EEG Feature Analysis

Contents

Introduction 1

Analysis preparation 1

Pre-processing 2

Analysis 5

Implications 86

Authors: Agata Belczyk, Jakub Ner

Introduction

We prepared EEG analysis using R library EEG Utils.

We analyze eeg datasets from "A Study on Mental State Classification using EEG-based Brain-Machine Interface", where 3 experiment epochs were introduced to cover the three mental states: relaxed, neutral and concentrating. The relaxed task required the participant to listen to low-tempo music and sound effects designed to aid in meditation whilst being instructed on relaxing their muscles and resting. For a neutral mental, a similar test was carried out, but without stimulus at all. For a concentration, the subject had to play a guessing game. The whole dataset consists of 22 eeg recording of 4 different subjects.

Analysis preparation

We install, import dependencies, set const values and import datasets:

```r
remotes::install_github("craddm/eegUtils")
library(ggplot2)
library(eegUtils)
library(readxl)
library(tibble)

options(digits=15) # show whole numbers

# CONSTS
SAMPLING_RATE <- 250


a_concentrating_1_init <- read.csv("./dataset//subjecta-concentrating-1.csv")
a_concentrating_2_init <- read.csv("./dataset//subjecta-concentrating-2.csv")
a_neutral_1_init <- read.csv("./dataset//subjecta-neutral-1.csv")
a_neutral_2_init <- read.csv("./dataset//subjecta-neutral-2.csv")
a_relaxed_1_init <- read.csv("./dataset//subjecta-relaxed-1.csv")
```

```
a_relaxed_2_init <- read.csv("./dataset//subjecta-relaxed-2.csv")

b_concentrating_1_init <- read.csv("./dataset//subjectb-concentrating-1.csv")
b_concentrating_2_init <- read.csv("./dataset//subjectb-concentrating-2.csv")
b_neutral_1_init <- read.csv("./dataset//subjectb-neutral-1.csv")
b_neutral_2_init <- read.csv("./dataset//subjectb-neutral-2.csv")
b_relaxed_1_init <- read.csv("./dataset//subjectb-relaxed-1.csv")
b_relaxed_2_init <- read.csv("./dataset//subjectb-relaxed-2.csv")

c_concentrating_1_init <- read.csv("./dataset//subjectc-concentrating-1.csv")
c_concentrating_2_init <- read.csv("./dataset//subjectc-concentrating-2.csv")
c_neutral_1_init <- read.csv("./dataset//subjectc-neutral-1.csv")
#c_neutral_2_init <- read.csv("./dataset//subjectc-neutral-2.csv")
c_relaxed_1_init <- read.csv("./dataset//subjectc-relaxed-1.csv")
c_relaxed_2_init <- read.csv("./dataset//subjectc-relaxed-2.csv")

d_concentrating_1_init <- read.csv("./dataset//subjectd-concentrating-1.csv")
# d_concentrating_2 has to few rows
d_neutral_1_init <- read.csv("./dataset//subjectd-neutral-1.csv")
d_neutral_2_init <- read.csv("./dataset//subjectd-neutral-2.csv")
d_relaxed_1_init <- read.csv("./dataset//subjectd-relaxed-1.csv")
d_relaxed_2_init <- read.csv("./dataset//subjectd-relaxed-2.csv")
```

```
head(d_neutral_2_init)
```

```
##       timestamps    TP9   AF7    AF8    TP10 Right.AUX
## 1 1533058130.472 -1.465 6.836 12.695 -77.148    33.691
## 2 1533058130.476  8.301 6.348 -2.930 -81.055   -18.555
## 3 1533058130.480 20.996 7.812  0.488 -75.195    24.902
## 4 1533058130.484 20.508 6.836 16.113 -64.453    65.430
## 5 1533058130.488 11.719 9.766 10.742 -62.988    76.172
## 6 1533058130.492  6.348 9.277  3.906 -70.801    75.195
```

