

# Multivariate statistical methods for the analysis, monitoring and optimization of processes

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# Some properties of PLS models

- At convergence,  $\mathbf{w}$ ,  $\mathbf{u}$ ,  $\mathbf{t}$ ,  $\mathbf{c}$  don't change.

$$\mathbf{w} = \mathbf{X}^T \mathbf{u} / \mathbf{u}^T \mathbf{u}$$

Substitute for  $\mathbf{u}$        $= \mathbf{X}^T \mathbf{Y} \mathbf{c} / ((\mathbf{c}^T \mathbf{c})(\mathbf{u}^T \mathbf{u}))$

Substitute for  $\mathbf{q}$        $= \mathbf{X}^T \mathbf{Y} \mathbf{Y}^T \mathbf{t} / ((\mathbf{t}^T \mathbf{t})(\mathbf{c}^T \mathbf{c})(\mathbf{u}^T \mathbf{u}))$

Substitute for  $\mathbf{t}$        $= \mathbf{X}^T \mathbf{Y} \mathbf{Y}^T \mathbf{X} \mathbf{w} / \underbrace{((\mathbf{w}^T \mathbf{w})(\mathbf{t}^T \mathbf{t})(\mathbf{c}^T \mathbf{c})(\mathbf{u}^T \mathbf{u}))}_{\text{Constant, denote as } \lambda}$

Constant, denote as  $\lambda$

$$\therefore \mathbf{X}^T \mathbf{Y} \mathbf{Y}^T \mathbf{X} \mathbf{w} = \lambda \mathbf{w}$$

**→  $\mathbf{w}$  is eigenvector of  $\mathbf{X}^T \mathbf{Y} \mathbf{Y}^T \mathbf{X}$**

# Some properties of PLS models

- Also,
  - $\mathbf{t}$  is eigenvector of  $\mathbf{X}^T\mathbf{X}\mathbf{Y}\mathbf{Y}^T$ .
  - $\mathbf{u}$  is eigenvector of  $\mathbf{Y}\mathbf{Y}^T\mathbf{X}\mathbf{X}^T$ .
  - $\mathbf{q}$  is eigenvector of  $\mathbf{Y}^T\mathbf{X}\mathbf{X}^T\mathbf{Y}$ .
- Orthogonal properties

$$\mathbf{w}_i^T \mathbf{w}_j = 0 \quad (i \neq j)$$

$$\mathbf{t}_i^T \mathbf{t}_j = 0 \quad (i \neq j)$$

$$\mathbf{w}_i^T \mathbf{p}_j = 0 \quad (i < j)$$

# Residuals

- Measure of size of residuals (same as in PCA)
  - $R_{X,k}^2$  measures how well the model **describe** the variable ( $x_k$ )
  - $R_{Y,m}^2$  measures how well the model **describe** the variable ( $y_m$ )
    - RV2X and RV2Y in Simca-p
  - $Q_{X,k}^2$  measures how well the model **predict** the variable ( $x_k$ )
  - $Q_{Y,m}^2$  measures how well the model **predict** the variable ( $y_m$ )
- $R^2 = 1 - [SS_{\text{residuals}}/SS_{\text{data}}]$  SS = sum of squares
- $Q^2 = 1 - [SS_{\text{predictive resid.}}/SS_{\text{data}}] = 1 - [\text{PRESS}/SS_{\text{data}}]$

# Residuals

- Residuals of observations (row-wise)

- Same as PCA, but two spaces, X and Y

- X-residuals,  $\mathbf{E} = \mathbf{X} - \mathbf{TP}^T$

row SD =  $D\text{Mod}X_i$

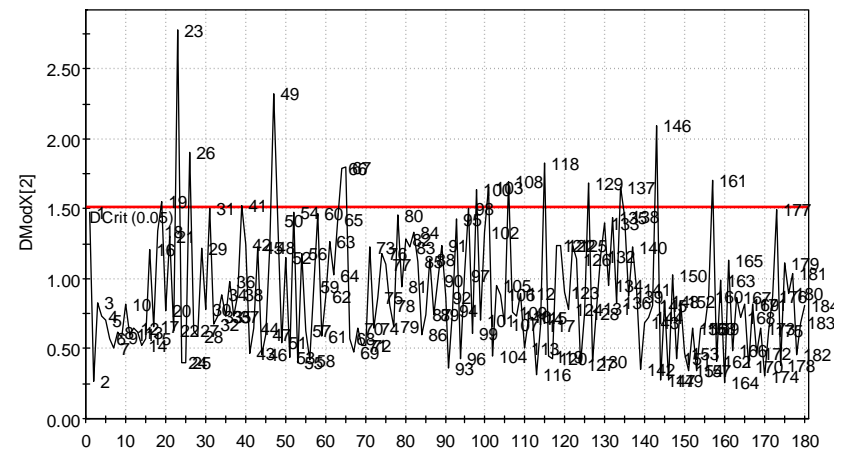
column criterion  $R_{X,k}^2$

- Y-residuals,  $\mathbf{F} = \mathbf{Y} - \mathbf{TC}^T$

row SD =  $D\text{Mod}Y_i$

column criterion  $R_{Y,m}^2$

- Critical values of  $D\text{Mod}X/D\text{Mod}Y$  from F-distribution



# Cross-validation

- Analogous to PCA, PLS model dimensionality can be chosen by CV
  - Data (rows of X and Y) divided into G groups (~7)
  - Model estimated for data minus one group (G rounds)
  - Y of deleted group predicted by model
  - PRESS (prediction error sum of squares) =  $\sum(y_i - y_{ip})^2$
  - $y_{ip}$  = predicted by model estimated from data after deleting the ith observation

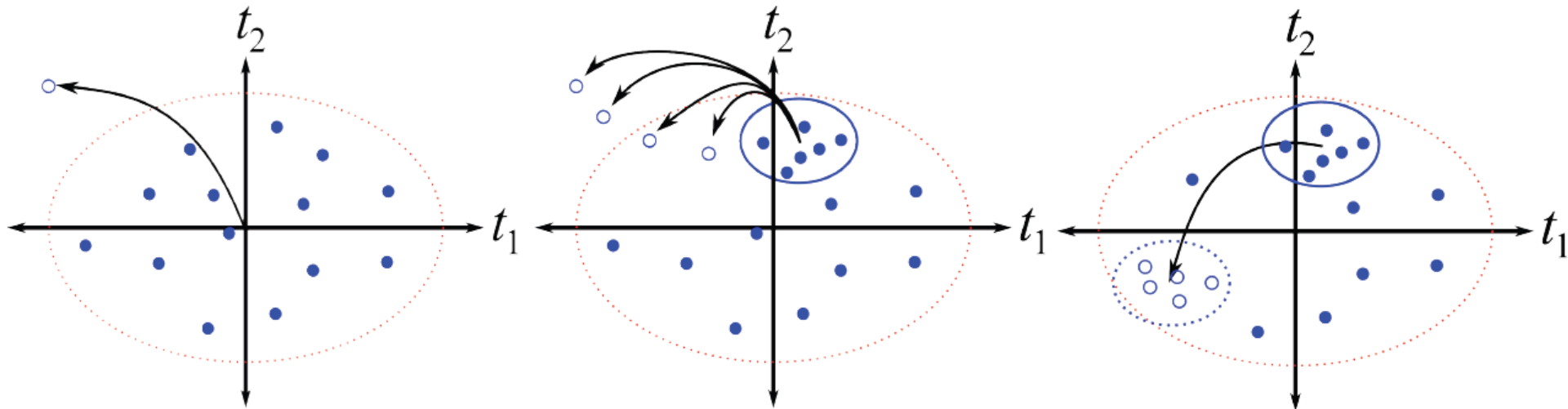
# VIP (Variable importance for the projection)

