning Algorithms. Cambridge University Press, 2003.
- C. Rasmussen, C. Williams. Gaussian Processes for Machine Learning. The MIT Press, 2006.

• Obrezanova et al. *J. Chem. Inf. Model.* E-publication ahead of print, 28 June, 2007.







- Gábor Csányi (Cavendish Laboratory, University of Cambridge)
- Joelle Gola
- Matthew Segall
- Ed Champness
- Chris Leeding
- Andre Kramer





# Spare slides







Method	Desc	R <sup>2</sup> (trn)	R <sup>2</sup> (test)	Time (min)	GP-Opt
PLS	166(2)	0.63	0.74	0.2	on test set: RMSE=0.6
RBF-GA	21	1	0.77		$R^2 = 0.81$
GP-Basic	166	0.79	0.76	2.3	R <sup>2</sup> corr=0.8
GP-FVS	17	0.76	0.80	19	
GP-Opt	26	0.82	0.81	13	
GP-Nest	166	0.81	0.77	170	
ASNN	166	0.94	0.69	100	<pre>VCCLAB</pre>
ASNN+kNN	166	0.94	0.77	188	

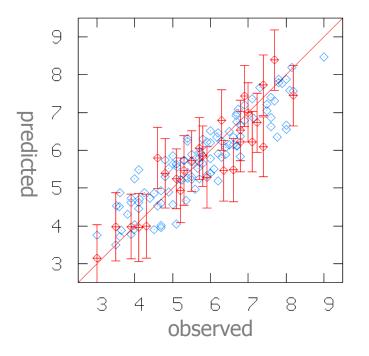
Training set - 110 compounds, test set - 27 compounds.



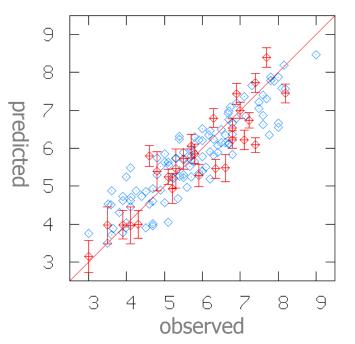




Predicted pIC50 values versus observed with errorbars. Training set in blue. Test set in red.



- Error bars include noise variance
- Confidence in prediction



• Original GP error bars, do not include experimental noise variance

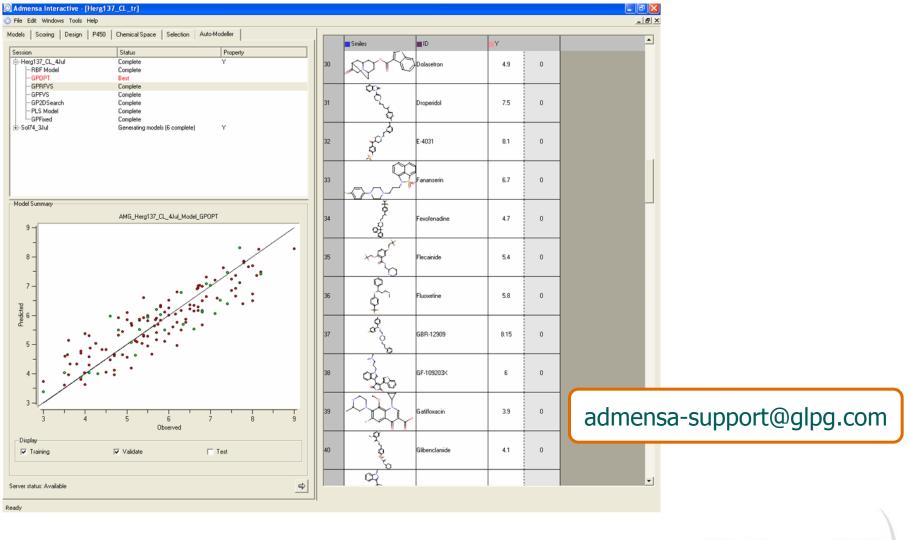
BioFocus

A **Galapa**gos Company

• Applicability of the model



# Admensa Interactive. Auto-Modeller.





**BioFocus DPI** 

A Galápagos Company

## Gaussian Processes: Practical steps

Structure of functions determined by covariance (kernel) function:

 $\operatorname{cov}(f(\boldsymbol{x}), f(\boldsymbol{x}')) = C(\boldsymbol{x}, \boldsymbol{x}')$ 

 Distribution of functions is multivariate Gaussian with zero mean and covariance matrix

$$\boldsymbol{K} = \boldsymbol{C} + \boldsymbol{\theta}_3 \boldsymbol{I}$$

• ARD covariance function (automatic relevance determination)

$$C(\mathbf{x}, \mathbf{x'}) = \theta_1 \exp\left[-\frac{1}{2} \sum_{i} (x_i - x'_i)^2 / r_i^2\right] + \theta_2$$

- Control fit and smoothness via hyperparameters.
  - $\succ \theta_3$  is a variance of noise present in the observed values.
  - >  $\{r_i\}$  are length scale parameters.



# Gaussian Processes: Hyperparameters

- Noise variance  $\theta_3$ : too small value leads to overtraining.
- Length scale parameters  $\{r_i\}$ : large values mean that corresponding descriptor does not influence the property values very much. Automatic relevance determination.

