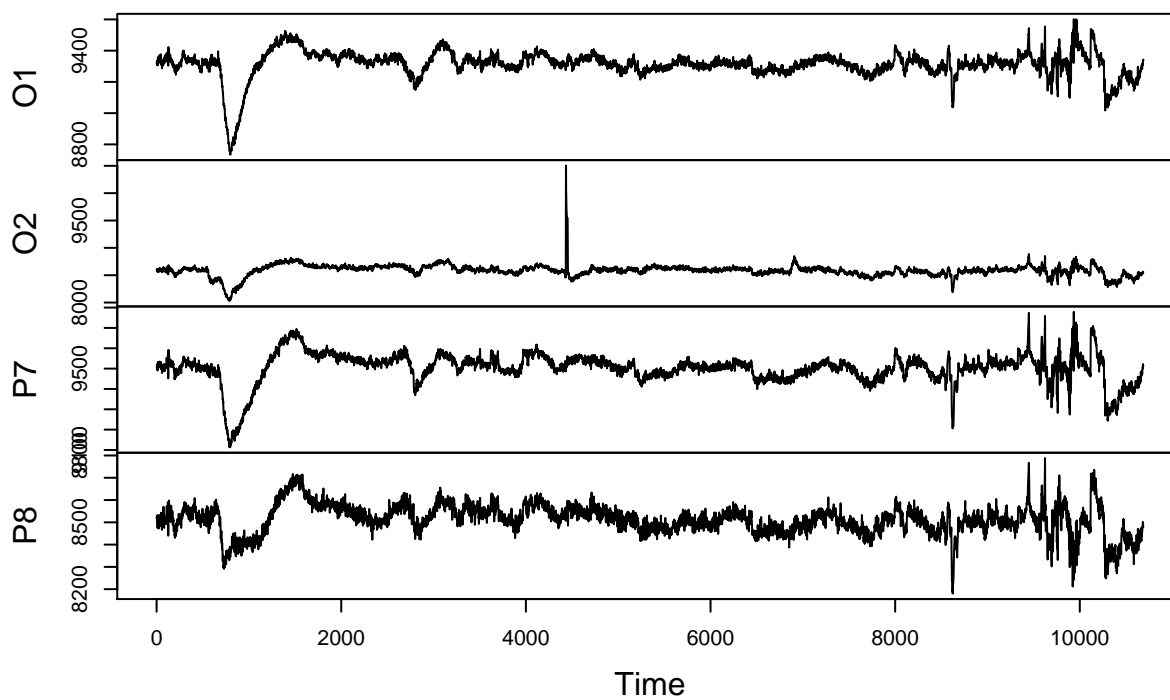


## EEG signaal

O1	O2	P7	P8
9317	8587	9507	8518
9327	8604	9510	8526
9334	8613	9517	8519
9334	8611	9521	8531
9326	8598	9512	8529
9311	8580	9507	8506

