PCA with missing data using the missMDA R package

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Using missMDA to deal with missing data

- > library(missMDA)
- > data(orange)

	Color intensity	Odor intensity		Sweet	Acid	Bitter	Pulp	Typicity
1	4.79	5.29	NA	NA	NA	2.83	NA	5.21
2	4.58	6.04	4.42	5.46	4.13	3.54	4.62	4.46
3	4.71	5.33	NA	NA	4.29	3.17	6.25	5.17
4	6.58	6.00	7.42	4.17	6.75	NA	1.42	3.42
5	NA	6.17	5.33	4.08	NA	4.38	3.42	4.42
6	6.33	5.00	5.38	5.00	5.50	3.63	4.21	4.88
7	4.29	4.92	5.29	5.54	5.25	NA	1.29	4.33
8	NA	4.54	4.83	NA	4.96	2.92	1.54	3.96
9	4.42	NA	5.17	4.62	5.04	3.67	1.54	3.96
10	4.54	4.29	NA	5.79	4.38	NA	NA	5.00
11	4.08	5.13	3.92	NA	NA	NA	7.33	5.25
12	6.50	5.88	6.13	4.88	5.29	4.17	1.50	3.50

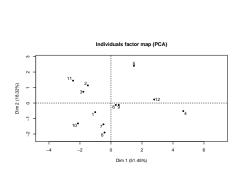
Some (bad) easy methods

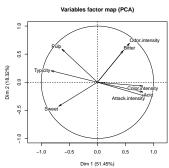
- Delete individuals or variables with missing data: usually not a good idea
- Replace missing data with the mean (default in several packages including FactoMineR)

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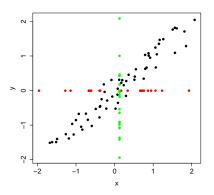
> res.pca <- PCA(orange)</pre>





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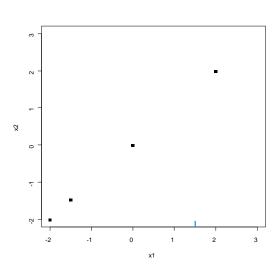
Big distortion of links between variables

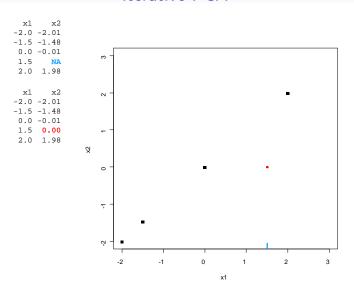
Ideas:

- As x and y strongly correlated : impute missing y value using x value
- if individuals i and j have similar values for all variables, impute missing i value using j value for that variable

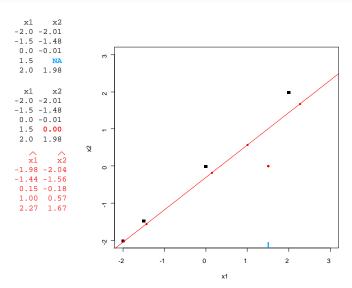
 \Rightarrow takes into account global similarity between individuals and links between variables

x1 x2 -2.0 -2.01 -1.5 -1.48 0.0 -0.01 1.5 NA 2.0 1.98

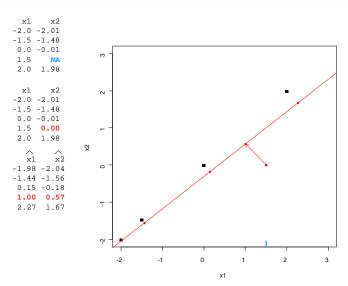




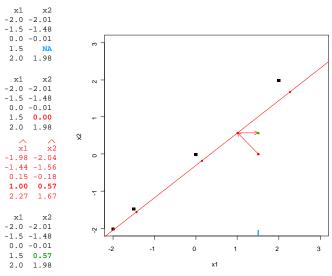
Initialize: impute the mean



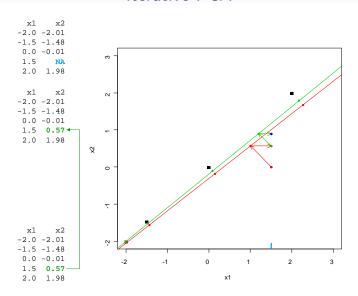
Do PCA on imputed table \rightarrow axes and components;

