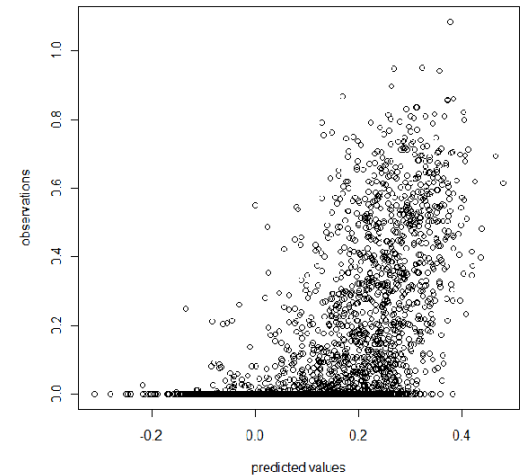
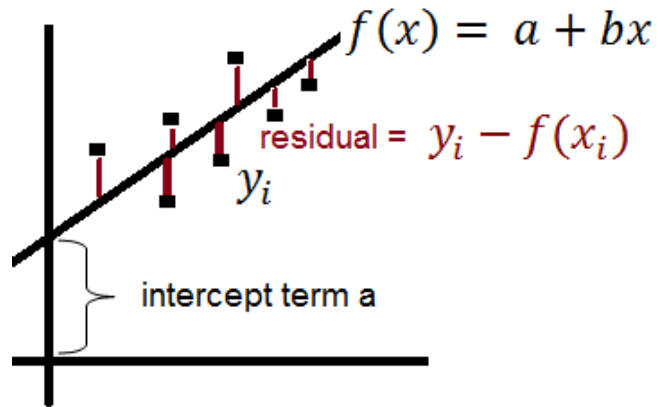
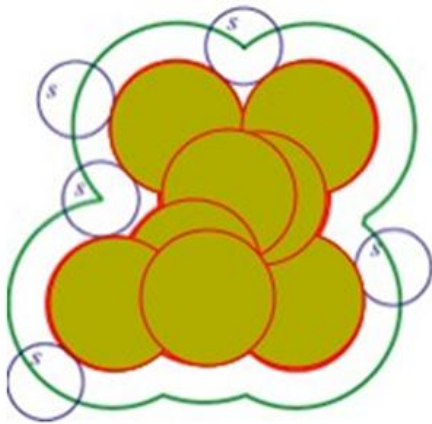


# Prediction of the burial status of transmembrane residues of helical membrane proteins (with Linear Regression)

Jing Cui

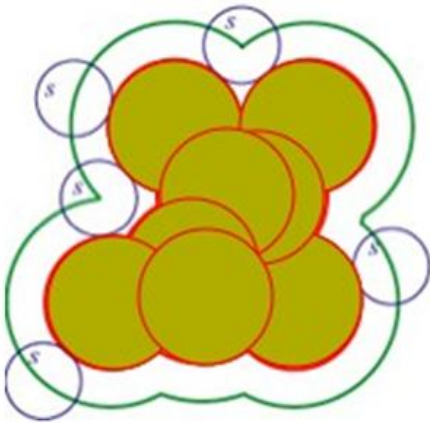
# Outline

- burial status
- linear regression
- practical



# Outline

## ➤ burial status



# HMPs

- Helical Membrane Proteins (HMPs)
  - play a crucial role in diverse cellular processes
- **Why we need to predict their structures ?**
  - hard by experimental techniques
    - <1% of proteins with known structure are HMPs
- **How to predict their structures ?**
  - solvent accessibility (burial status)

# Burial Status

➤ **Prediction Burial Status** : transmembrane(TM) residues of HMPs buried in the protein structure vs. exposed to the membrane

➤ rSASA value  buried vs. exposed

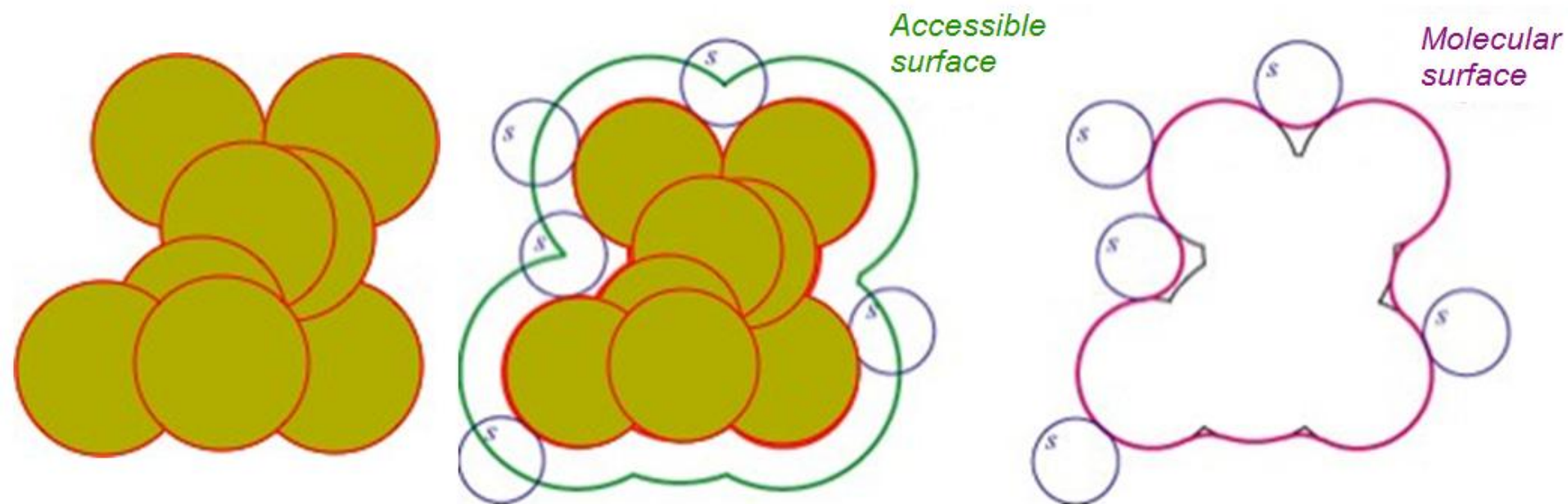
➤ rSASA value = 
$$\frac{SASA}{reference\ value}$$