## EEG signaal



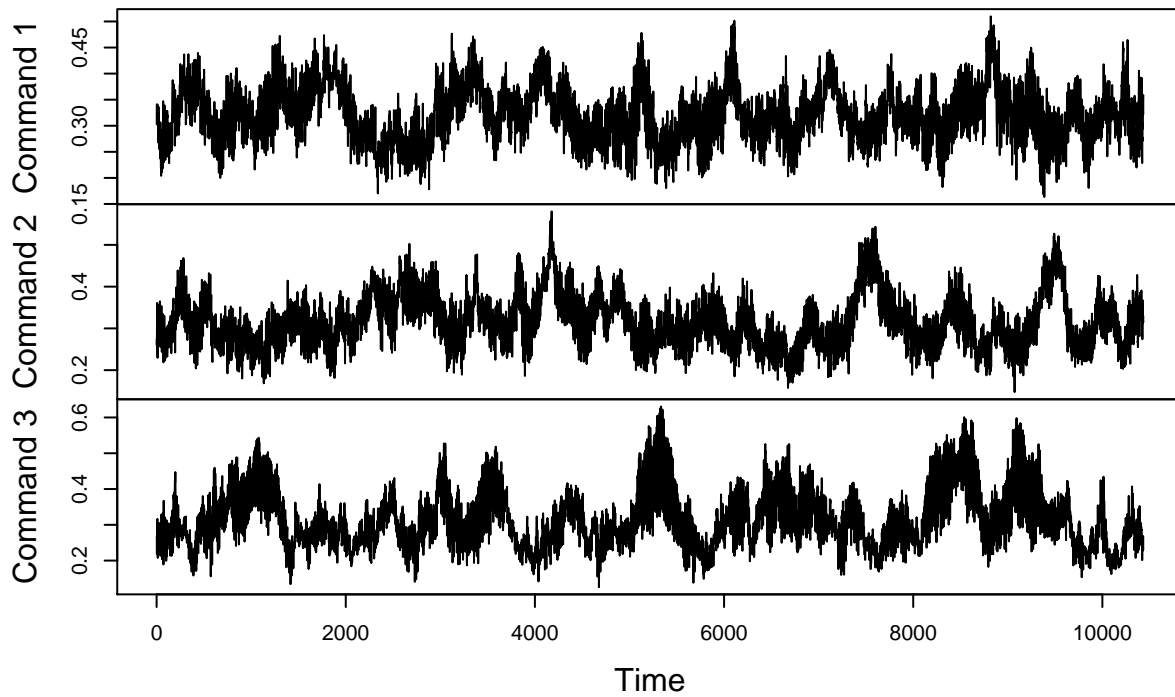
## Kasutatud sagedused

ID	Frequency
1	6.666667
2	7.500000
3	8.571429

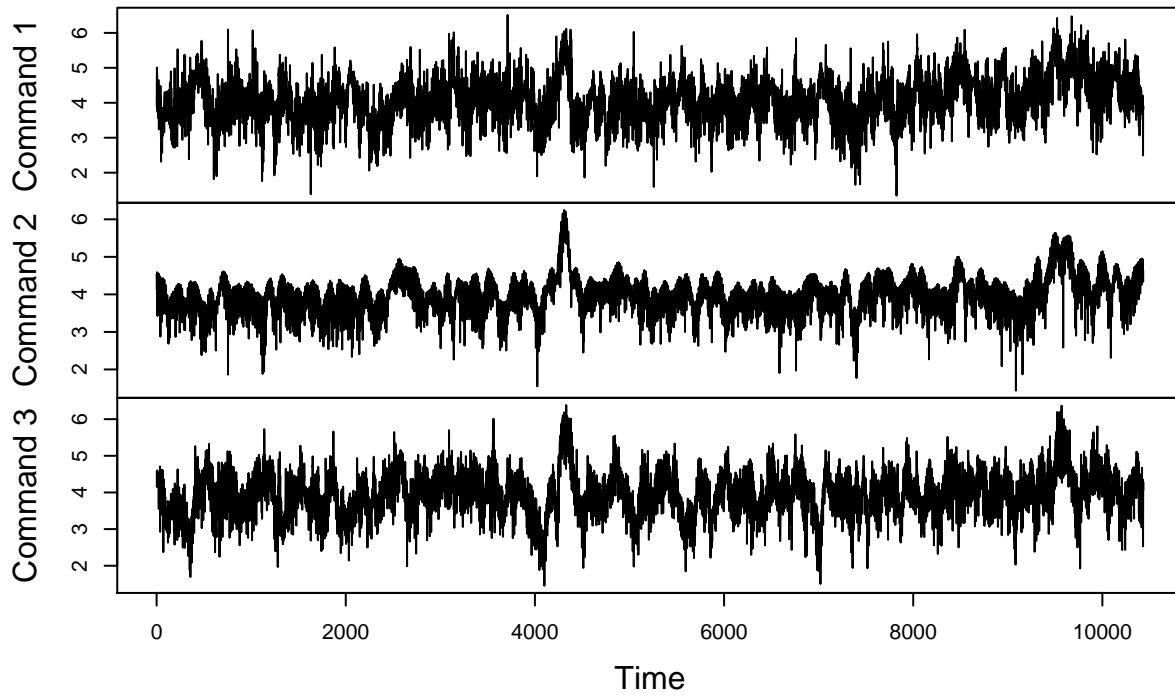
## EEG signaalist eraldatud tunnused

PSDA_sum_f1	PSDA_sum_f2	PSDA_sum_f3	CCA_f1	CCA_f2	CCA_f3
3.896971	4.119254	4.575920	0.3028430	0.2741514	0.2669149
4.474294	4.549097	4.406292	0.3335525	0.2597220	0.2564238
5.010334	4.474692	4.151357	0.3411201	0.2703358	0.2189455
4.915839	4.368423	4.323578	0.3289583	0.3110394	0.2421184
4.867986	4.590158	4.520489	0.3165068	0.3610076	0.2756416
4.702446	4.580038	4.602424	0.3026591	0.3378599	0.2960716

### Features extracted by CCA



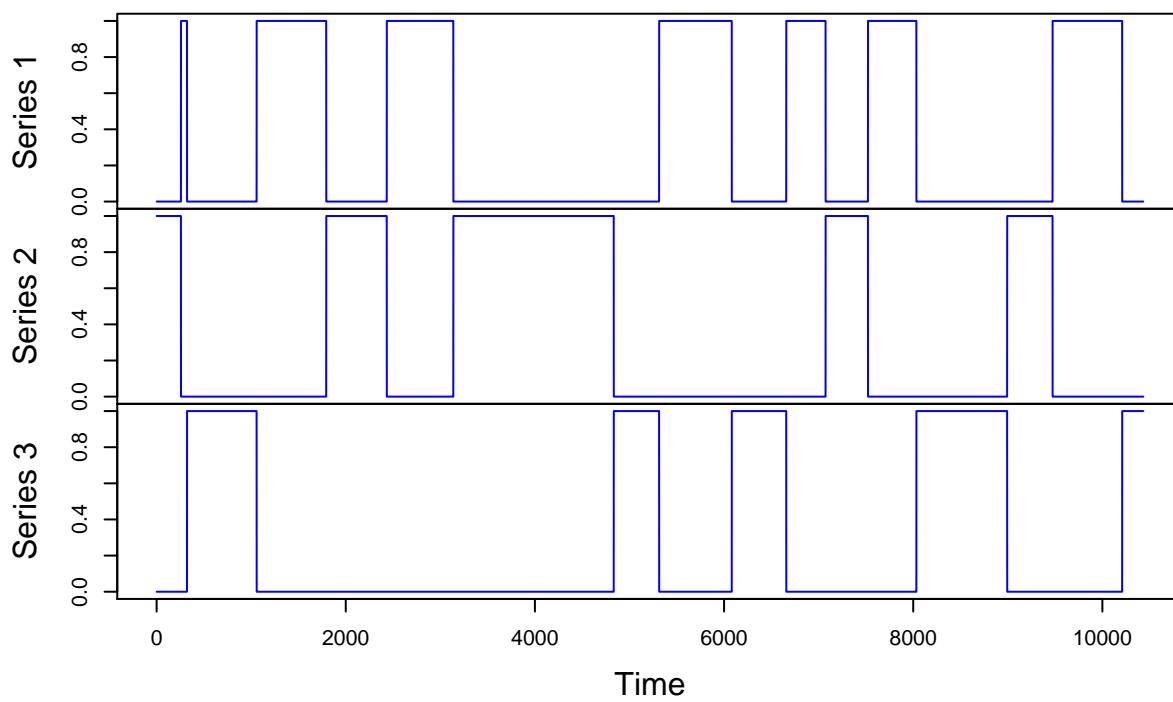
## Features extracted by PSDA for channel O1