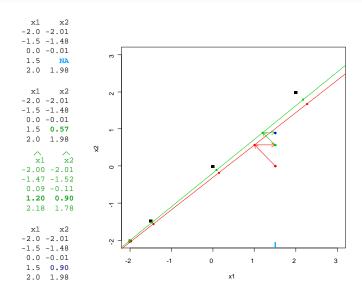


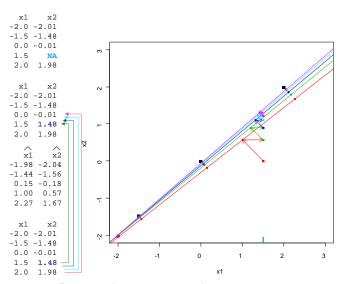
Missing data imputed using PCA



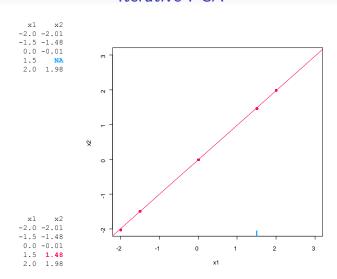
New imputed data table







Repeat these steps until convergence



Do PCA on imputed data table

- 1. initialization: impute using the mean
- 2. Step ℓ :
 - (a) do PCA on imputed data table S dimensions retained
 - (b) missing data imputed using PCA
 - (c) means (and standard deviations) updated
- 3. iterate the estimation and imputation steps

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Overfitting problem due to believing too much in links between variables

⇒ regularized iterative PCA

Running missMDA in R

```
> library(missMDA)
> data(orange)
> nb <- estim_ncpPCA(orange, scale=TRUE)</pre>
                                                       ## Estimate no. of dimensions
> comp <- imputePCA(orange, ncp=2, scale=TRUE)</pre>
                                                       ## Impute the table
> res.pca <- PCA(comp$completeObs)</pre>
                                                       ## Do the PCA
> orange
                                         > comp$completeObs
 Sweet Acid Bitter Pulp Typicity
                                         Sweet Acid Bitter Pulp Typicity
  NΑ
       NA 2.83
                    NΑ
                            5.21
                                          5.54 4.13 2.83 5.89
                                                                        5.21
5.46 4.13 3.54 4.62 4.46
                                          5.46 4.13 3.54 4.62
                                                                        4.46
  NA 4.29 3.17 6.25
                            5.17
                                          5.45 4.29 3.17 6.25
                                                                        5.17
4.88 5.29 4.17 1.50
                            3.50
                                          4.88 5.29 4.17 1.50
                                                                        3.50
                   Individuals factor map (PCA)
                                                                Variables factor map (PCA)
                              5
                                                                        Odori
                                                         Typicit
Dim 2 (17.16%)
                                                  Dim 2 (17.
                                                         Swe
```

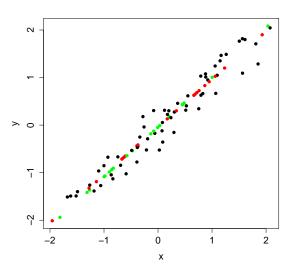
Dim 1 (71 34%)

7

8

Dim 1 (71.34%)

Is running the imputation algorithm once sufficient?



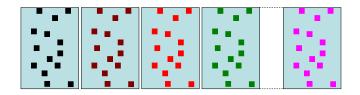
What confidence can we give to the results? Idea of variance?

 \Rightarrow A single value cannot show variability in the predicted value



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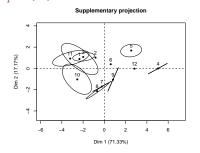
 \Rightarrow A single value cannot show variability in the predicted value

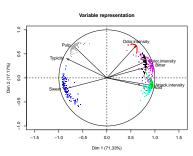


 \Rightarrow Multiple imputation : generate several plausible values for each missing data point

```
> mi <- MIPCA(orange, scale = TRUE, ncp=2)
> plot(mi)
```

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> mi <- MIPCA(orange, scale = TRUE, ncp=2)</pre> > plot(mi) Variable representation Supplementary projection 2 Dim 2 (17.17%) Jim 2 (17.17%) -0.5 4 1.0 -1.0 -1.5 -0.5 1.0 1.5 Dim 1 (71.33%) Dim 1 (71.33%) Projection of the Principal Components Multiple imputation using Procrustes Dim 2 (17.17%)

Dim 2 (17.17%)

Dim 1 (71.33%)

-1.0

Dim 1 (71.33%)

1.0