rSASA	Burial Status
> 0.00	exposed residue
0.00	buried residue

# Solvent Accessible Surface Area (SASA)

**VDW Representation**

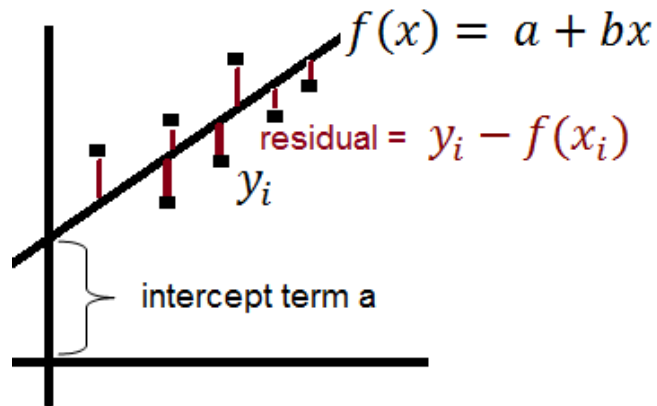
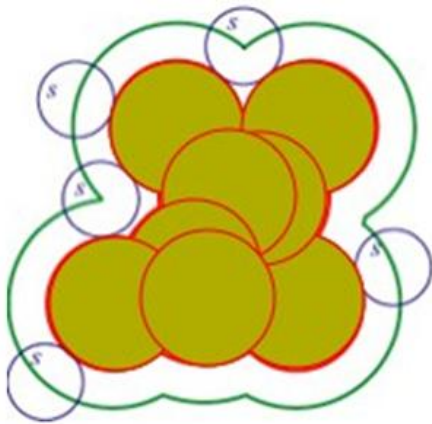
**Accessible Surface Area**



**Solvent Accessible Surface** is the surface defined by rolling a sphere the size of solvent over the molecule.


# Outline

- burial status
- linear regression



# Multiple Linear Regression Models

- Simple
- Interpretable description of how the inputs affect the output

*input vector* :  $X^T = (X_1, X_2, \dots, X_p)$    $Y$

*linear regression model* :  $f(x) = \beta_0 + \sum_{j=1}^p X_j \beta_j$

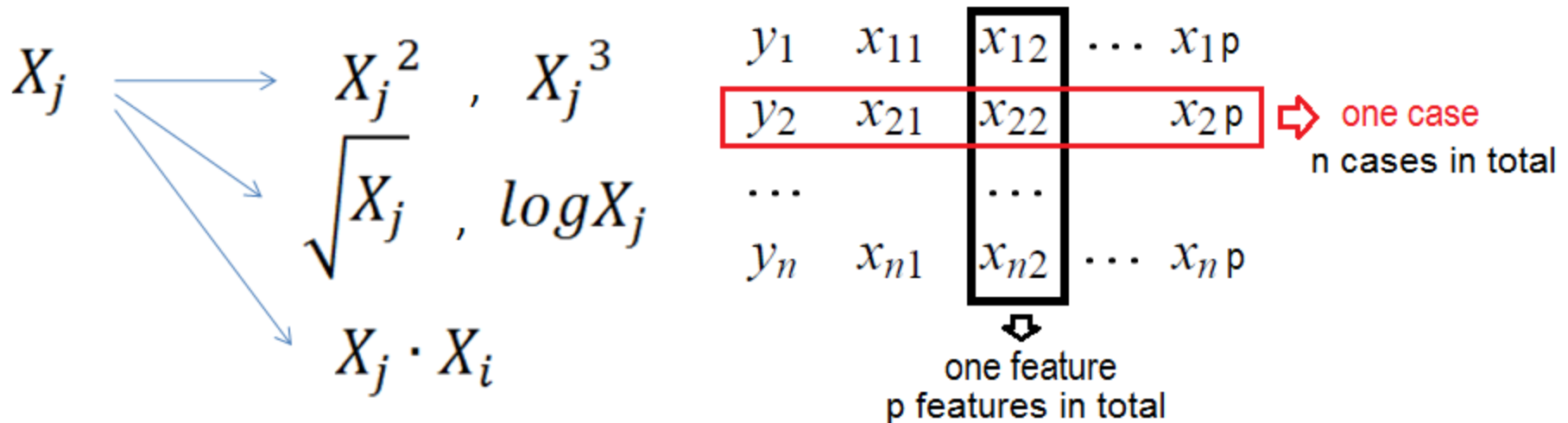
$\beta_0, \beta_1, \dots, \beta_p$  : parameters or coefficients