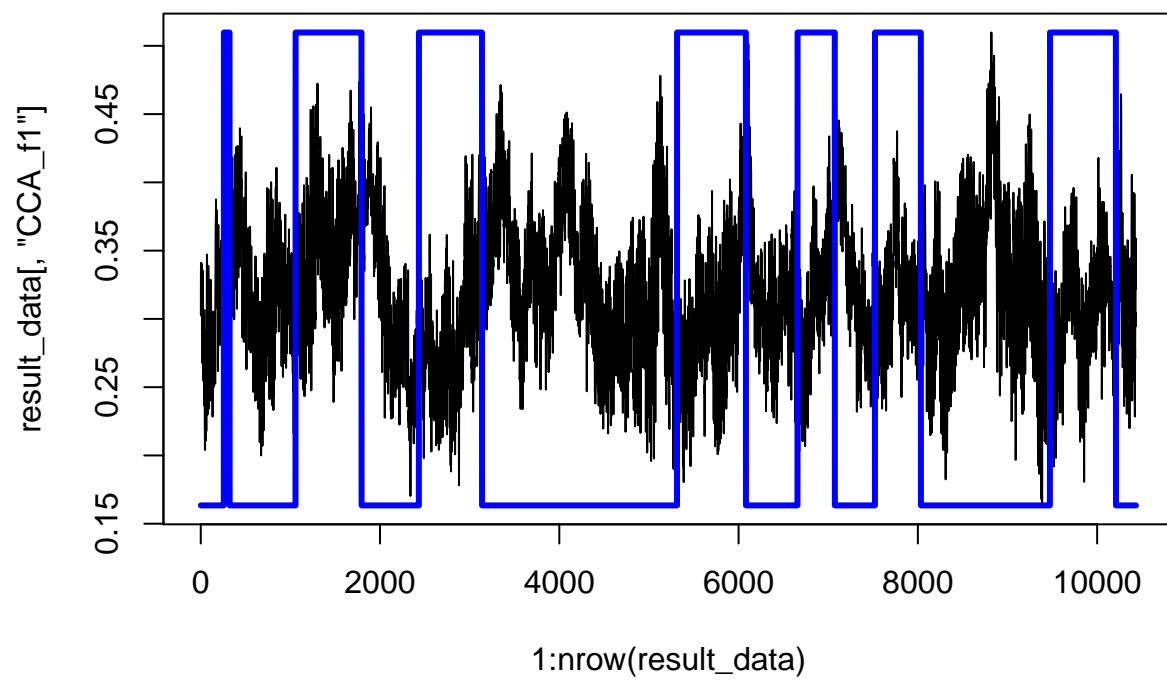
```
plot(ts(result_data[c("CCA_f1", "CCA_f2", "CCA_f3")]), main="Kanoonilise korrelatsioonanalüüsi  
eraldatud tunnused") plot(ts(result_data[c("PSDA_sum_f1", "PSDA_sum_f2", "PSDA_sum_f3")]),  
main="Võimsusspektri analüüsi eraldatud tunnused") # Oodatav (perfektne) tulemus
```

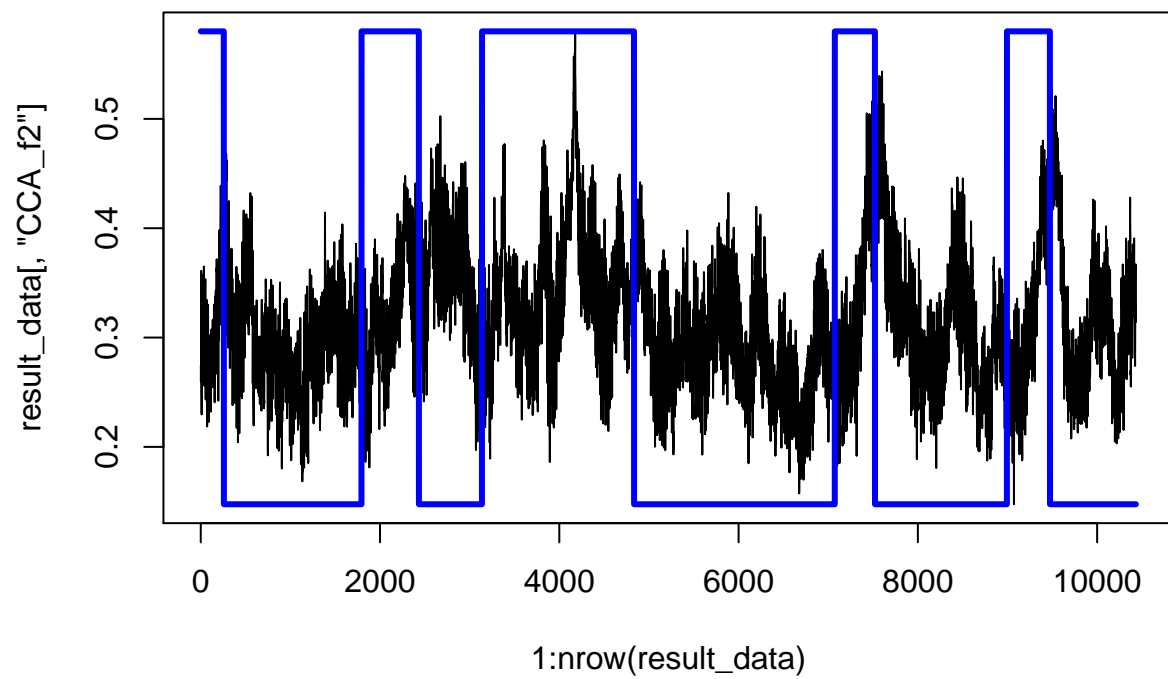
Start	Stop	Target
1	512	2
513	576	1
577	1312	3
1313	2048	1
2049	2688	2
2689	3392	1
3393	5088	2
5089	5568	3
5569	6336	1
6337	6912	3
6913	7328	1
7329	7776	2
7777	8288	1
8289	9248	3
9249	9728	2
9729	10464	1
10465	10688	3