Pre-processing

Firstly we drop first and last 2 seconds of recordings, because it takes time for a subject to obtain a state (concentration, neutral, relaxation).

```
ROWS_TO_DROP <-2 * SAMPLING_RATE
drop <- function(dataset) {
  dataset <- dataset[-c(1:ROWS_TO_DROP, (nrow(dataset) - ROWS_TO_DROP + 1):10000), ]
  return(dataset)
}

a_concentrating_1 <- drop(a_concentrating_1_init)
a_concentrating_2 <- drop(a_concentrating_2_init)
a_neutral_1 <- drop(a_neutral_1_init)
a_neutral_2 <- drop(a_neutral_2_init)
a_relaxed_1 <- drop(a_relaxed_1_init)
a_relaxed_2 <- drop(a_relaxed_2_init)

b_concentrating_1 <- drop(b_concentrating_1_init)
```

```r
b_concentrating_2 <- drop(b_concentrating_2_init)
b_neutral_1 <- drop(b_neutral_1_init)
b_neutral_2 <- drop(b_neutral_2_init)
b_relaxed_1 <- drop(b_relaxed_1_init)
b_relaxed_2 <- b_relaxed_2_init[0:9998,]

c_concentrating_1 <- drop(c_concentrating_1_init)
c_concentrating_2 <- drop(c_concentrating_2_init)
c_neutral_1 <- drop(c_neutral_1_init)
#c_neutral_2 <- drop(c_neutral_2_init)
c_relaxed_1 <- drop(c_relaxed_1_init)
c_relaxed_2 <- drop(c_relaxed_2_init)

d_concentrating_1 <- drop(d_concentrating_1_init)
d_neutral_1 <- drop(d_neutral_1_init)
d_neutral_2 <- drop(d_neutral_2_init)
d_relaxed_1 <- drop(d_relaxed_1_init)
d_relaxed_2 <- drop(d_relaxed_2_init)
```

In the experiment Right.AUX was used for calibration purposes. More specifically as NZ. That's why we rename the mentioned column

```r
rename_to_NZ <- function(dataset){
  names(dataset)[names(dataset) == "Right.AUX"] <- "NZ"
  return(dataset)
}


a_concentrating_1 <- rename_to_NZ(a_concentrating_1)
a_concentrating_2 <- rename_to_NZ(a_concentrating_2)
a_neutral_1 <- rename_to_NZ(a_neutral_1)
a_neutral_2 <- rename_to_NZ(a_neutral_2)
a_relaxed_1 <- rename_to_NZ(a_relaxed_1)
a_relaxed_2 <- rename_to_NZ(a_relaxed_2)

b_concentrating_1 <- rename_to_NZ(b_concentrating_1)
b_concentrating_2 <- rename_to_NZ(b_concentrating_2)
b_neutral_1 <- rename_to_NZ(b_neutral_1)
b_neutral_2 <- rename_to_NZ(b_neutral_2)
b_relaxed_1 <- rename_to_NZ(b_relaxed_1)
#b_relaxed_2 <- rename_to_NZ(b_relaxed_2)

c_concentrating_1 <- rename_to_NZ(c_concentrating_1)
c_concentrating_2 <- rename_to_NZ(c_concentrating_2)
c_neutral_1 <- rename_to_NZ(c_neutral_1)
#c_neutral_2 <- rename_to_NZ(c_neutral_2)
c_relaxed_1 <- rename_to_NZ(c_relaxed_1)
c_relaxed_2 <- rename_to_NZ(c_relaxed_2)

d_concentrating_1 <- rename_to_NZ(d_concentrating_1)
d_neutral_1 <- rename_to_NZ(d_neutral_1)
d_neutral_2 <- rename_to_NZ(d_neutral_2)
d_relaxed_1 <- rename_to_NZ(d_relaxed_1)
```

```
d_relaxed_2 <- rename_to_NZ(d_relaxed_2)

head(a_concentrating_1)
```

```
##          timestamps    TP9    AF7     AF8   TP10      NZ
## 501 1533222561.792 11.719 41.016 -45.410 -4.883 -40.039
## 502 1533222561.796 18.066 36.621   6.836 -7.812  13.672
## 503 1533222561.800 35.156 35.645  89.355 -4.395 -30.762
## 504 1533222561.804 40.527 36.133  76.660  3.906 -46.387
## 505 1533222561.808 23.438 37.109 -40.527 -1.953  34.668
## 506 1533222561.812  1.465 35.156 -41.992 -9.766  67.871
```