- VIP is a weighted combination over all components of the squared PLS weights  $w_{ak}$ .
- $SSY_a/SSY_{tot}$  is amount of Y variance explained by component a.
- Suggestions for usage
  - “Normal” VIP value is 1.0.
  - $VIP < 0.5$  indicates unimportant X's in explaining Y & the projection in X

$$VIP_k^2 = K \sum_a (w_{ak}^2 SSY_a) / SSY_{tot}$$

# Contribution plot

- Same as PCA
  - Also have for Y variables



From the model center to a point

Four separate contribution plots to learn why the sequence of deviations occurred

From one group to another group



# PLS regression coefficients

- PLS model

$$\begin{aligned}\mathbf{Y} &= \mathbf{T}\mathbf{C}^T + \mathbf{F} \\ &= \mathbf{t}_1\mathbf{c}_1^T + \mathbf{t}_2\mathbf{c}_2^T + \cdots + \mathbf{F} \\ &= \mathbf{X}\mathbf{w}_1\mathbf{c}_1^T + (\mathbf{X} - \mathbf{t}_1\mathbf{p}_1^T)\mathbf{w}_2\mathbf{c}_2^T + \mathbf{F}\end{aligned}$$

Making all substitutions for  $\mathbf{t}$ 's

$$\mathbf{Y} = \mathbf{X}\mathbf{B} + \mathbf{F} \quad \text{where} \quad \mathbf{B} = \mathbf{W}(\mathbf{P}^T\mathbf{W})^{-1}\mathbf{C}^T$$

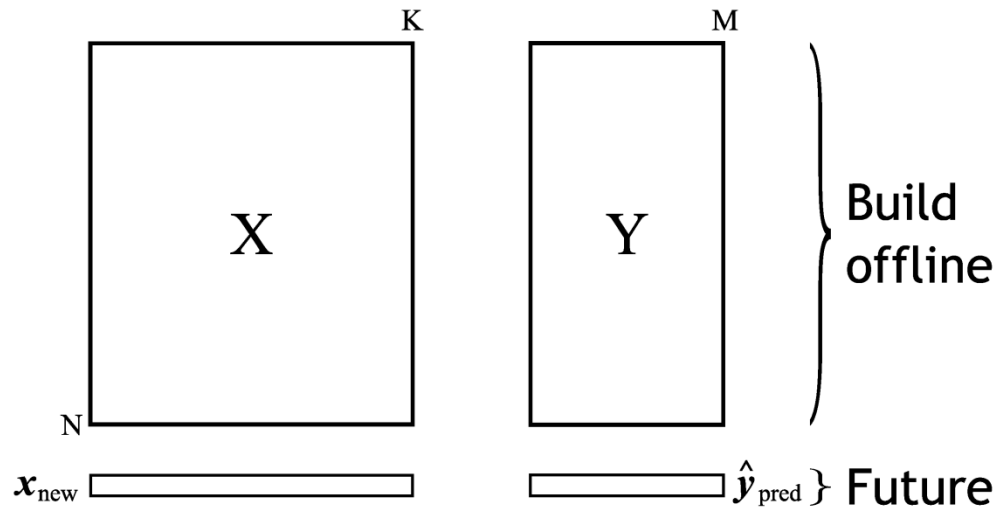
i.e.,

$$y_m \cong b_{1m}x_1 + b_{2m}x_2 + \cdots + b_{Km}x_K$$

Size and sign of scaled and centered regression coefficients

$(b_{km})$  indicates influence of  $x_k$  term on model for  $y_m$ .

# Prediction via PLS model



$$\begin{aligned}
 t_{1,\text{new}} &= \mathbf{x}_{\text{new}}^T \mathbf{w}_1 \\
 \mathbf{x}_{\text{new}}^T &= \mathbf{x}_{\text{new}}^T - t_{1,\text{new}} \mathbf{p}_1^T \\
 t_{2,\text{new}} &= \mathbf{x}_{\text{new}}^T \mathbf{w}_2 \\
 \mathbf{x}_{\text{new}}^T &= \mathbf{x}_{\text{new}}^T - t_{2,\text{new}} \mathbf{p}_2^T \\
 &\text{etc}
 \end{aligned}$$

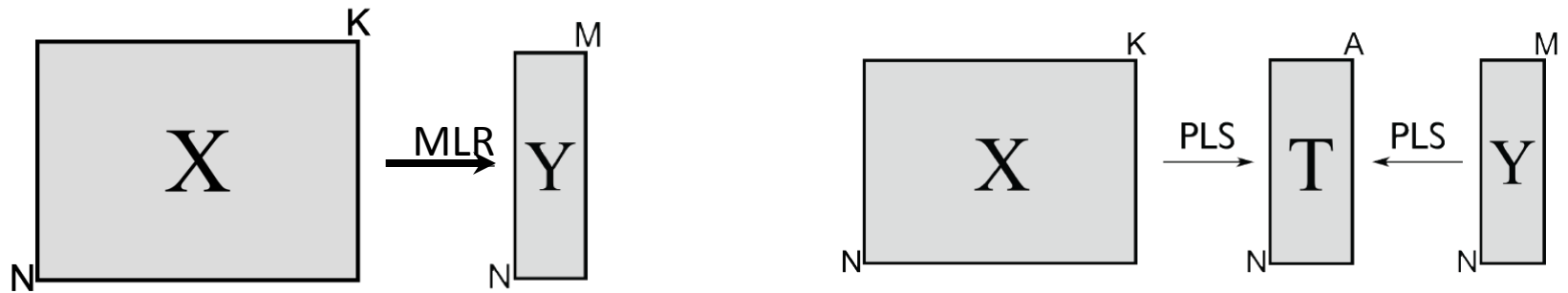
Using this approach, we not only get prediction of  $y$  but also get  $t_a$ 's and  $D_{\text{mod}}X$ .