$X_1, X_2, \dots, X_p$  : variables or features

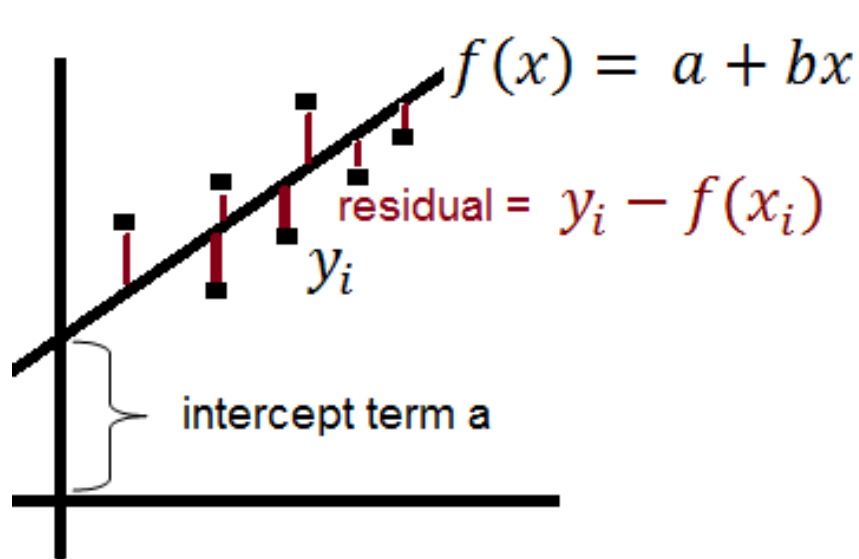


# Multiple Linear Regression Models

The model is linear in the **parameters**.



# Multiple Linear Regression Models



$$(x_1, y_1)$$

.

.

$$(x_N, y_N)$$



estimation method : *least squares*

$$\beta = (\beta_0, \beta_1, \dots, \beta_p)^T$$

minimize



$RSS(\beta)$ : residual sum of squares

$$= \sum_{i=1}^N (y_i - f(x_i))^2$$

# Multiple Linear Regression Models

$$f(x) = \beta_0 + \sum_{j=1}^p X_j \beta_j \quad \xrightarrow{X = \begin{pmatrix} 1 & x_{11} & x_{12} & \dots & x_{1p} \\ 1 & x_{21} & x_{22} & & x_{2p} \\ \dots & & & \dots & \\ 1 & x_{n1} & x_{n2} & \dots & x_{np} \end{pmatrix}} \quad f(x) = X\beta$$