To make analysis easier we wrap our dataframes with eeg_epochs

```
wrap <- function(dataset) return(eeg_epochs(
  dataset[,-1],
  srate = SAMPLING_RATE,
  epochs=tibble(epoch=c(1)),
  timings=data.frame(time=seq(1, nrow(dataset)), epoch=rep(1, nrow(dataset)))
  )
)

a_concentrating_1_obj <- wrap(a_concentrating_1)
a_concentrating_2_obj <- wrap(a_concentrating_2)
a_neutral_1_obj <- wrap(a_neutral_1)
a_neutral_2_obj <- wrap(a_neutral_2)
a_relaxed_1_obj <- wrap(a_relaxed_1)
a_relaxed_2_obj <- wrap(a_relaxed_2)

b_concentrating_1_obj <- wrap(b_concentrating_1)
b_concentrating_2_obj <- wrap(b_concentrating_2)
b_neutral_1_obj <- wrap(b_neutral_1)
b_neutral_2_obj <- wrap(b_neutral_2)
b_relaxed_1_obj <- wrap(b_relaxed_1)
b_relaxed_2_obj <- wrap(b_relaxed_2)

c_concentrating_1_obj <- wrap(c_concentrating_1)
c_concentrating_2_obj <- wrap(c_concentrating_2)
c_neutral_1_obj <- wrap(c_neutral_1)
#c_neutral_2_obj <- wrap(c_neutral_2)
c_relaxed_1_obj <- wrap(c_relaxed_1)
c_relaxed_2_obj <- wrap(c_relaxed_2)

d_concentrating_1_obj <- wrap(d_concentrating_1)
d_neutral_1_obj <- wrap(d_neutral_1)
d_neutral_2_obj <- wrap(d_neutral_2)
d_relaxed_1_obj <- wrap(d_relaxed_1)
d_relaxed_2_obj <- wrap(d_relaxed_2)

a_concentrating_1_obj
```

```
## Epoched EEG data
```

```
##
## Number of channels   : 5
## Number of epochs : 1
## Epoch limits     : 1 - 9998 seconds
## Electrode names      : TP9 AF7 AF8 TP10 NZ
## Sampling rate        : 250  Hz
## Reference        :
```