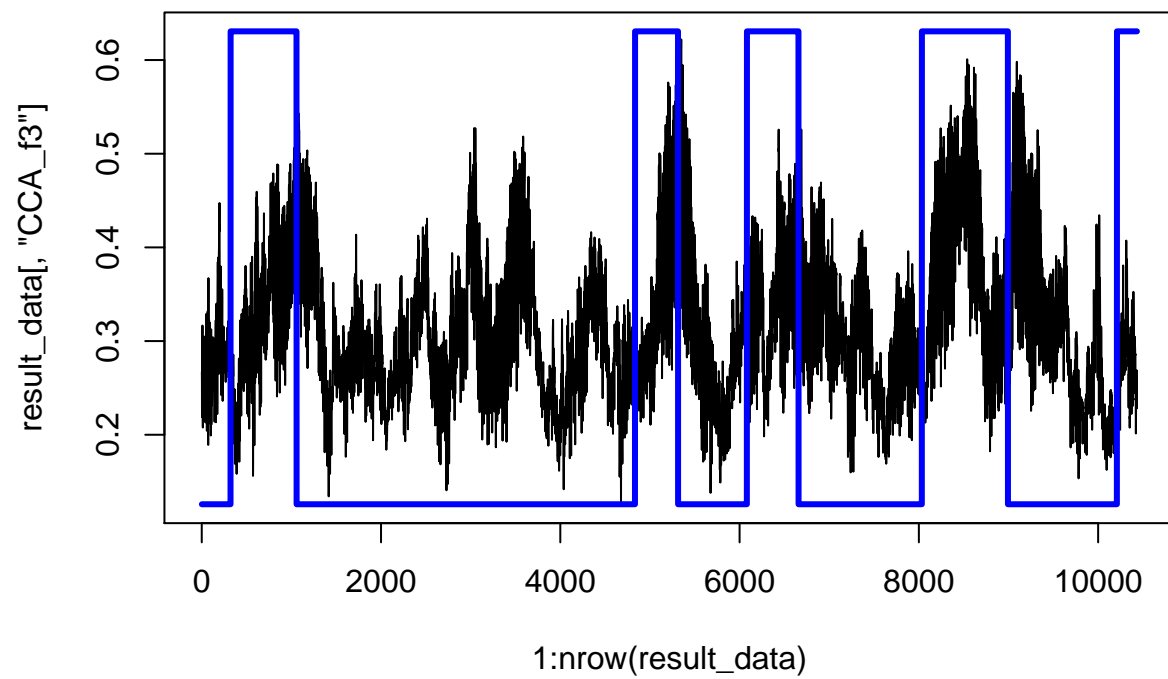
## Oodatav tulemus



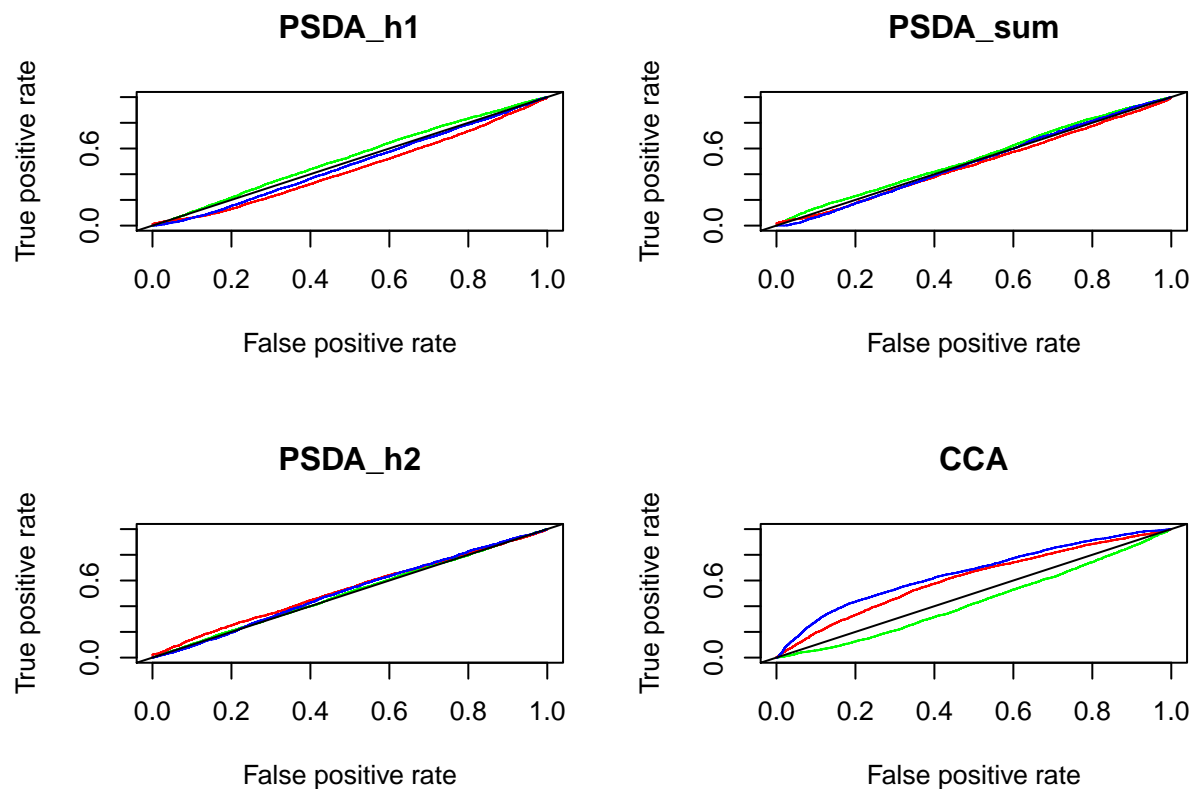
Eraldatud tunnused + oodatav (perfektne) tulemus







## ROC kőver



```
## Warning in read.table("prinoneh.txt"): incomplete final line found by
## readTableHeader on 'prinoneh.txt'

## Warning in read.table("prinmaxh.txt"): incomplete final line found by
## readTableHeader on 'prinmaxh.txt'

## Warning in read.table("prinsmch.txt"): incomplete final line found by
## readTableHeader on 'prinsmch.txt'

## Warning in read.table("prinitmaxh.txt"): incomplete final line found by
## readTableHeader on 'prinitmaxh.txt'

## Warning in read.table("prinitismch.txt"): incomplete final line found by
## readTableHeader on 'prinitismch.txt'

## Warning in read.table("prinoneh2.txt"): incomplete final line found by
## readTableHeader on 'prinoneh2.txt'

## Warning in read.table("prinmaxh2.txt"): incomplete final line found by
## readTableHeader on 'prinmaxh2.txt'

## Warning in read.table("prinsmch2.txt"): incomplete final line found by
## readTableHeader on 'prinsmch2.txt'
```