Collect all the  $t_{a,\text{new}}$  score values in  $\mathbf{t}_{\text{new}}$

$$\text{Then, } \hat{\mathbf{y}}_{\text{new}}^T = \mathbf{t}_{\text{new}}^T \mathbf{C}^T$$

# Relation to MLR

- PLS contains MLR as a special case
  - When the  $X$  variables are few and fairly independent
  - And  $A \rightarrow K$  ( $A$  is the number of PLS component)
  - Then  $T \rightarrow$  reformulation of  $X$
  - PLS  $\rightarrow$  MLR

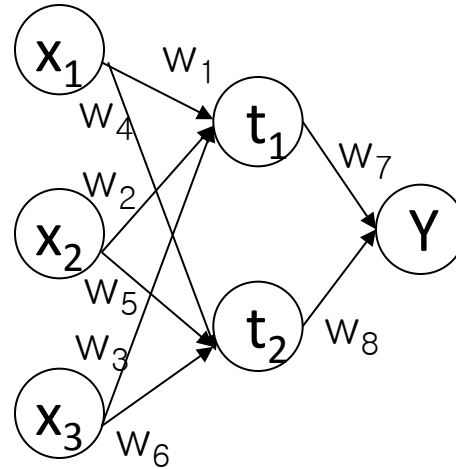


# Relation to Neural Networks

- In the linear case:

- $Y = \sum t_a c_a$

- $t_a = \sum x_k w_{ak} *$



Identical to PLS, but PLS gives a unique solution (the  $t_a$ 's are orthogonal and anchored due to modeling of the x-space)

(McAvoy & Qin, Computers and Chemical Engineering, 16(1992) 379-391)

# Tutorials

- Drug discovery
  - New drugs: chemicals that are biologically active.
  - Testing chemicals for biological activity is very expensive.
  - Prediction of biological activity from cheaper chemical measurements is desirable
  - Measurements: size, lipophilicity, and polarity at various sites on the molecule
- Dataset
  - 30 chemical compounds
  - 16 measurements including the activity (represented by the logarithm of relative activity)

Originally from

Ufkes *et al.* (1978), "Structure-Activity Relationships of Bradykinin-Potentiating Peptides," *European Journal of Pharmacology*, 50, 119.

Ufkes *et al.* (1982), "Further Studies on the Structure-Activity Relationships of Bradykinin-Potentiating Peptides," *European Journal of Pharmacology*, 79, 155.

# Tutorials

```
data penta;
  input obsnam $ S1 L1 P1 S2 L2 P2
          S3 L3 P3 S4 L4 P4
          S5 L5 P5 log_RAI @@;

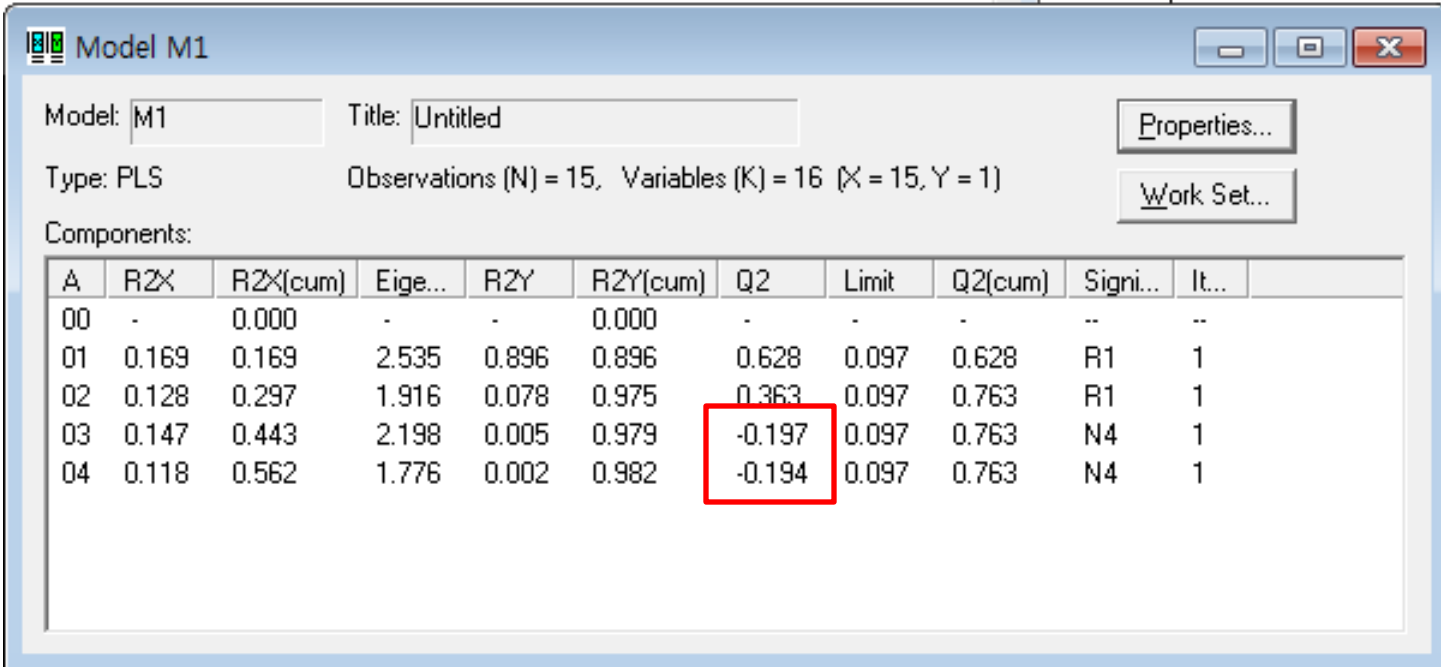
  n = _n_;
  datalines;
VESSK   -2.6931 -2.5271 -1.2871  3.0777  0.3891 -0.0701
         1.9607 -1.6324  0.5746  1.9607 -1.6324  0.5746
         2.8369  1.4092 -3.1398                0.00
VESAK   -2.6931 -2.5271 -1.2871  3.0777  0.3891 -0.0701
         1.9607 -1.6324  0.5746  0.0744 -1.7333  0.0902
         2.8369  1.4092 -3.1398                0.28
VEASK   -2.6931 -2.5271 -1.2871  3.0777  0.3891 -0.0701
         0.0744 -1.7333  0.0902  1.9607 -1.6324  0.5746
         2.8369  1.4092 -3.1398                0.20
VEAAK   -2.6931 -2.5271 -1.2871  3.0777  0.3891 -0.0701
         0.0744 -1.7333  0.0902  0.0744 -1.7333  0.0902
         2.8369  1.4092 -3.1398                0.51
VKAAK   -2.6931 -2.5271 -1.2871  2.8369  1.4092 -3.1398
         0.0744 -1.7333  0.0902  0.0744 -1.7333  0.0902
         2.8369  1.4092 -3.1398                0.11
VEWAK   -2.6931 -2.5271 -1.2871  3.0777  0.3891 -0.0701
         -4.7548  3.6521  0.8524  0.0744 -1.7333  0.0902
         2.8369  1.4092 -3.1398                2.73
VEAAP   -2.6931 -2.5271 -1.2871  3.0777  0.3891 -0.0701
         0.0744 -1.7333  0.0902  0.0744 -1.7333  0.0902
         -1.2201  0.8829  2.2253                0.18
VEHAK   -2.6931 -2.5271 -1.2871  3.0777  0.3891 -0.0701
         2.4064  1.7438  1.1057  0.0744 -1.7333  0.0902
         2.8369  1.4092 -3.1398                1.53
VAAAK   -2.6931 -2.5271 -1.2871  0.0744 -1.7333  0.0902
         0.0744 -1.7333  0.0902  0.0744 -1.7333  0.0902
```

# Tutorials

- Goal
  - To predict biological activity with chemical measurements (that are easily available)
  - To understand latent structure of chemical measurements
  - To find which measurements are more important in predicting biological activity

# Tutorials

- Two components seems adequate.