In order to remove artifacts we apply bandpass filter. High-pass filter at 1 Hz removes muscle activity, blinking. Low-pass filter at 100 Hz drops electrical interference and environmental artifacts. Also we applied notch filter to remove electrical interference (50 Hz in UK)

```
apply_filter <- function(eeg_obj){
  eeg_obj <- eeg_filter(eeg_obj, method = "iir", low_freq = 50, high_freq = 49)
  return(
    eeg_filter(eeg_obj, method = "iir", low_freq = 1, high_freq = 100)
  )
}

a_concentrating_1_obj <- apply_filter(a_concentrating_1_obj)
a_concentrating_2_obj <- apply_filter(a_concentrating_2_obj)
a_neutral_1_obj <- apply_filter(a_neutral_1_obj)
a_neutral_2_obj <- apply_filter(a_neutral_2_obj)
a_relaxed_1_obj <- apply_filter(a_relaxed_1_obj)
a_relaxed_2_obj <- apply_filter(a_relaxed_2_obj)

b_concentrating_1_obj <- apply_filter(b_concentrating_1_obj)
b_concentrating_2_obj <- apply_filter(b_concentrating_2_obj)
b_neutral_1_obj <- apply_filter(b_neutral_1_obj)
b_neutral_2_obj <- apply_filter(b_neutral_2_obj)
b_relaxed_1_obj <- apply_filter(b_relaxed_1_obj)
b_relaxed_2_obj <- apply_filter(b_relaxed_2_obj)

c_concentrating_1_obj <- apply_filter(c_concentrating_1_obj)
c_concentrating_2_obj <- apply_filter(c_concentrating_2_obj)
c_neutral_1_obj <- apply_filter(c_neutral_1_obj)
#c_neutral_2_obj <- apply_filter(c_neutral_2_obj)
c_relaxed_1_obj <- apply_filter(c_relaxed_1_obj)
c_relaxed_2_obj <- apply_filter(c_relaxed_2_obj)

d_concentrating_1_obj <- apply_filter(d_concentrating_1_obj)
d_neutral_1_obj <- apply_filter(d_neutral_1_obj)
d_neutral_2_obj <- apply_filter(d_neutral_2_obj)
d_relaxed_1_obj <- apply_filter(d_relaxed_1_obj)
d_relaxed_2_obj <- apply_filter(d_relaxed_2_obj)
```

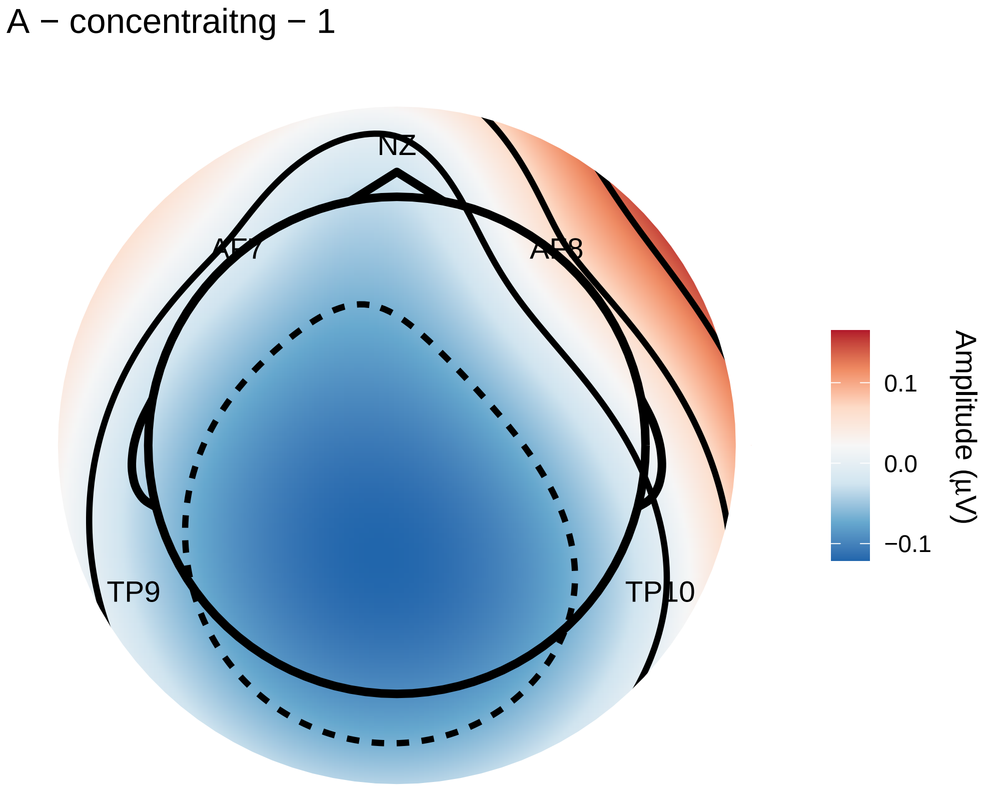
Analysis

In order to analyse Brain-Computer-Interface data, we need to utilize simplifications, due to low spatial resolution and noise sensitivity. We leverage left-brain, right-brain dominance theory (Corballis, 2014; Joseph, 1988).

