Cluster Analysis: Identifying Parkinson's Disease Subtypes

July 22, 2015

1 Preprocessing

1.1 Dataset Description

951 subjects, 145 metrics, collected 15-4-2012 from Pablo Martinez Martín. Only 19 features used for clustering and/or interpretation. 50 subjects with missing values of the features to be used in clustering (brought down to 901). Imputation may be a good idea later on.

1.2 Selected Features

Combination of non-motor scale (NMS) symptoms and standard motor symptoms. Note: PIGD was deleted after 2015-07-16 meeting.

Name	Type	Format	Description
nms_d1	byte	%8.0g	cardiovascular
nms_d2	byte	%8.0g	sleep/fatigue
nms_d3	byte	%8.0g	mood/cognition
$nms_{-}d4$	byte	%8.0g	percep/hallucinations
$nms_{-}d5$	byte	%8.0g	attention/memory
$nms_{-}d6$	byte	%8.0g	gastrointestinal
$\mathrm{nms}_{-}\mathrm{d}7$	byte	%8.0g	urinary
nms_d8	byte	%8.0g	sexual function
nms_d9	byte	%8.0g	miscellaneous
tremor	float	%9.0g	tremor
bradykin	float	%9.0g	bradykinesia ¹
rigidity	float	%9.0g	rigidity
axial	float	%9.0g	$axial^2$

Table 1: Selected Features and Details

¹Impaired ability to adjust the body's position.

²Issues affecting the middle of the body.

Name	μ	σ	min-max
nms_d1	1.73	3.35	0-24
nms_d2	8.75	8.70	0-48
$nms_{-}d3$	8.68	11.55	0-60
nms_d4	1.64	3.86	0-33
nms_d5	5.42	7.43	0-36
nms_d6	5.53	6.79	0-36
$\mathrm{nms_d7}$	8.08	8.94	0-36
nms_d8	3.52	5.97	0-24
nms_d9	7.13	7.79	0-48
tremor	2.59	2.58	0-12
bradykin	2.40	1.41	0-6
rigidity	2.24	1.36	0-6
axial	3.25	2.68	0-12

Table 2: Descriptive Statistics

$\mathbf{2}$ k-means

k-means clustering with k = 4 was tried. k = 2, 3 provided models that were too simplistic. k = 5 did not provide any new information, but rather just fragmented existing groups.

Table 3: Cluster statistics

Cluster	n
1	189
2	88
3	221
4	406

2.1 Decision tree

2.2 Interpretation of Clusters

2.2.1 Cluster summaries

Available in Figure 2. Error bar is standard error.

2.2.2 Interpretation

2.2.3 Statistical Significance Tests, k = 4

Using one-way ANOVA for multiple means, we reject the null hypothesis that the means are the same with p < 0.05 for every variable except pdonset.

Post-hoc analysis using Tukey's HSD:

```
age insignificant differences:
          diff
                     lwr
                               upr
                                       p adj
3-1 0.9947808 -1.458184 3.4477455 0.7236845
4-1 -1.2838898 -3.464063 0.8962832 0.4284274
sex insignificant differences:
           diff
                       lwr
                                  upr
                                           p adj
2-1 -0.05044493 -0.2106093 0.10971941 0.84945412
4-1 -0.09897829 -0.2082638 0.01030726 0.09181043
3-2 -0.12633690 -0.2827741 0.03010026 0.16087872
4-2 -0.04853336 -0.1944676 0.09740091 0.82744866
4-3 0.07780354 -0.0259428 0.18154987 0.21607772
pdonset insignificant differences:
          diff
                      lwr
                               upr
                                       p adj
2-1 2.9315777 -0.6232172 6.486373 0.1466742
3-1 1.7136632 -1.0153886 4.442715 0.3699280
4-1 0.7453932 -1.6801637 3.170950 0.8585776
3-2 -1.2179144 -4.6899860 2.254157 0.8033301
4-2 -2.1861845 -5.4251477 1.052779 0.3049434
4-3 -0.9682701 -3.2708860 1.334346 0.7004488
durat_pd insignificant differences:
          diff
                     lwr
                                upr
3-1 -0.7188824 -2.140915 0.7031499 5.624040e-01
cisitot insignificant differences:
          diff
                       lwr
                                            p adj
3-1 0.4942421 -0.4388731 1.427357 5.228228e-01
nms_d1 insignificant differences:
          diff
                      lwr
4-3 -0.3798787 -0.9604053 0.2006478 3.325894e-01
nms_d4 insignificant differences:
          diff
                      lwr
                                 upr
4-3 -0.3362459 -0.9972012 0.3247094 5.571480e-01
nms_d5 insignificant differences:
           diff
                       lwr
                                   upr
4-3 -0.4117201 -1.743630
                             0.9201902 8.564409e-01
nms_d8 insignificant differences:
          diff
                      lwr
                                 upr
4-3 -0.9953302 -2.1560641 0.1654036 1.220509e-01
nms_d9 insignificant differences:
                     lwr
          diff
                                upr
2-1 0.8708514 -1.297413 3.03911557 0.72966265
4-3 -1.3221920 -2.726684 0.08229967 0.07350641
tremor insignificant differences:
          diff
                       lwr
                                  upr
```