Model M1

Model: M1 Title: Untitled

Type: PLS Observations (N) = 15, Variables (K) = 16 (X = 15, Y = 1)

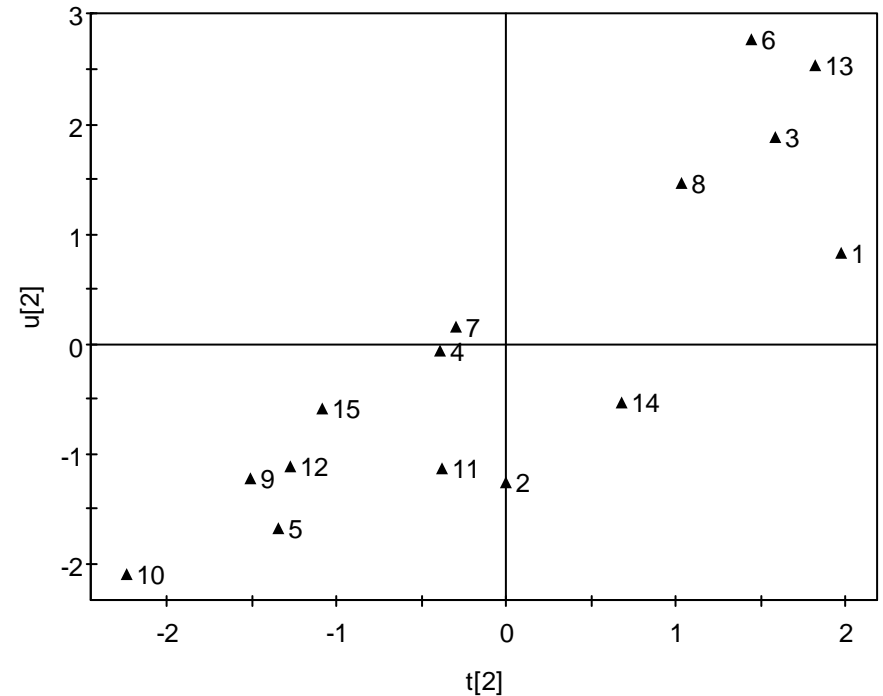
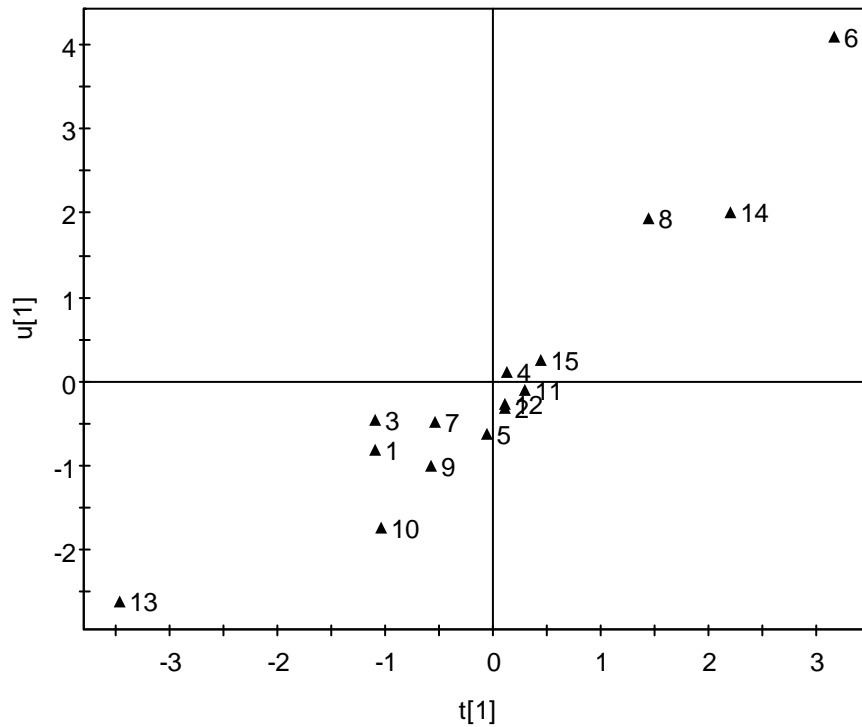
Components:

A	R2X	R2X(cum)	Eige...	R2Y	R2Y(cum)	Q2	Limit	Q2(cum)	Signi...	It...
00	-	0.000	-	-	0.000	-	-	-	--	--
01	0.169	0.169	2.535	0.896	0.896	0.628	0.097	0.628	R1	1
02	0.128	0.297	1.916	0.078	0.975	0.363	0.097	0.763	R1	1
03	0.147	0.443	2.198	0.005	0.979	-0.197	0.097	0.763	N4	1
04	0.118	0.562	1.776	0.002	0.982	-0.194	0.097	0.763	N4	1