```
## Warning in read.table("prinitmaxh2.txt"): incomplete final line found by
## readTableHeader on 'prinitmaxh2.txt'
```

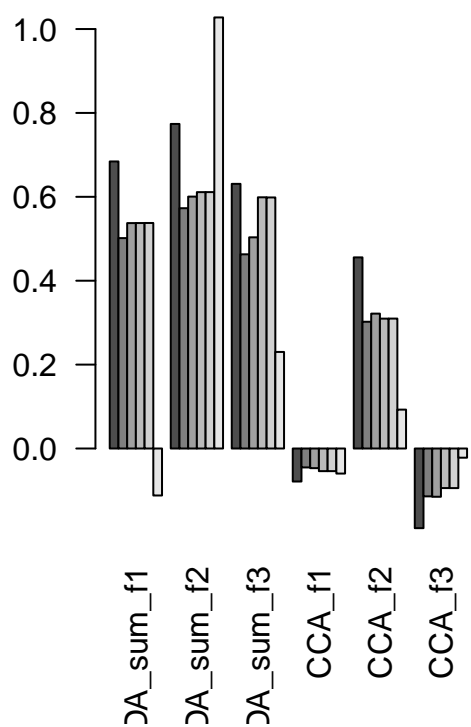
```
## Warning in read.table("prinitismch2.txt"): incomplete final line found by
## readTableHeader on 'prinitismch2.txt'
```

```
## Warning in read.table("tsfah2.txt"): incomplete final line found by
## readTableHeader on 'tsfah2.txt'
```

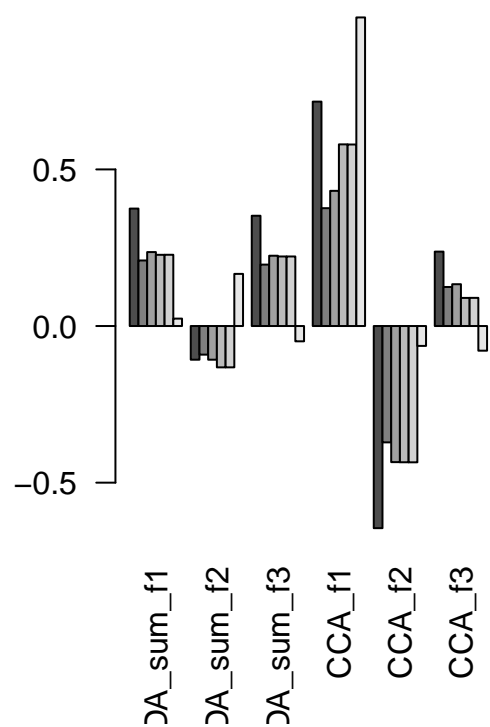
	PK1	PK2	PK3	h^2	PF1max	PF2max	PF3max	h^2	PF1smc	PF2smc	PF3smc
PSDA_sum_f1	0.684	0.375	-0.175	0.639	0.502	0.209	-0.108	0.307	0.537	0.236	-0.144
PSDA_sum_f2	0.774	-0.107	0.057	0.613	0.573	-0.091	0.021	0.337	0.600	-0.108	0.019
PSDA_sum_f3	0.631	0.352	0.397	0.680	0.463	0.196	0.196	0.291	0.503	0.224	0.255
CCA_f1	-0.079	0.716	-0.480	0.750	-0.045	0.376	-0.213	0.189	-0.047	0.431	-0.266
CCA_f2	0.456	-0.645	-0.123	0.639	0.302	-0.371	-0.066	0.234	0.322	-0.434	-0.094
CCA_f3	-0.190	0.238	0.826	0.775	-0.114	0.125	0.333	0.140	-0.115	0.134	0.392

