

Supplementary information for the paper

Title: Determinants of Antibiotic Consumption - Development of a Model using Partial Least Squares Regression based on Data from India

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The general underlying model of PLS regression

$$X = TP^T + E \quad \text{Equation S1}$$

$$Y = UQ^T + F$$

where,

$\mathbf{X} = n$ (rows) \times m (columns) matrix of determinants; $\mathbf{Y} = n$ (rows) \times p (columns) matrix of responses (antibiotic consumption); \mathbf{T} and $\mathbf{U} = n$ (rows) \times l (columns) matrices that are, respectively, projections of \mathbf{X} (the X score, component or factor matrix) and projections of \mathbf{Y} (the Y scores); \mathbf{P} and $\mathbf{Q} = m$ (rows) \times l (columns) and p (rows) \times l (columns) orthogonal loading matrices; matrices \mathbf{E} and \mathbf{F} are the error terms, assumed to be independent and identically distributed random normal variables. The decompositions of \mathbf{X} and \mathbf{Y} are made so as to maximise the covariance between \mathbf{T} and \mathbf{U} .

R code for building the prediction model to estimate human antibiotic consumption in India

Note: Comments to explain each line of code are in italics starting with "#"

```
# Import the data for model building
```

```
ind.subset = read.csv(file.choose(), header=T)
```

```
# 75% of the sample size
```

```
set.seed(896)
```

```
smp_size<- floor(0.75 * nrow(ind.subset))
```

```
# set the seed to make your partition reproducible
```

```
set.seed(457)
```

```
train_ind<- sample(seq_len(nrow(ind.subset)), size = smp_size)
```

```
# Create training set
```

```
train.subset<- ind.subset[train_ind, ]
```

```
# Create test set
```

```
test.subset<- ind.subset[-train_ind, ]
```

```
# Call the library pls to run PLSR
```

```
library(pls)
```

```
# Regression command
```

```
mod.subset<- pls(ab_use~., ncomp=6, data = train.subset, validation = "LOO")
```

```
summary(mod.subset)
```

```
# Command to plot the RMSEP graph
```

```
plot(RMSEP(mod.subset))
```

```
# 2 components plot with loading values
```

```
par(mar = c(10,4,2,2), mgp = c(7, 1, 0))
```

```
plot(mod.subset, plottype="loadings", comps = 2, ylim=c(-1,1.5), xlab="Determinants", ylab="",  
xaxt="n")
```

```
axis(1, at=1:38, labels=prednames(mod.subset), las=3)
```

```
title(ylab = "loading value", mgp = c(2.5, 1, 0))
```

```
abline(h = 0)
```

```
# Predict the antibiotic consumption values for test set
```

```
predict(mod.subset, ncomp = 2, newdata = test.subset)
```

```
# Command to plot the predicted vs. measured value of the test data
```

```
par(mar = c(10,4,2,2), mgp = c(4, 1, 0))
```

```
predplot(mod.subset, ncomp=2, newdata = test.subset, asp=1, line=TRUE, xlab="Measured  
value")
```

```
title(ylab = "Predicted value", mgp = c(2.5, 1, 0))
```