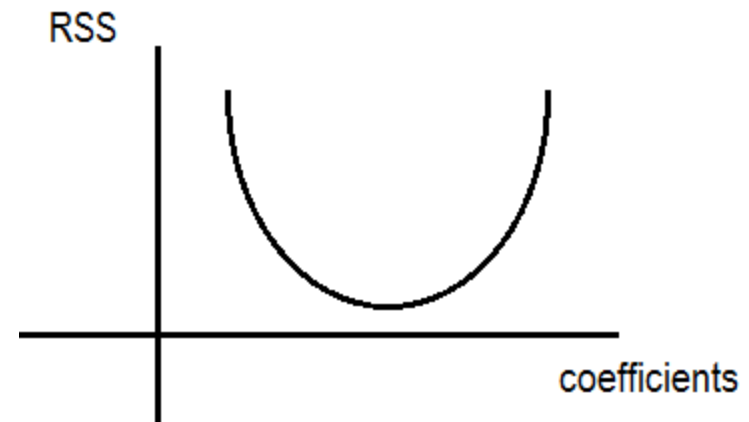
$RSS(\beta)$ : residual sum of squares

$$= \sum_{i=1}^N (y_i - f(x_i))^2 = (y - X\beta)^T (y - X\beta)$$

$$\frac{\partial RSS}{\partial \beta} = -2X^T (y - X\beta)$$

$$\frac{\partial RSS}{\partial \beta \partial \beta^T} = 2X^T X$$

$$\Rightarrow \hat{\beta} = (X^T X)^{-1} X^T y$$



# Assumptions

- The Gauss-Markov Theorem

$$Y = \beta_0 + \sum_{j=1}^p X_j \beta_j + \varepsilon$$

With  $E[\varepsilon|X = x] = 0$ , errors have expectation zero

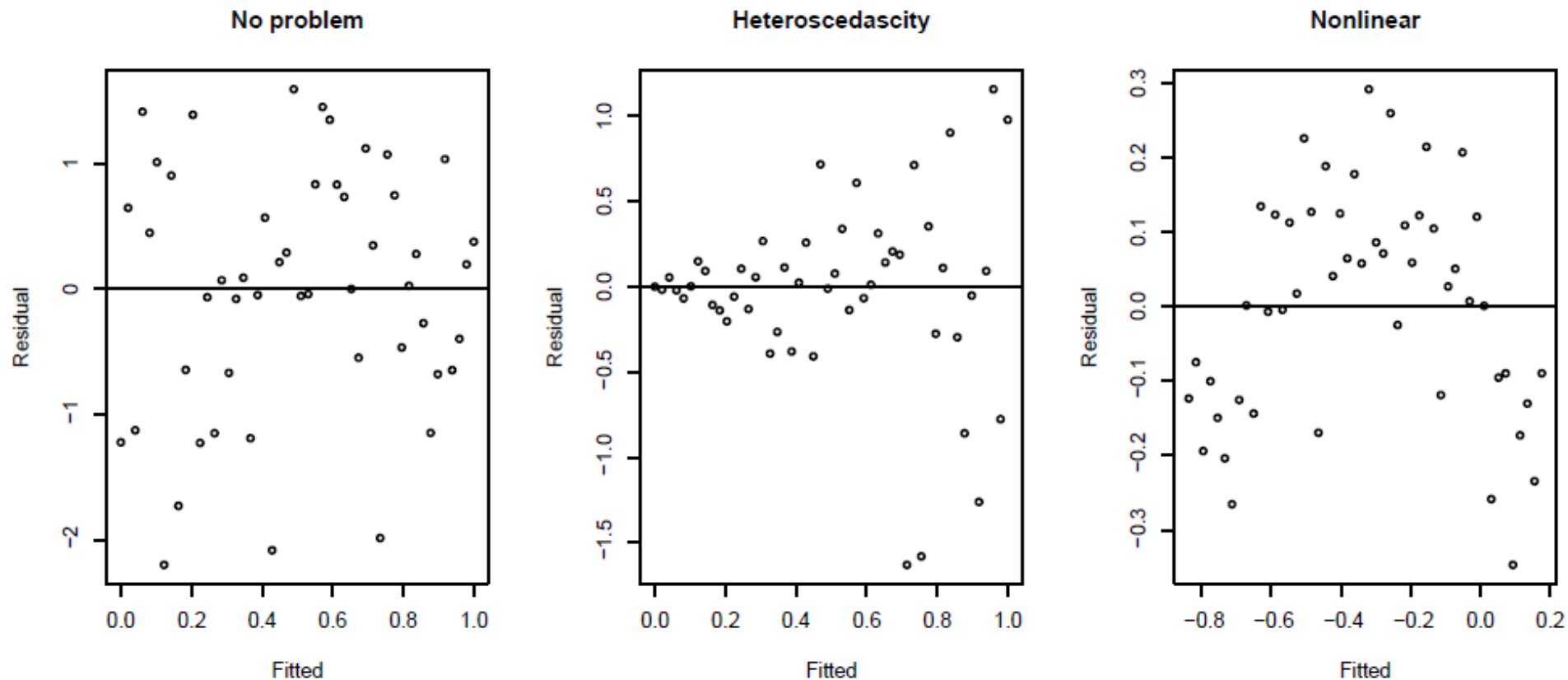
$Var[\varepsilon|X = x] = \sigma^2$ , constant variance

$E[\varepsilon_x \varepsilon_z] = 0$  the errors are uncorrelated

*Under these assumptions, the maximum likelihood is given by the method of least squares.*

# Model Assessment and Selection

- Model checking



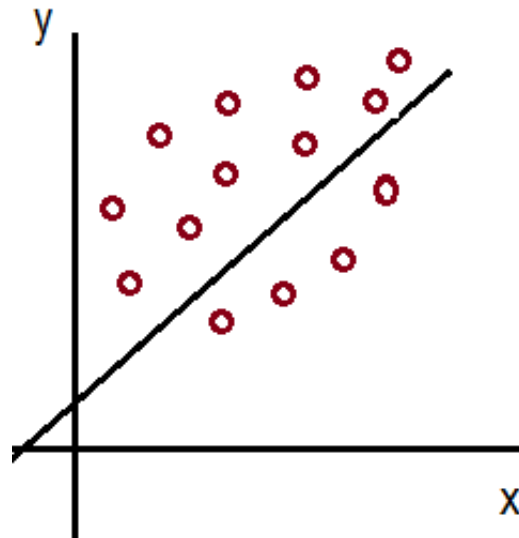
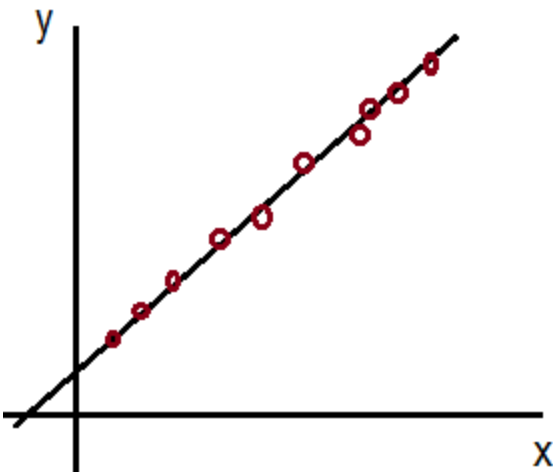
# Model Assessment and Selection