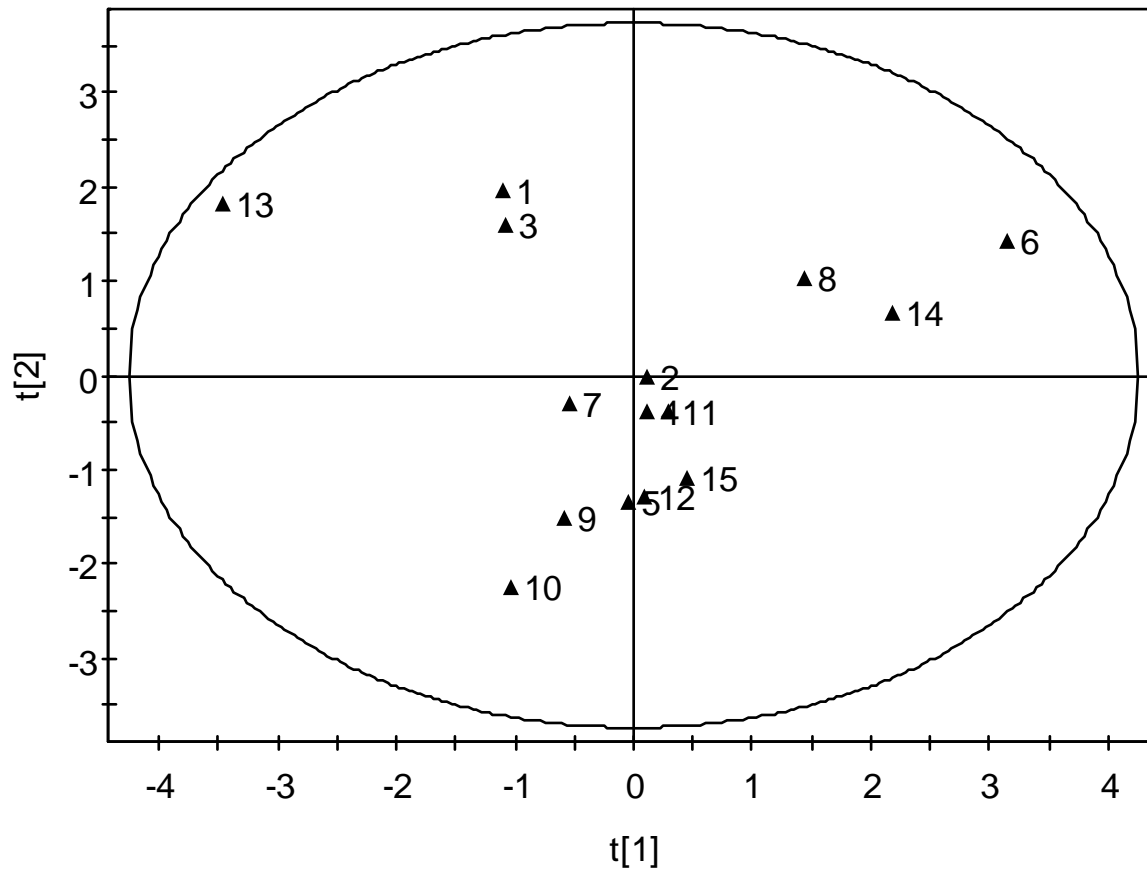
# Tutorials

- t vs. u plots verify linear relationships ( $t_i = u_i + e$ )



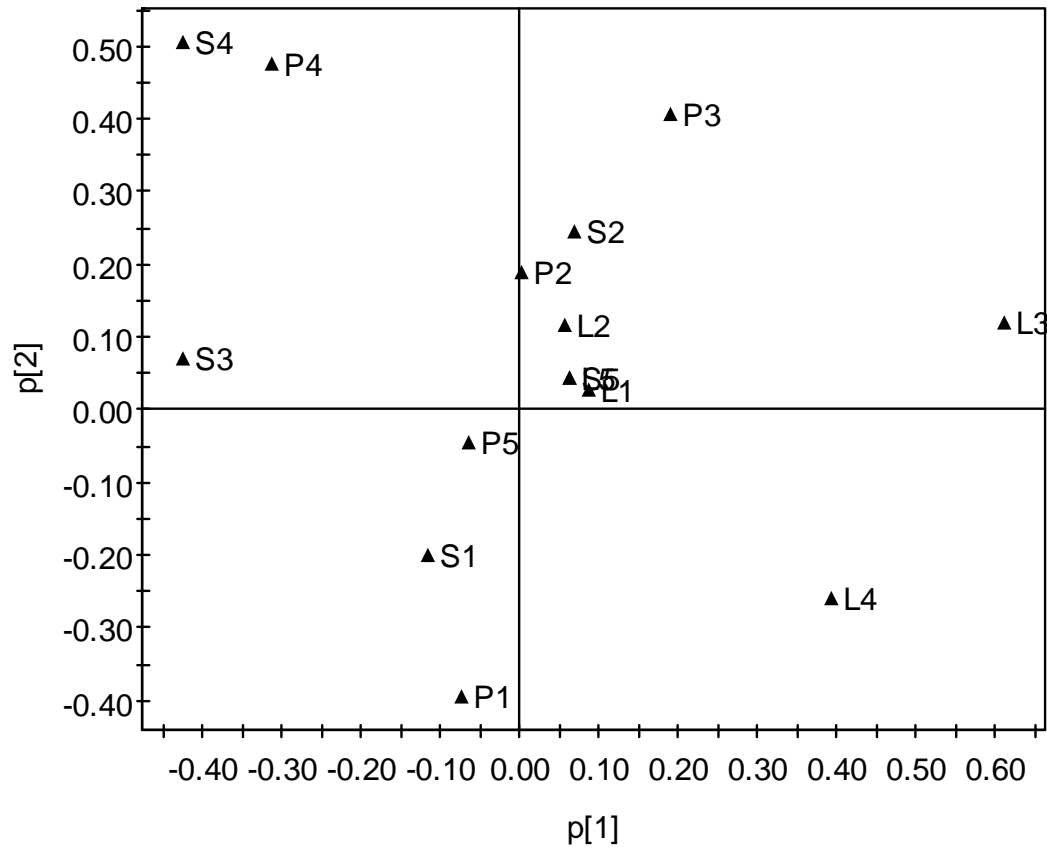
# Tutorials

- Groups/clusters or outliers can be found in x-score plots.



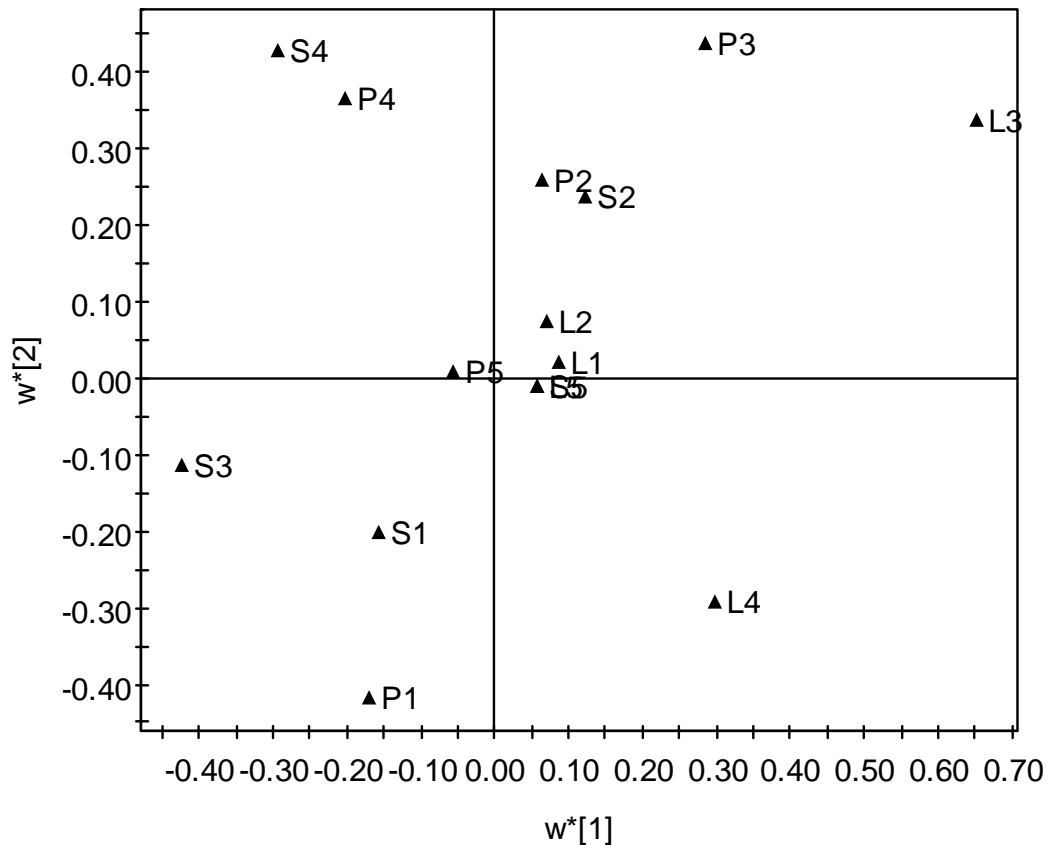
# Tutorials

- And which measurements may be responsible for that clusters and/or outliers.