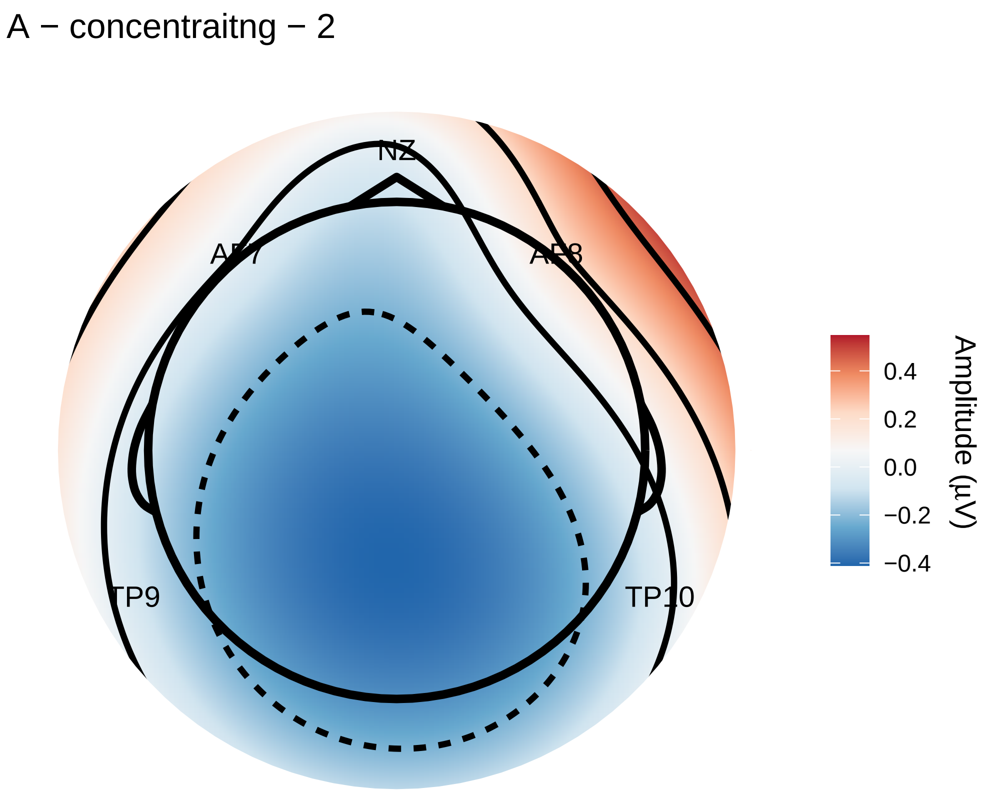
Spatial analysis

Below we visualize placement of **TP9** (temporal-parietal) **AF7** (auricular-frontal) **AF8** **TP10** **NZ** electrodes on the subjects heads with averaged signals around the area. Blue areas suggest decreased activity, while red increased. Due to low spatial resolution (non-invasive and small amount of channels), analysis results are ambiguous and it's hard to draw conclusions.

