

```
> library("pls")
> metfull.pcr <- pcr(m~g*F*A, data=alkohol)
> summary(metfull.pcr)
Data:   X dimension: 32 7
        Y dimension: 32 1
Fit method: svdpc
Number of components considered: 7
TRAINING: % variance explained
```

	1 comps	2 comps	3 comps	4 comps	5 comps	6 comps	7 comps
X	39.7	73.39	93.78	98.56	99.53	99.94	100.00
m	56.6	76.91	79.48	80.48	80.97	82.51	82.77

*

```
> metfull.pcr4v <- pcr(m~g*F*A, 4, validation="LOO", data=alkohol)
> coef(metfull.pcr4v)
, , 4 comps
```

```

      m
g      2.0785781
F     -0.5822384
A     -0.1634464
g:F    -0.8650668
g:A    -0.2757334
F:A     0.2348700
g:F:A   0.3351248
```

*

```
> summary(metfull.pcr4v)
Data:   X dimension: 32 7
        Y dimension: 32 1
Fit method: svdpc
Number of components considered: 4

VALIDATION: RMSEP
Cross-validated using 32 leave-one-out segments.
      (Intercept)  1 comps  2 comps  3 comps  4 comps
CV           2.701    2.330    1.507    1.413    1.421
adjcv        2.701    2.321    1.490    1.409    1.417

TRAINING: % variance explained
      1 comps  2 comps  3 comps  4 comps
X       39.7    73.39    93.78    98.56
m       56.6    76.91    79.48    80.48
```

* CV – cross validation error, "adjCV" (for RMSEP and MSEP) is the bias-corrected cross-validation estimate

```
> MSEP(metfull.pcr4v)
      (Intercept)  1 comps  2 comps  3 comps  4 comps
CV           7.296    5.430    2.271    1.998    2.019
adjcv        7.296    5.388    2.219    1.987    2.007
```

*

```
> summary(lm(m~g+F+g:F,alkohol))
```

Call:

```
lm(formula = m ~ g + F + g:F, data = alkohol)
```

Residuals:

Min	1Q	Median	3Q	Max
-2.4427	-0.6111	-0.0326	0.5436	3.8759

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.1858	0.7117	-1.666	0.1068
g	2.3439	0.2801	8.367	4.22e-09 ***
F	0.9885	1.0724	0.922	0.3645
g:F	-1.5069	0.5591	-2.695	0.0118 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.207 on 28 degrees of freedom
Multiple R-squared: 0.8137, Adjusted R-squared: 0.7938
F-statistic: 40.77 on 3 and 28 DF, p-value: 2.386e-10

```
> metfull.pcr3 <-pcr(m~g*F*A,3,data=alkohol)
```

```
> coef(metfull.pcr3)
```

```
, , 3 comps
```

	m
g	2.06006735
F	-0.65907155
A	-0.09085652
g:F	-0.66906881
g:A	0.01263040
F:A	-0.12407708
g:F:A	-0.15666630

*

```
> metfull.pcr3v <-pcr(m~g*F*A,3,validation="LOO",data=alkohol)
```

```
> summary(metfull.pcr3v)
```

Data: X dimension: 32 7

Y dimension: 32 1

Fit method: svdpc

Number of components considered: 3

VALIDATION: RMSEP

Cross-validated using 32 leave-one-out segments.

	(Intercept)	1 comps	2 comps	3 comps
CV	2.701	2.330	1.507	1.413
adjcv	2.701	2.321	1.490	1.409

TRAINING: % variance explained

	1 comps	2 comps	3 comps
X	39.7	73.39	93.78
m	56.6	76.91	79.48

*

```
> MSEP(metfull.pcr3v)
```

	(Intercept)	1 comps	2 comps	3 comps
CV	7.296	5.430	2.271	1.998
adjcv	7.296	5.388	2.219	1.987

```
> R2(metfull.pcr3v)
```

	(Intercept)	1 comps	2 comps	3 comps
	-0.06556	0.20692	0.66828	0.70823

```
> loadings(metfull.pcr3v)
```

Loadings:

	Comp 1	Comp 2	Comp 3
g	0.522	0.693	0.475
F	-0.434		
A		-0.335	0.328
g:F	-0.706	0.351	0.392
g:A	0.155	-0.492	0.578
F:A		-0.114	0.234
g:F:A		-0.153	0.340

	Comp 1	Comp 2	Comp 3
SS loadings	1.000	1.000	1.000
Proportion Var	0.143	0.143	0.143
Cumulative Var	0.143	0.286	0.429