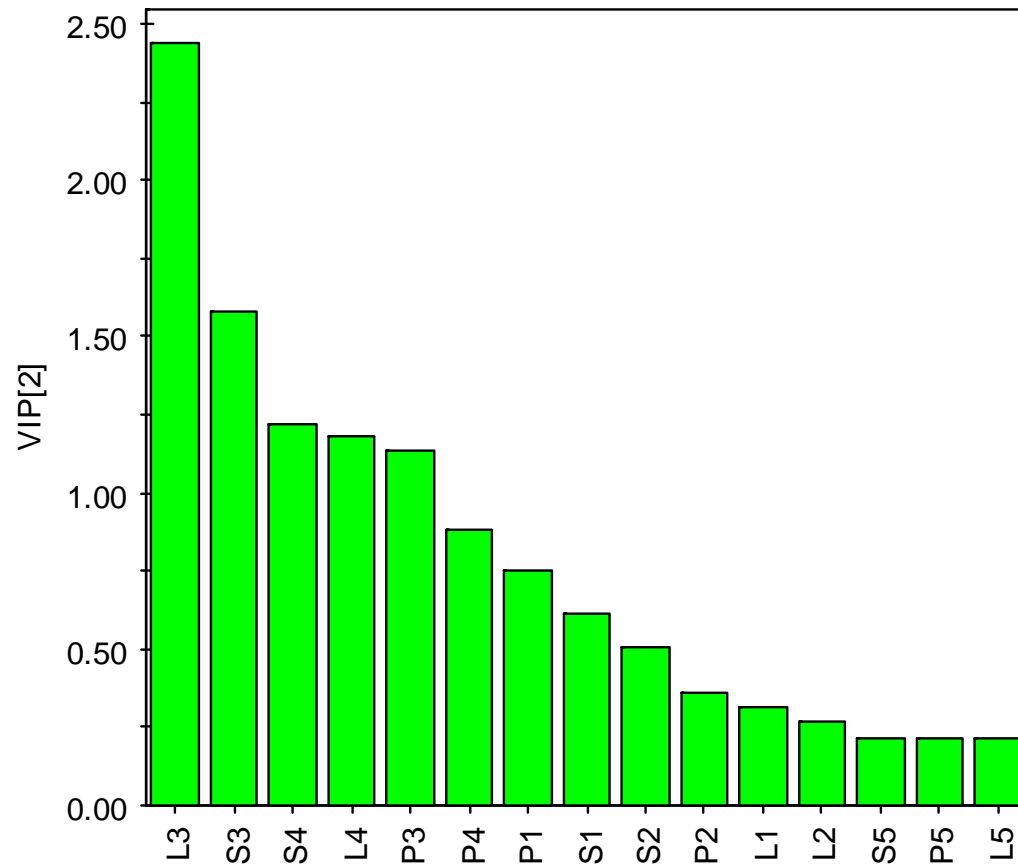
# Tutorials

- Weight ( $w^*$ ) plots can tell relative importance of chemical measurements in predicting biological activity..



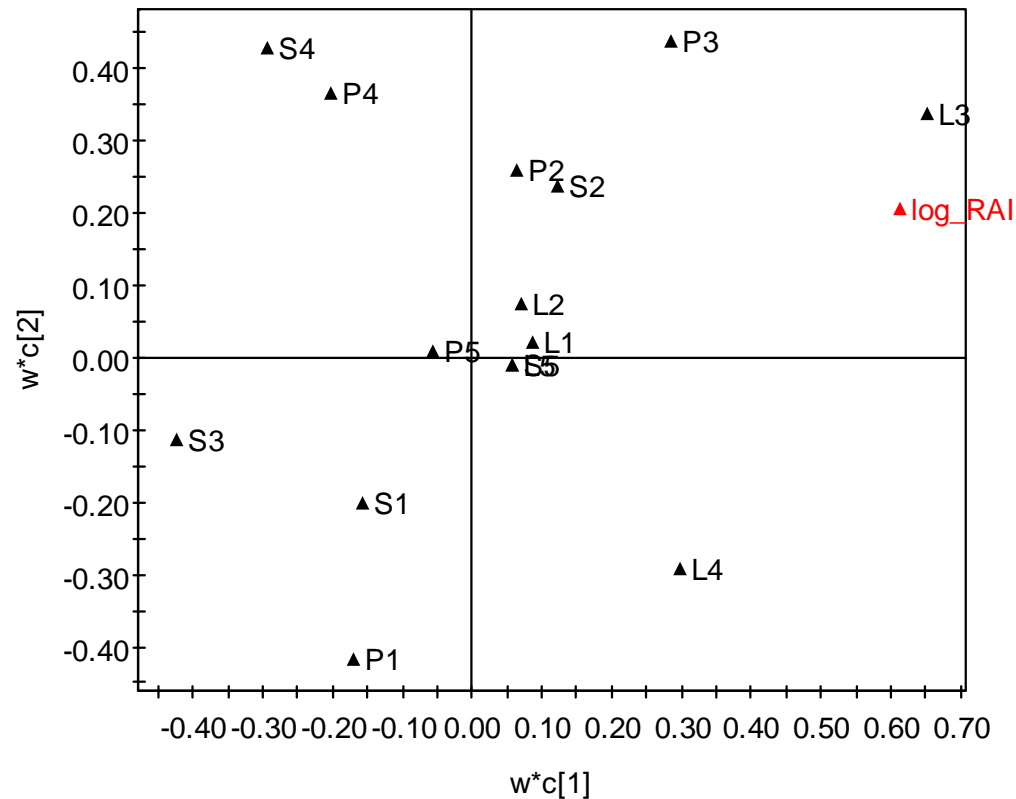
# Tutorials

- A VIP plot can reveal this more easily.