	PFit1max	PFit2max	PFit3max	h^2	PFit1smc	PFit2smc	PFit3smc	h^2	TSFA1	TSFA2
PSDA_sum_f1	0.538	0.227	-0.165	0.368	0.538	0.227	-0.165	0.368	-0.112	0.019
PSDA_sum_f2	0.611	-0.132	-0.058	0.394	0.611	-0.132	-0.058	0.394	1.028	0.101
PSDA_sum_f3	0.599	0.222	0.347	0.528	0.598	0.222	0.347	0.528	0.230	-0.041
CCA_f1	-0.054	0.580	-0.292	0.424	-0.054	0.580	-0.292	0.424	-0.060	0.981
CCA_f2	0.310	-0.435	-0.198	0.324	0.310	-0.435	-0.198	0.324	0.093	-0.001
CCA_f3	-0.094	0.090	0.400	0.177	-0.094	0.090	0.400	0.177	-0.022	-0.001

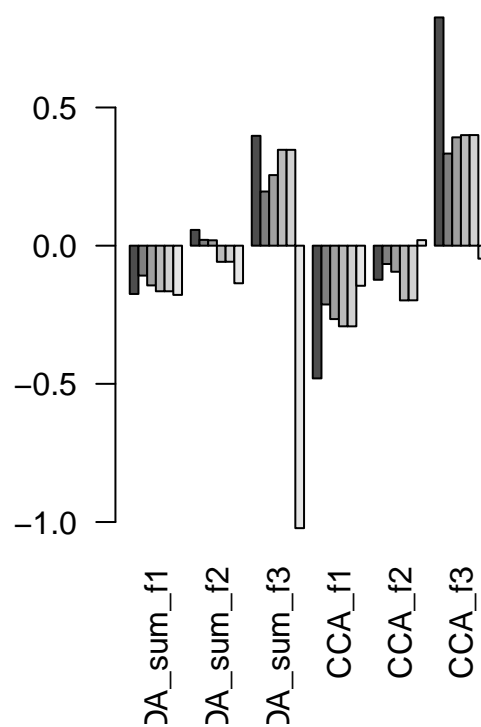