4-1 0.3346105 -0.19270261 0.8619236 3.603863e-01

2.2.4 Ranked Features by Information Gain

Table 4: Features ranked by information gain

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	variable	information gain
	bradykin	0.31574672
	rigidity	0.29560018
	nms_d2	0.24218407
	cisitot	0.22920103
	axial	0.22780750
	nms_d3	0.20480570
	nms_d9	0.15782743
	nms_d7	0.15290569
	nms_d5	0.14454931
	$nms_{-}d6$	0.14025139
	nms_d1	0.13212756
	tremor	0.10937168
	nms_d4	0.10710526
	nms_d8	0.10005480
	$durat_pd$	0.02876190
	age	0.02346158
	sex	0.00000000
	pdonset	0.00000000

2.2.5 Correlation Plots

Figure 3.

2.2.6 One vs all decision trees

Figures 4, 5, 6, 7.

3 Other Work

3.1 Bayesian Networks

In Figure 8. Structure is too sparse, need to discretize or use some kind of regularization (e.g. a lasso)

UNSCALED Pruned Tree, 4 clusters

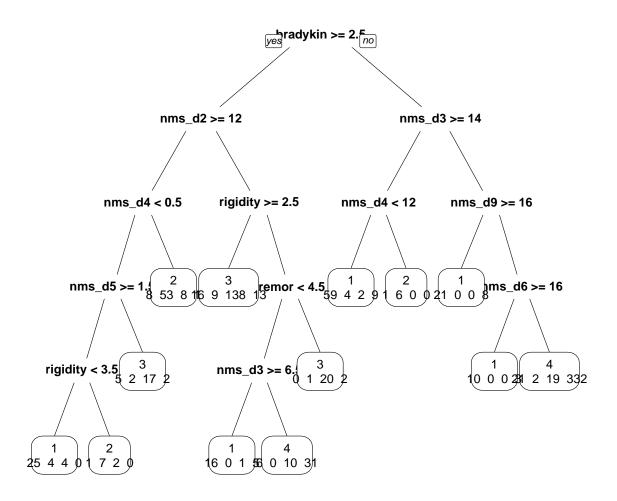


Figure 1: Decision Tree from k-means clustering, 4 clusters

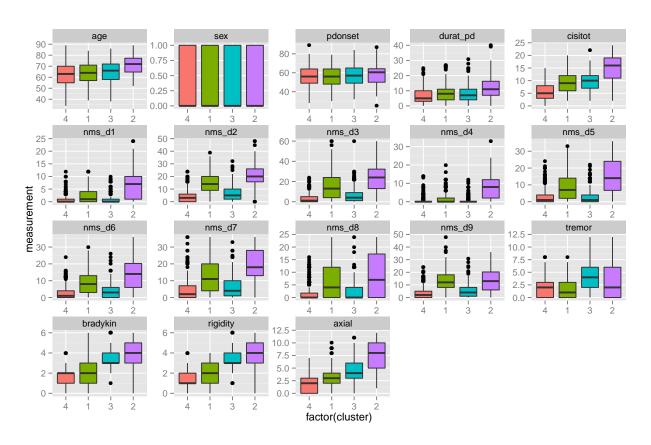


Figure 2: Cluster Summaries, k=4

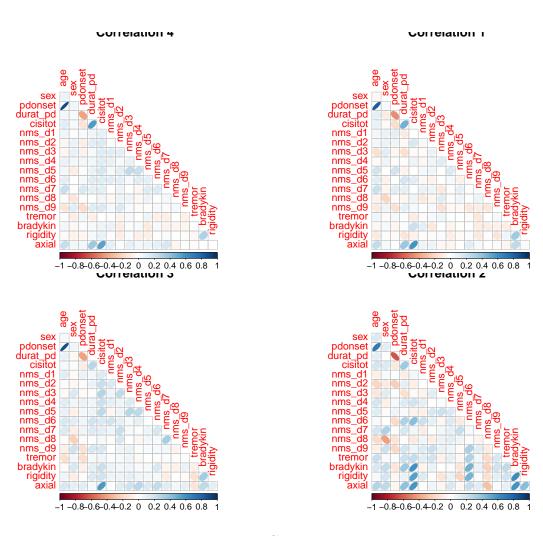


Figure 3: Correlation plots

Pruned 1 vs all

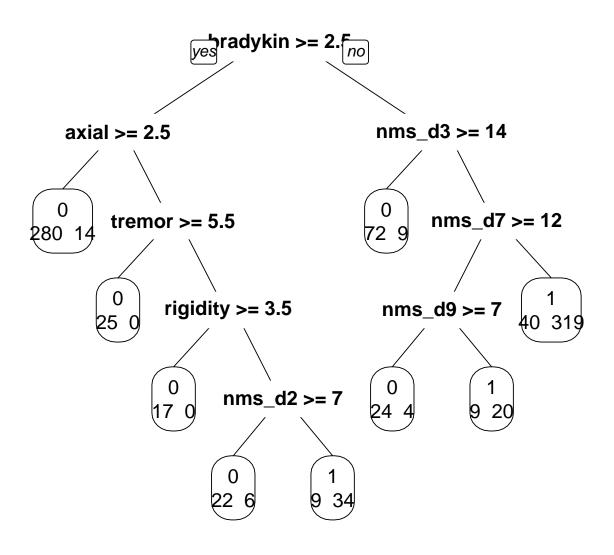


Figure 4: Cluster 1 vs all

Pruned 2 vs all

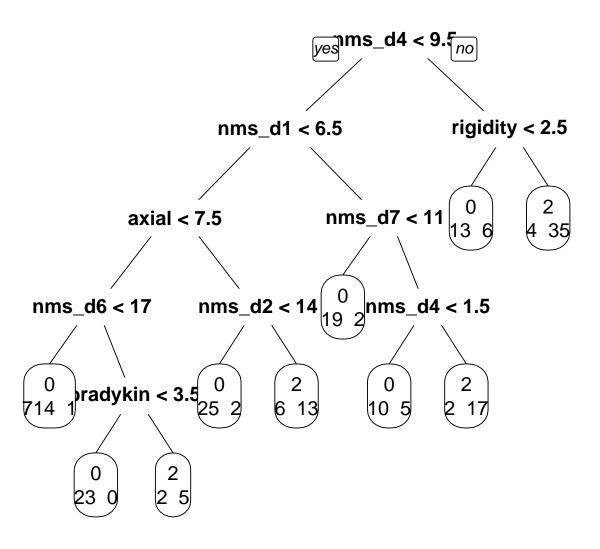


Figure 5: Cluster 2 vs all

Pruned 3 vs all

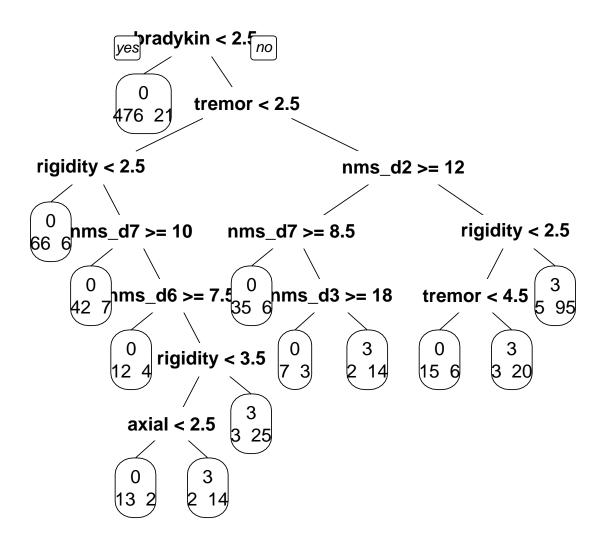


Figure 6: Cluster 3 vs all

Pruned 4 vs all

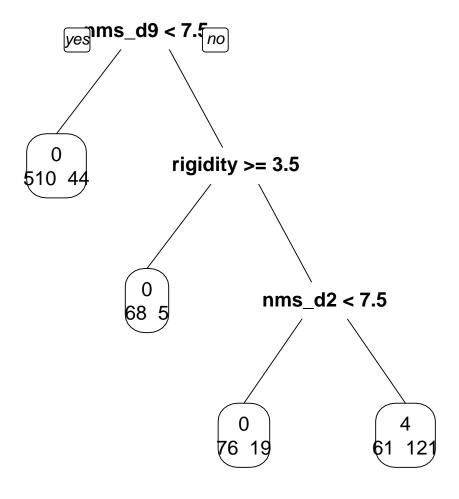


Figure 7: Cluster 4 vs all

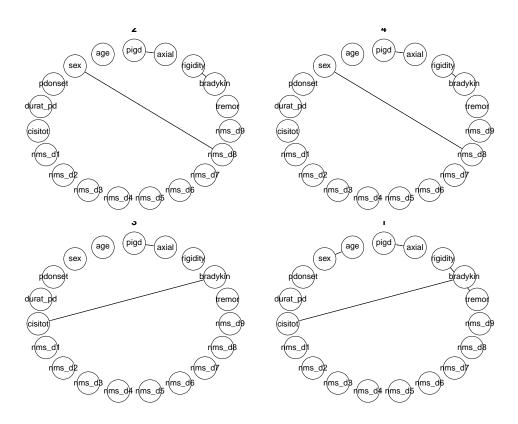


Figure 8: Bayesian Networks