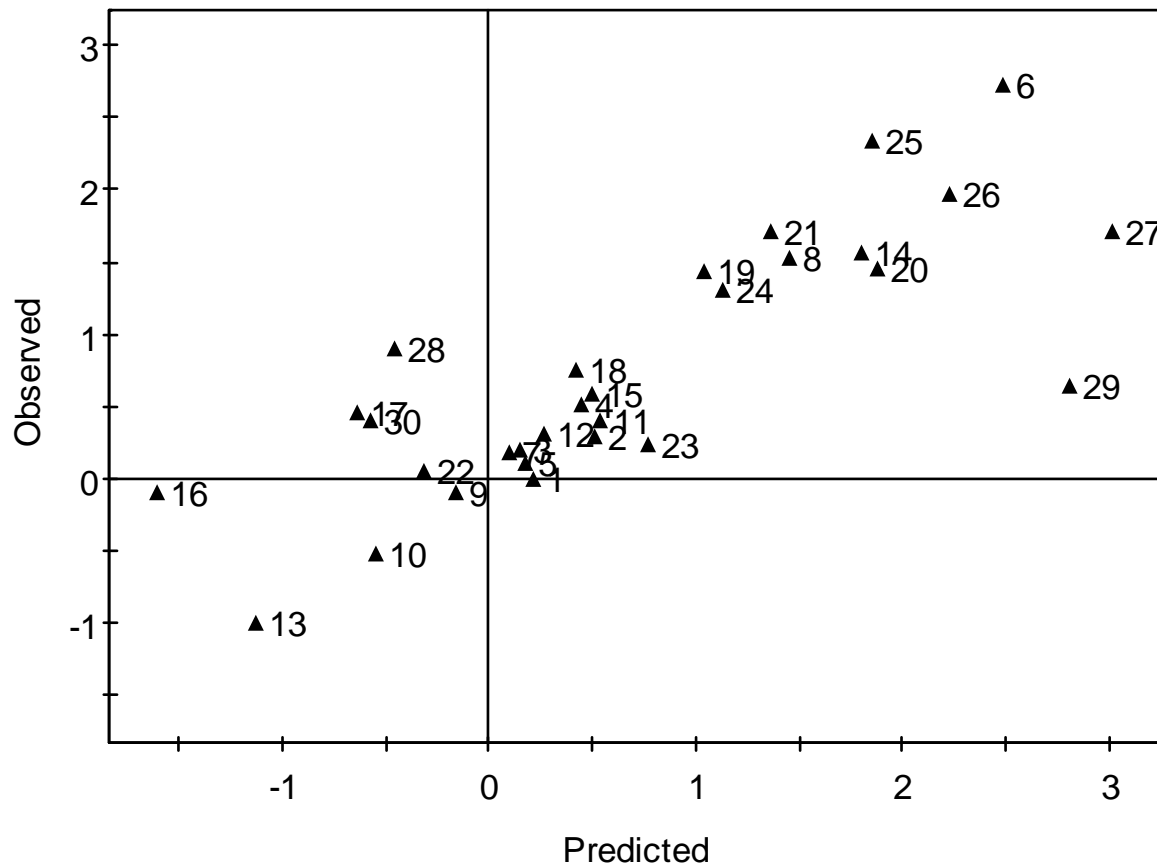
# Tutorials

- $w^*c$  plots show the correlation structure between X and Y. One sees how the X and Y variables combine in the projections, and how the X variables relate to the Y variables.



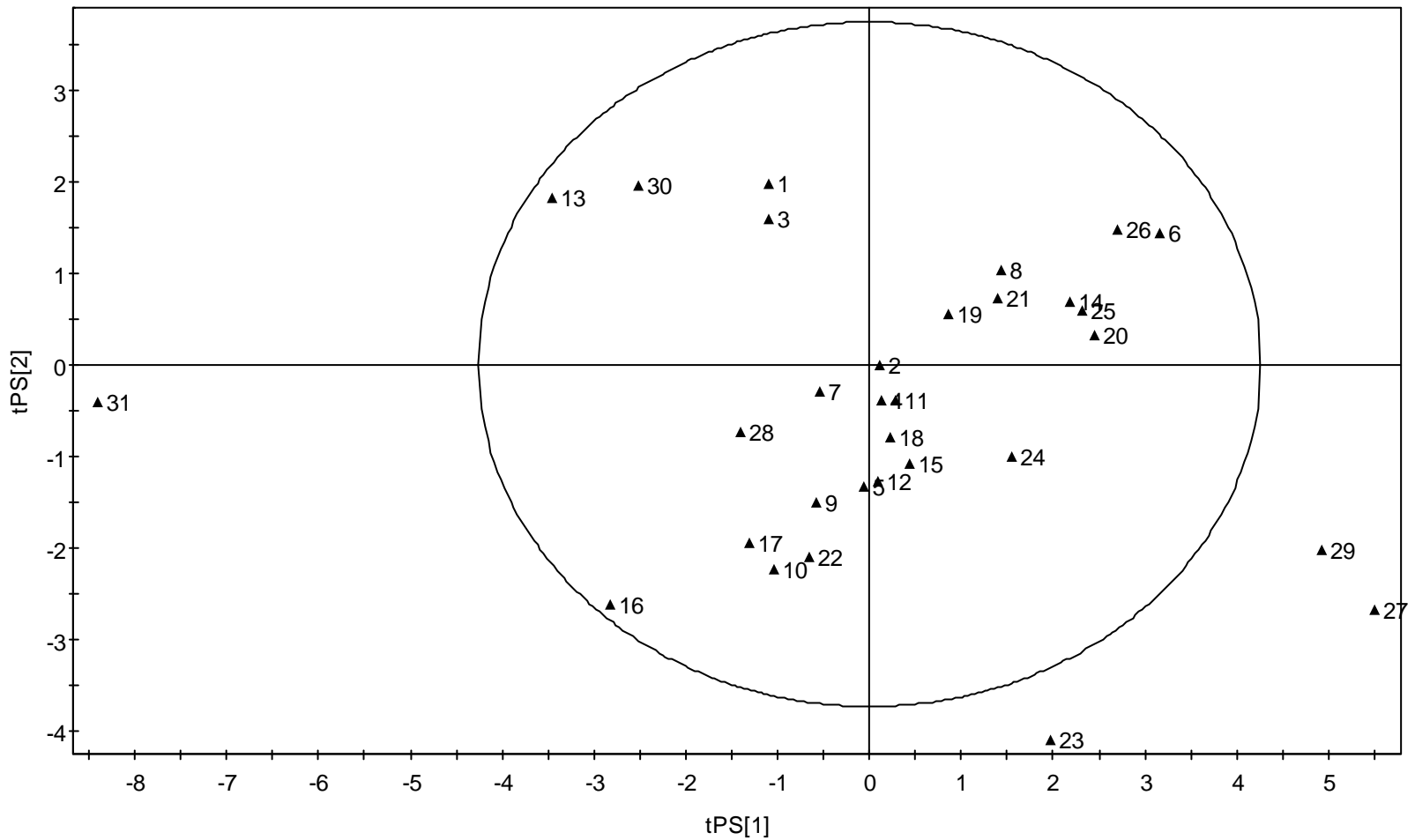
# Tutorials

- Prediction for remaining 15 compounds



# Tutorials

- Prediction for remaining 15 compounds





# Confidence interval in PCA & PLS

- Approximate confidence interval/regions based on distribution assumption
  - Since  $t_a (= \mathbf{p}_a^T \mathbf{x})$  is a linear function of many  $x$ 's, by the **Central Limit Theorem**,  $t_a \sim N(0, \sigma_t^2)$  even if the individual  $x$ 's are not normally distributed.
  - Use normal theory (or t-distribution if # observation is not large) to obtain confidence intervals/regions for  $t_a$ 's

※ Confidence interval: for single variable

※ Joint confidence interval for more than two variable? → confidence region

# Confidence interval in PCA & PLS

- 100(1- $\alpha$ )% confidence interval of  $t_a$

$$\pm t_{\alpha/2}(df) \cdot s_{t_a} \quad \text{statistic} \pm A \times \sigma_{\text{statistic}}$$