**Faktor 1 faktorkaalud**



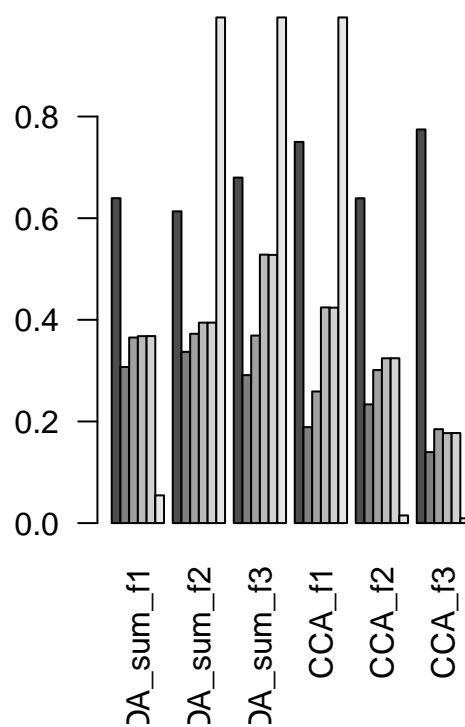
**Faktor 2 faktorkaalud**



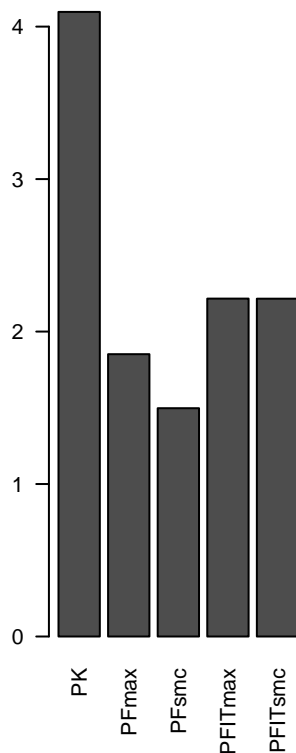
**Faktor 3 faktorkaalud**



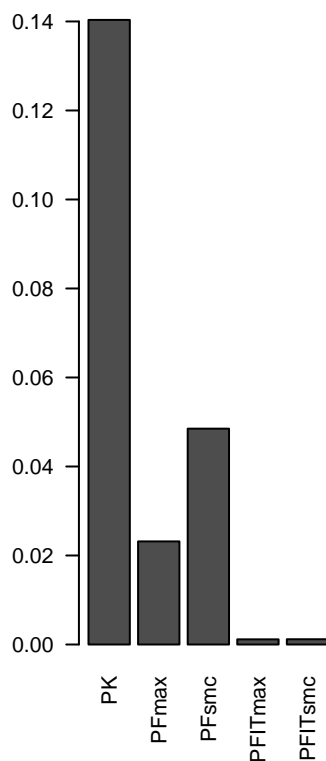
**Kommunaliteetid**



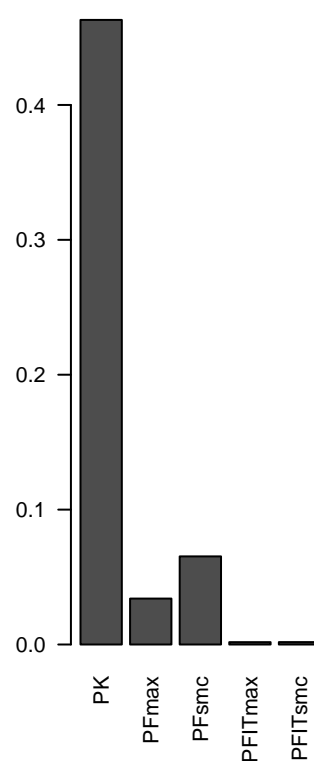
Summaarne kirjeldatus



RMS jääkkorrelatsioon



RMS osakorrelatsioon

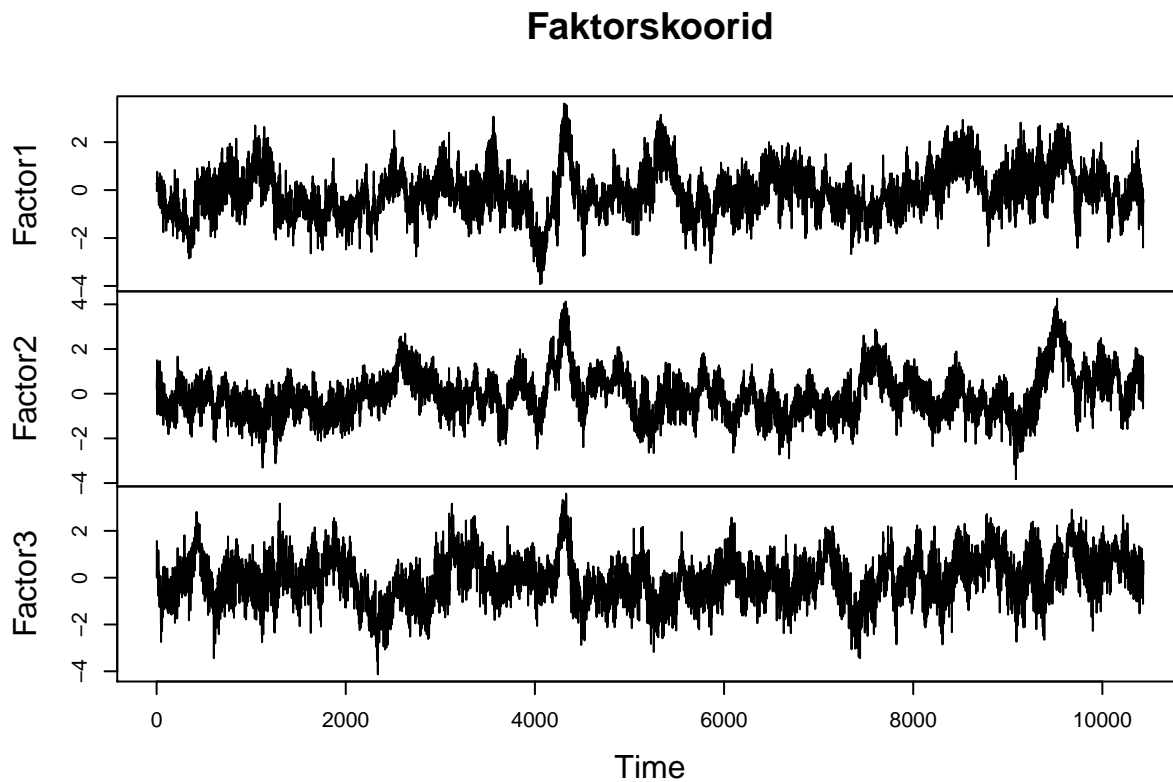


TSFA stats	
chisq	21.142
df	0.000
pval	0.000
delta	21.142
RMSEA	Inf
RNI	0.978
CFI	0.978
MCI	0.999
GFI	0.999
AGFI	-Inf
AIC	21.142
CAIC	236.447
SIC	215.447
CAK	0.006
CK	0.006