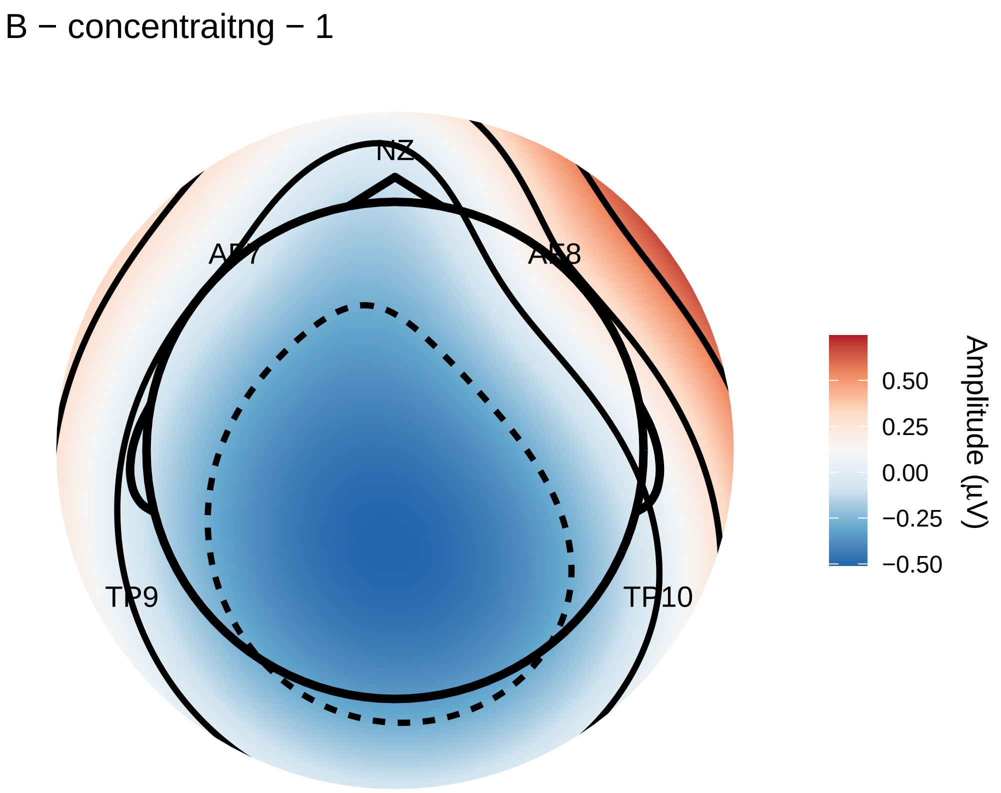
```
show_topplot <- function(eeg_obj, plot_title) {
  return (topoplot(electrode_locations(eeg_obj), chan_marker = "name") + ggtitle(plot_title))
}


show_topplot(a_concentrating_1_obj, "A - concentraitng - 1")
```



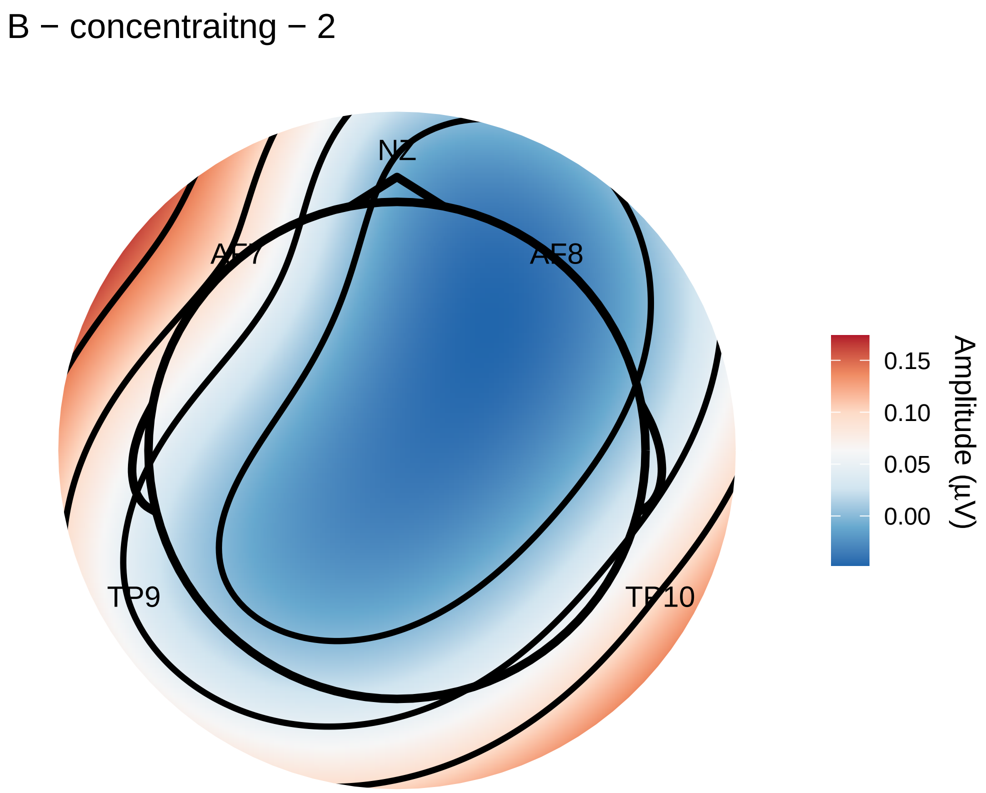
```
show_topplot(a_concentrating_2_obj, "A - concentraitng - 2")
```