- Goodness of Fit

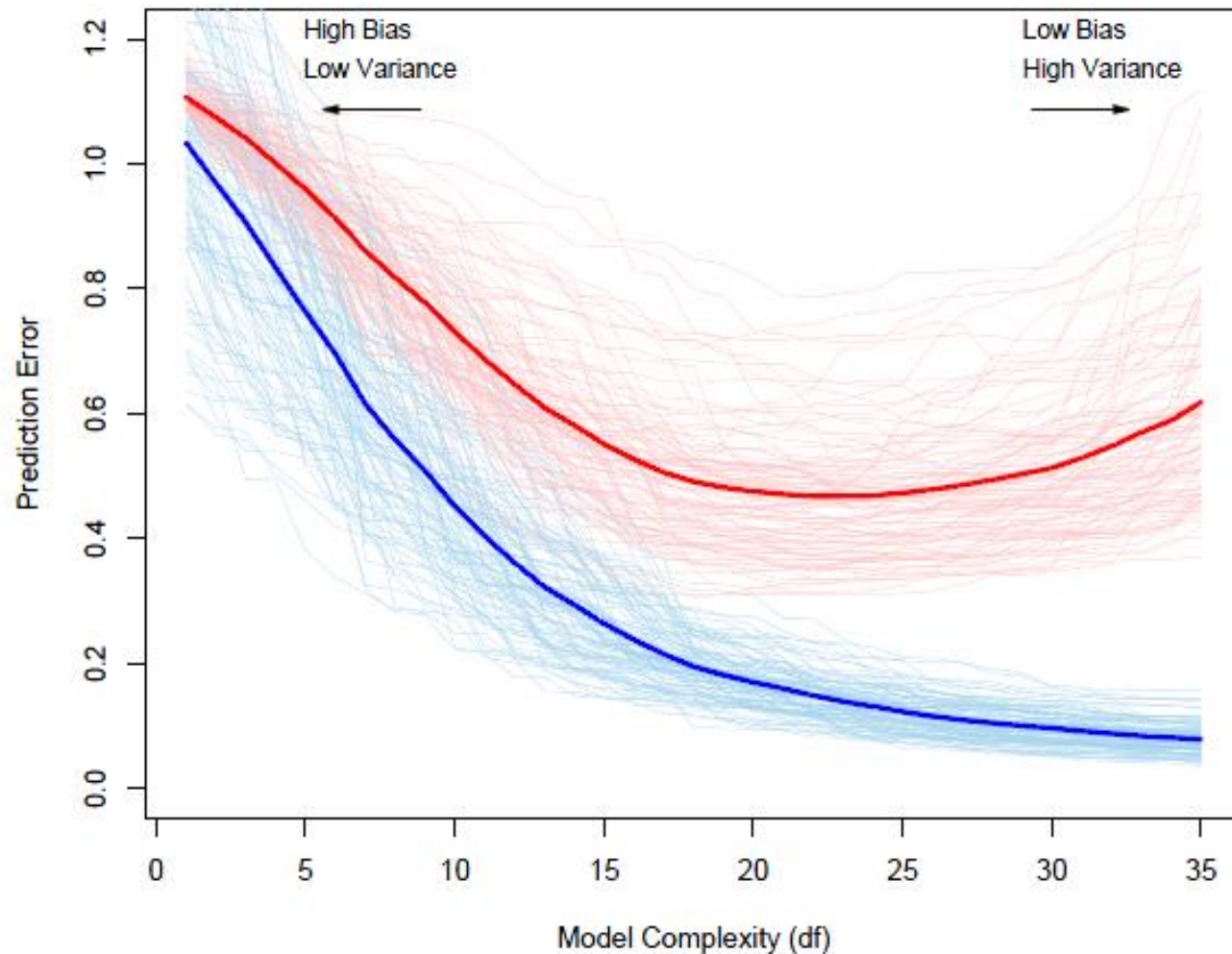
➤ Coefficient of determination  $R^2$

$$R^2 = 1 - \frac{RSS}{Total\ SS} = 1 - \frac{\sum(\hat{y}_i - y_i)^2}{\sum(y_i - \bar{y})^2}$$

perfect fit will get 1



# Test Error and Training Error



# Model Assessment and Selection

- AIC (Akaike information criterion)

$$AIC = -\frac{2}{N} * \loglik + 2 * \frac{d}{N}$$

d : the number of parameters in the model

N: sample size

log-likelihood loss function is used



# Cross Validation

1	2	3	4	5
Train	Train	Validation	Train	Train

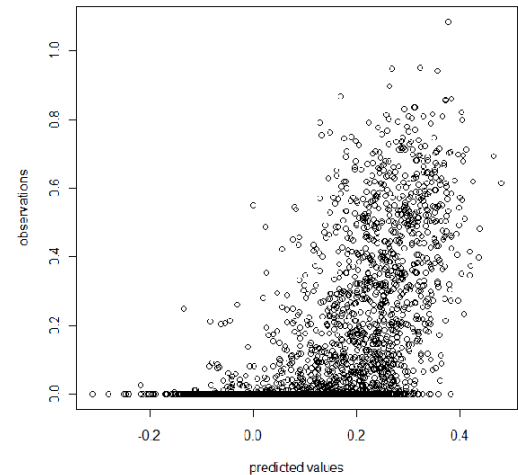
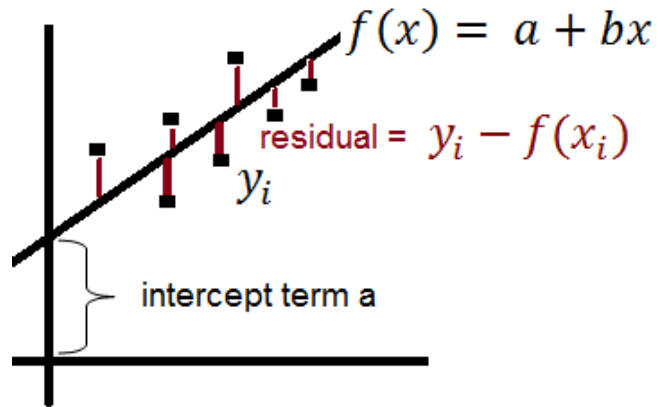
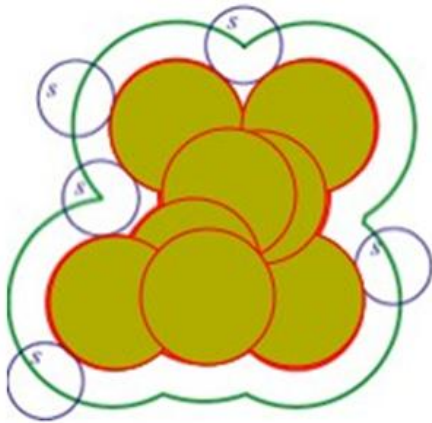
K-Fold Cross-Validation