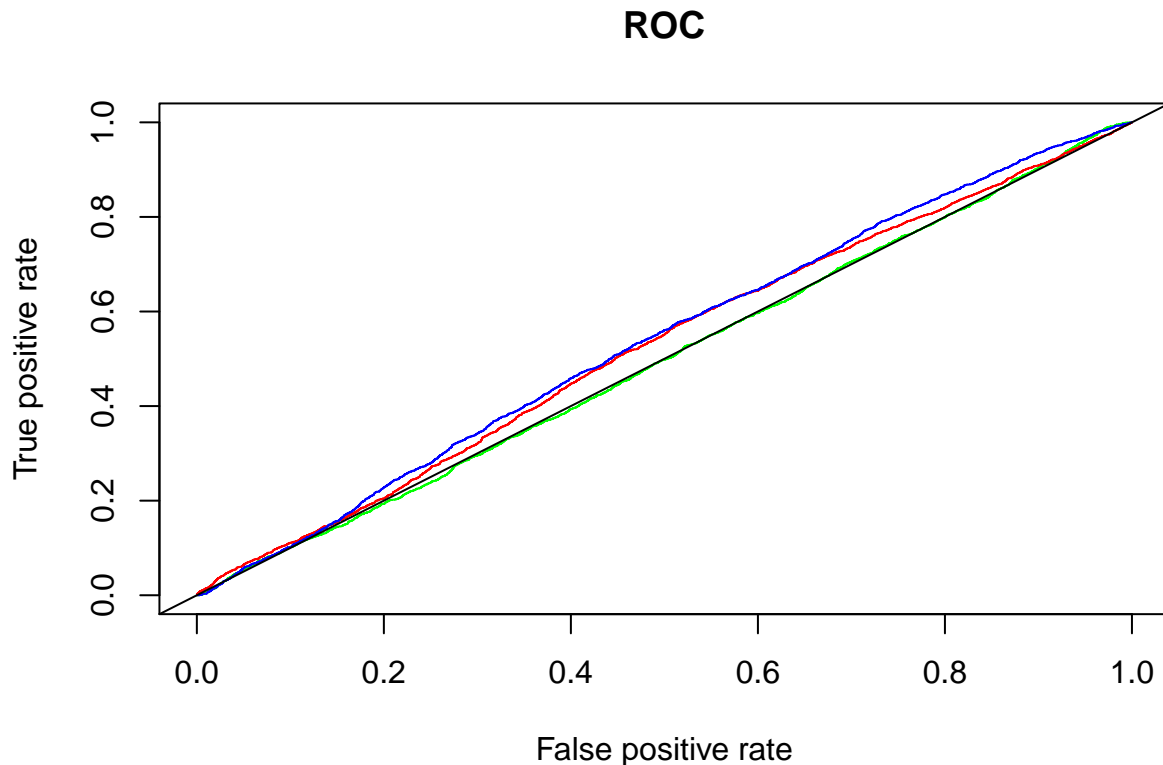
```
setwd("C:\\Users\\Anti\\Desktop\\sas\\SASUniversityEdition\\myfolders")
factor_data <- read.csv("RESULT.csv", header=TRUE)[c("Factor1", "Factor2", "Factor3")]
setwd("C:\\Users\\Anti\\Desktop\\sas\\tables")
kaalud <- read.table("kaalud.txt")
knitr::kable(kaalud)
```

	Factor1	Factor2	Factor3
PSDA_sum_f1	0.62812	0.30874	0.13446
PSDA_sum_f2	0.13817	0.68518	0.17718
PSDA_sum_f3	0.27704	0.24354	0.63875
CCA_f1	0.82040	-0.50680	-0.17655
CCA_f2	-0.30542	0.80031	-0.26788
CCA_f3	-0.32417	-0.36382	0.80956

```
plot(ts(factor_data), main="Faktorskoorid")
```



```
plot_rocs(factor_data, true_labels, list(ROC=c("Factor1", "Factor2", "Factor3")))
```



```
library(TTR)
#avg <- as.data.frame(apply(factor_data, 2, function(x){SMA(x, 64)})[64:nrow(factor_data),])
#plot_rocs(avg, true_labels[64:length(true_labels)], list(Faktor=c("Factor1", "Factor2", "Factor3")))

# setwd("C:\\Users\\Anti\\Desktop\\PycharmProjects\\MAPProject\\data")
# trial_data <- read.csv("test5_targets_3.csv", header=TRUE, sep=" ")
# setwd("C:\\Users\\Anti\\Desktop\\PycharmProjects\\MAPProject\\data")
# result_data <- read.csv("test5_results_3_all.csv", header=TRUE, sep=" ")
# setwd("C:\\Users\\Anti\\Desktop\\sas\\SASUniversityEdition\\myfolders")
# factor_data <- read.csv("RESULT123.csv", header=TRUE)[c("Factor1", "Factor2", "Factor3")]
#
# true_labels = get_true_labels(trial_data)
# plot_rocs(result_data, true_labels, method_names)
#
# plot_rocs(factor_data, true_labels[1:11884], list(ROC=c("Factor1", "Factor2", "Factor3")))

classify_results <- function(input_data, method_names) {
  result = matrix(NA, nrow=nrow(input_data), ncol=length(method_names)*3)
  overall = matrix(NA, nrow=nrow(input_data), 2)
  for (j in 1:length(method_names)) {
    for (i in 1:nrow(input_data)) {
      method_data <- input_data[i, method_names[[j]]]
      index <- order(method_data, decreasing=TRUE)
      result[i, (j-1)*3+index[1]] <- method_data[index[1]]/sum(method_data)+2
      result[i, (j-1)*3+index[2]] <- method_data[index[2]]/sum(method_data)+1
      result[i, (j-1)*3+index[3]] <- method_data[index[3]]/sum(method_data)
    }
  }
}
```

```

        overall[i,] <- c(index[1], method_data[index[1]]/sum(method_data))
    }
}
colnames(result) <- unlist(method_names)
list(result=as.data.frame(result), overall=overall)
}

#classified = classify_results(factor_data, list(Faktor=c("Factor1", "Factor2", "Factor3")))

```