Value that depends on P.D.F of the statistic & confidence level  $\alpha$

Standard error of the statistic

- Joint 100(1- $\alpha$ )% confidence region of  $t$ 's

$$T^2 = (\mathbf{x} - \bar{\mathbf{x}})^T \mathbf{S}_x^{-1} (\mathbf{x} - \bar{\mathbf{x}})$$

$$\mathbf{S}_x = \hat{\Sigma}_x = \frac{1}{N} \mathbf{X}^T \mathbf{X} = \frac{1}{N} \mathbf{P} (\mathbf{T}^T \mathbf{T}) \mathbf{P}^T = \mathbf{P} \mathbf{S}_t \mathbf{P}^T$$

$$T^2 = (\mathbf{x} - \bar{\mathbf{x}})^T \mathbf{P} \mathbf{S}_t^{-1} \mathbf{P}^T (\mathbf{x} - \bar{\mathbf{x}})$$

$$= \mathbf{t}^T \mathbf{S}_t^{-1} \mathbf{t}$$

$$= \sum_{a=1}^K \frac{t_a^2}{s_{t_a}^2}$$

$$\mathbf{S}_t = \begin{bmatrix} s_{t_1}^2 & 0 & \cdots & 0 \\ 0 & s_{t_2}^2 & 0 & \vdots \\ \vdots & 0 & \ddots & 0 \\ 0 & \cdots & 0 & s_{t_K}^2 \end{bmatrix}$$

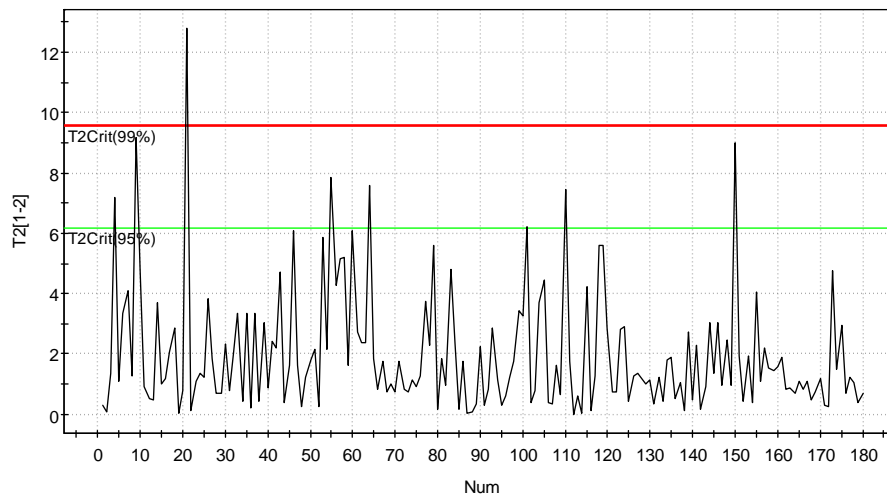
# Confidence interval in PCA & PLS

- Upper 100(1- $\alpha$ )% confidence limit on  $T^2$  is given by

$$T_{\alpha}^2 = \frac{(N-1)(N+1)K}{N(N-K)} F_{\alpha}(K, N-K)$$

- If only A component are used,

$$T_A^2 = \sum_{a=1}^A \frac{t_a^2}{s_{t_a}^2} \sim \frac{(N-1)(N+1)A}{N(N-A)} F_{\alpha}(A, N-A)$$

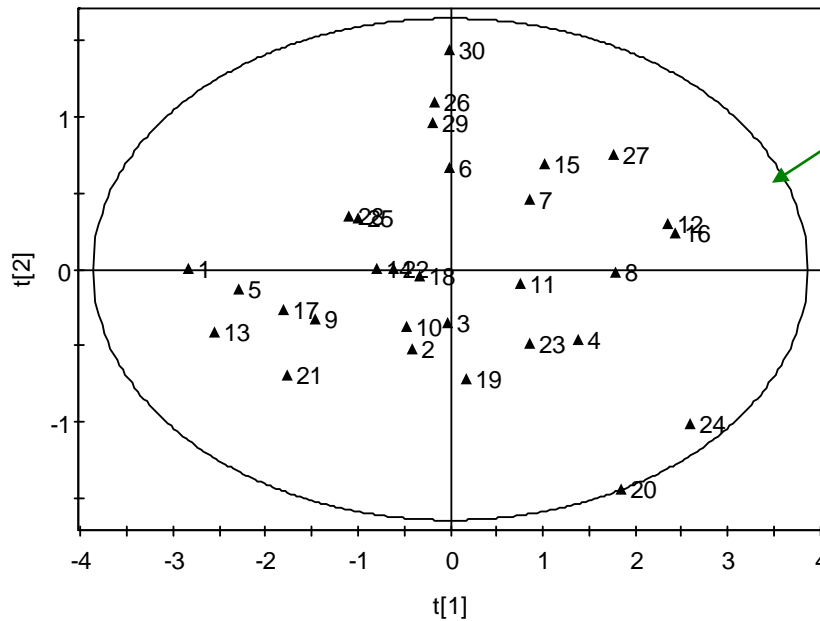


# Confidence interval in PCA & PLS

- Or in space of  $t_1, t_2, \dots$

$$\frac{t_1^2}{s_{t_1}^2} + \frac{t_2^2}{s_{t_2}^2} = \frac{(N-1)(N+1)2}{N(N-2)} F_\alpha(2, N-2) \quad \text{constant}$$

This is the equation of an ellipse in space of  $t_1$  and  $t_2$ .



# Confidence interval in PCA & PLS

## 3. SPE confidence interval (by Jackson, 1991)

$$Q = (\mathbf{x} - \hat{\mathbf{x}})^T (\mathbf{x} - \hat{\mathbf{x}}) (\equiv SPE)$$

Critical upper 100(1- $\alpha$ )% confidence limit on Q is give by

$$Q_\alpha = \theta_1 \left[ \frac{Z_\alpha \sqrt{2\theta_2 h_0^2}}{\theta_1} + \frac{\theta_2 h_0 (h_0 - 1)}{\theta_1^2} + 1 \right]^{1/h_0}$$

Where

$$\begin{aligned} \theta_1 &= \sum_{a=A+1}^K \lambda_a = Tr(\mathbf{E}) & \theta_3 &= \sum_{a=A+1}^K \lambda_a^3 = Tr(\mathbf{E}^3) \\ \theta_2 &= \sum_{a=A+1}^K \lambda_a^2 = Tr(\mathbf{E}^2) & h_0 &= 1 - \frac{2\theta_1\theta_3}{3\theta_2} \end{aligned}$$

※ Some S/W's use resampling methods (bootstrap, jackknife) to calculate C.I.

# Readings

- Theory
  - Burnham, A.J., Viveros, R., MacGregor, J.F., “Frameworks for latent variable multivariate regression,” J. Chemometrics **10**, 31-45, (1996)
  - Hoskuldsson, A., “PLS regression methods” J. Chemometrics **2**, 211-228, (1988)
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  - Wold, S., Sjöström, M., and Eriksson, L., “PLS regression: A basic tool of chemometrics,” Chemometrics and Intelligent Laboratory Systems, 58, 109-130, (2001)
- Applications
  - Gossen, P.D., MacGregor, J.F., Pelton, R.H., “composition and particle diameter for styren/methyl methacrylate copolymer latex using UV and NIR spectroscopy,” applied spectroscopy, **47**(11), 1852-1870
  - MacGregor, J.F., Jaeckle, D., Kiparissides, C. and Koutoudi, M., “process monitoring and diagnosis by multi-block PLS methods,” AIChE J., 40(5) 826-838, (1994)