Leave-One-Out cross-validation     $K = N$

$$CV(\hat{f}) = \frac{1}{N} \sum_{i=1}^N L(y_i, \hat{f}^{-\kappa(i)}(x_i))$$

# Outline

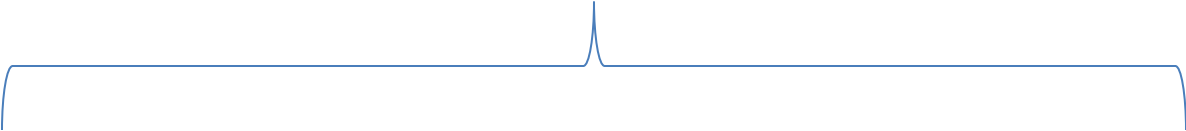
- burial status
- linear regression
- practical



# Dataset

```
pdbid chain number type rsasa freq1 freq2 freq3 freq4 freq5 freq6 freq7 freq8 freq9 freq10  
3ddl A 18 F 0.642 0.0 0.234043 0.0 0.0 0.531915 0.085106 0.148936 0.0 0.0 0.0 0.0 0.0 0.0  
3ddl A 19 T 0.0 0.0 0.0 0.0 0.0 0.0 0.06383 0.425532 0.191489 0.0 0.234043 0.0 0.06383 0.0  
3ddl A 20 V 0.168 0.0 0.021277 0.021277 0.0 0.021277 0.170213 0.042553 0.021277 0.042553 0.  
3ddl A 21 A 0.792 0.0 0.021277 0.0 0.148936 0.0 0.0 0.021277 0.787234 0.0 0.021277 0.0 0.0
```

41 features

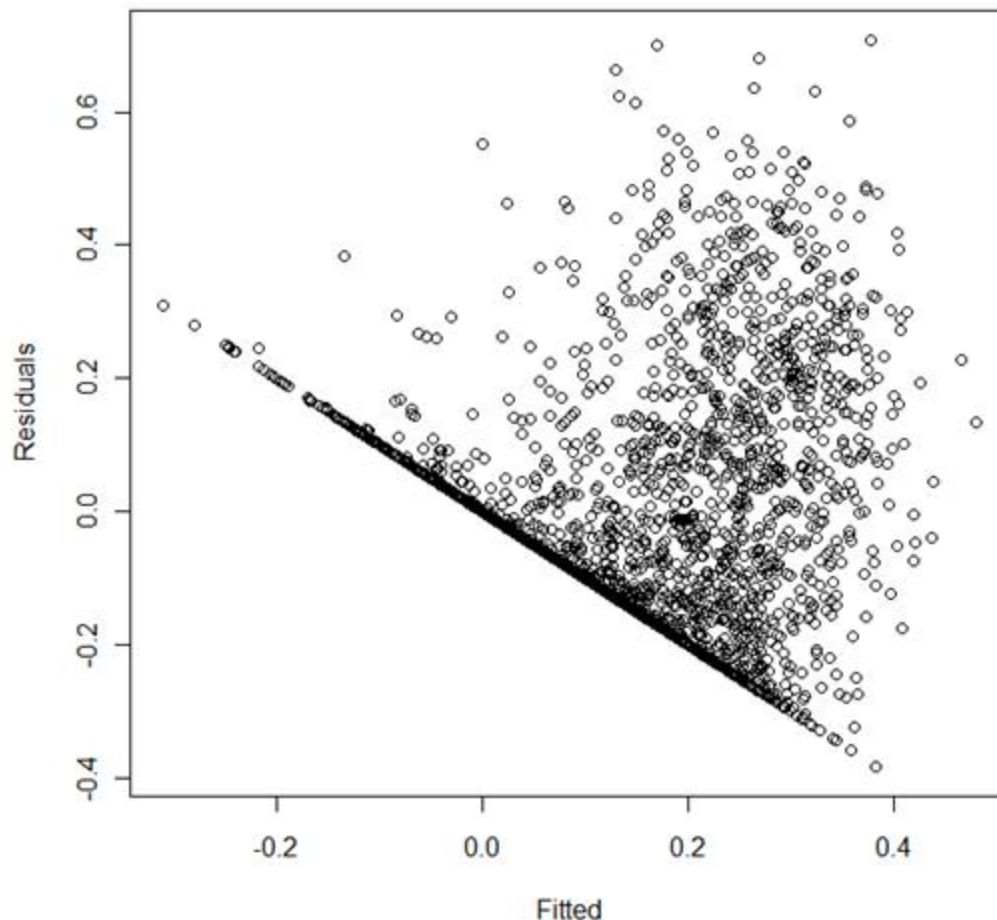


rSASA	frequencies per aa (20)	PSSM (PSI-Blast results) (20)	conservation index
2595	2595	2595	2595

2595 cases without missing values

# 1<sup>st</sup> Linear Regression Model

$$f(x) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_{41} X_{41}$$



**correlation coefficient**  
= 0.5949052

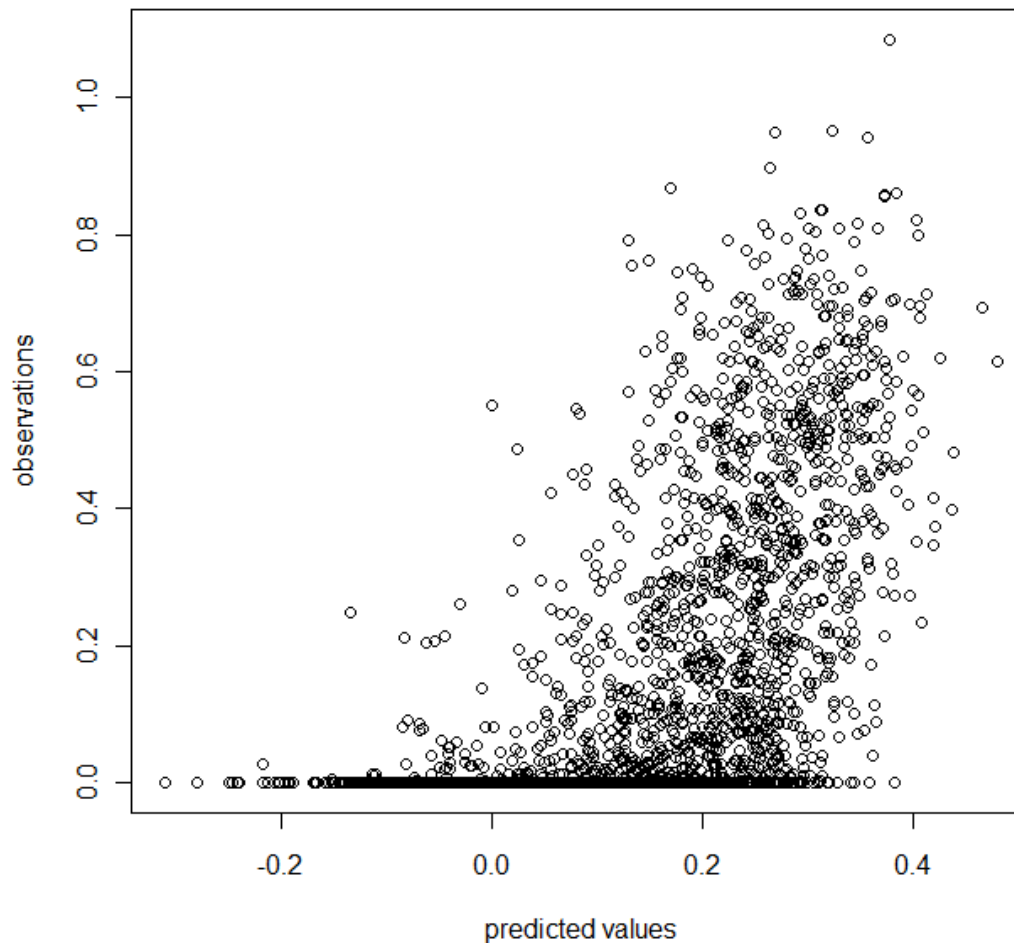
**$R^2$**  = 0.353912197

**prediction error** = 0.02994921  
(cross-validation estimate)

**AIC** = -1653.624

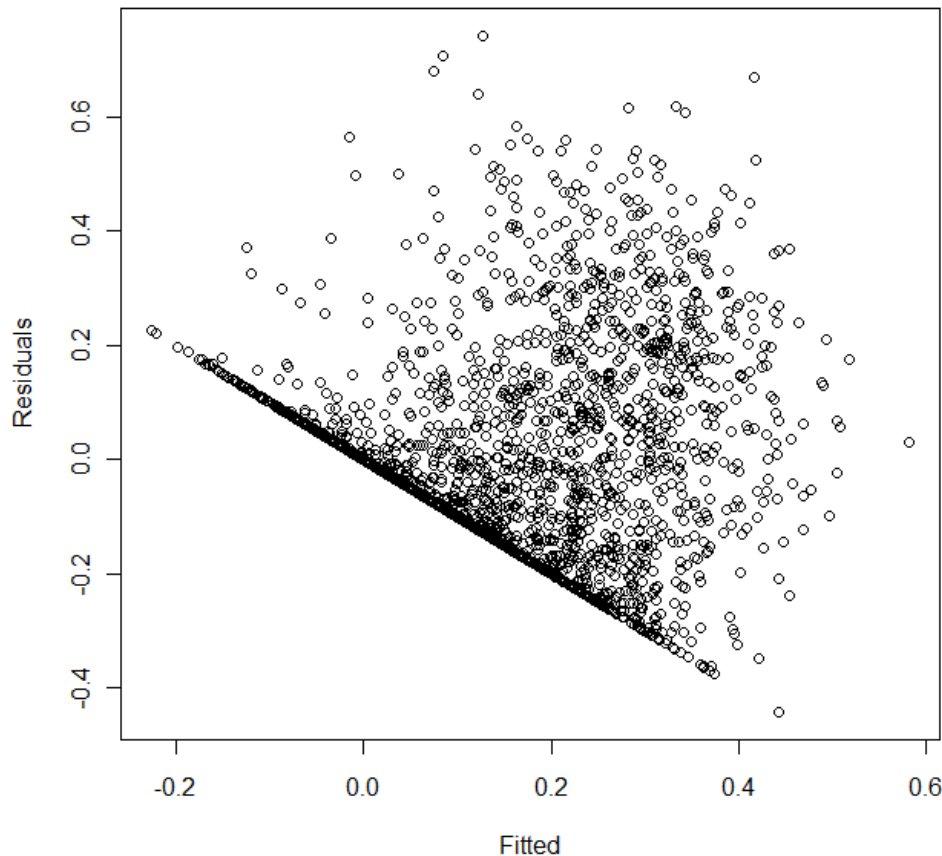
# 1<sup>st</sup> Linear Regression Model

$$f(x) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_{41} X_{41}$$



# 2<sup>nd</sup> Linear Regression Model

features : *conservation*, *score11*, *freq2*, *score13*,  
*score20*, *score17*, *freq4* with quadratic term



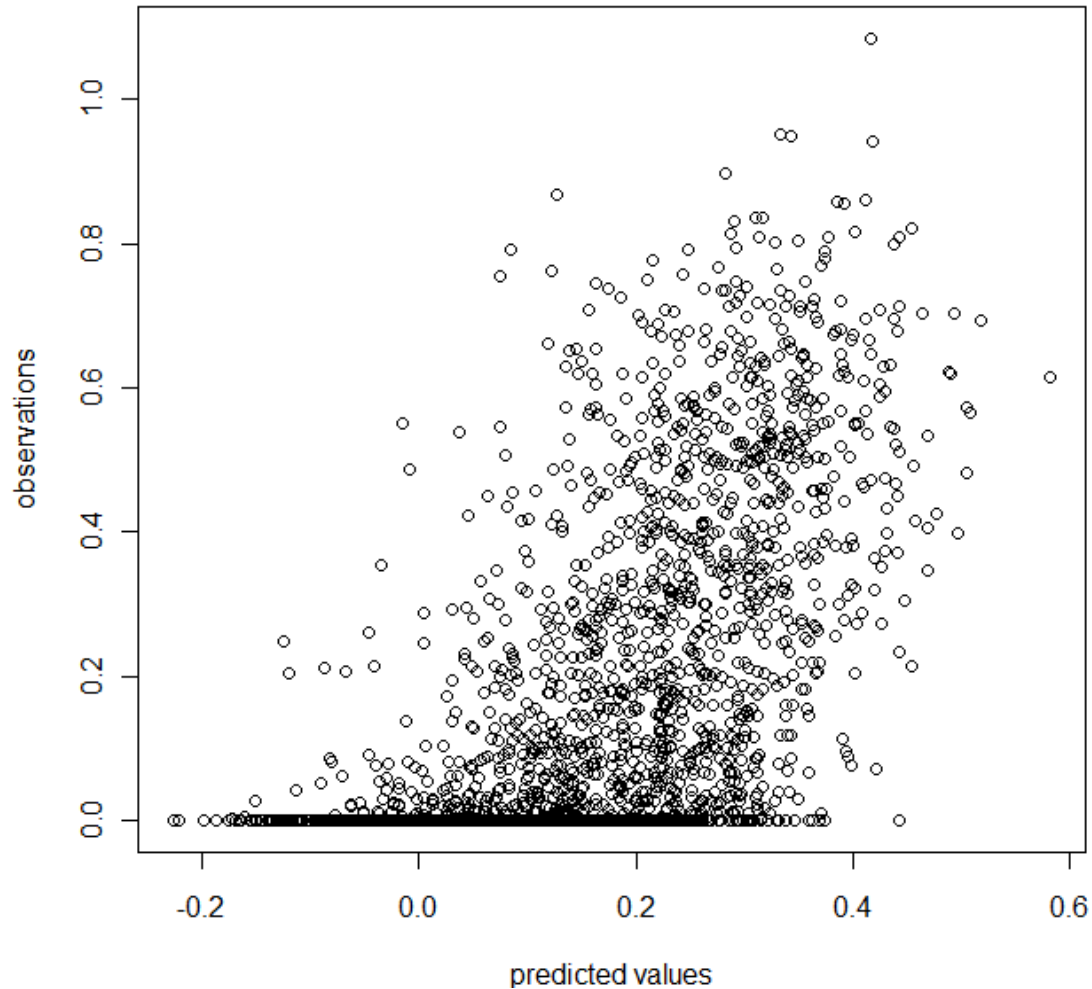
**correlation coefficient**  
=0.6233053

**$R^2$**  = 0.3885095

**prediction error** = 0.02834546  
(cross-validation estimate)

**AIC** = -1794.442

# 2<sup>nd</sup> Linear Regression Model



# References

- **Park, Y. Prediction of the burial status of transmembrane residues of helical membrane proteins.**(2007)*BMC Bioinformatics*
- **Richards, F. M. Areas, volumes, packing and protein structure.**(1977) *Annu Rev Biophys Bioeng*
- **Kavraki, L.E. Molecular Shapes and Surfaces.**(2007) *The Connexions Project*
- **Faraway, J.J. Practical Regression and Anova using R.**(2002)*CRAN*
- **Hastie, T. The Elements of Statistical Learning.**(2009)*Springer*
- **Crawley, M.J. The R book.** (2007)*Wiley*



Thank you for your attention