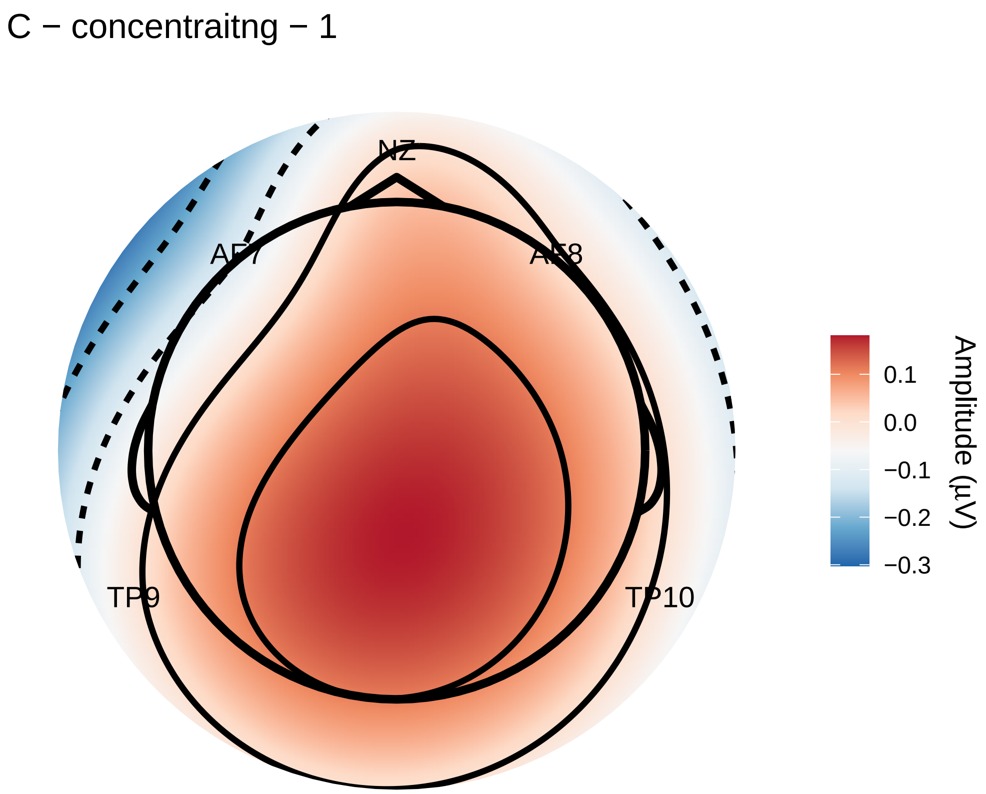
```r
show_topplot(b_concentrating_1_obj, "B - concentraitng - 1")
```



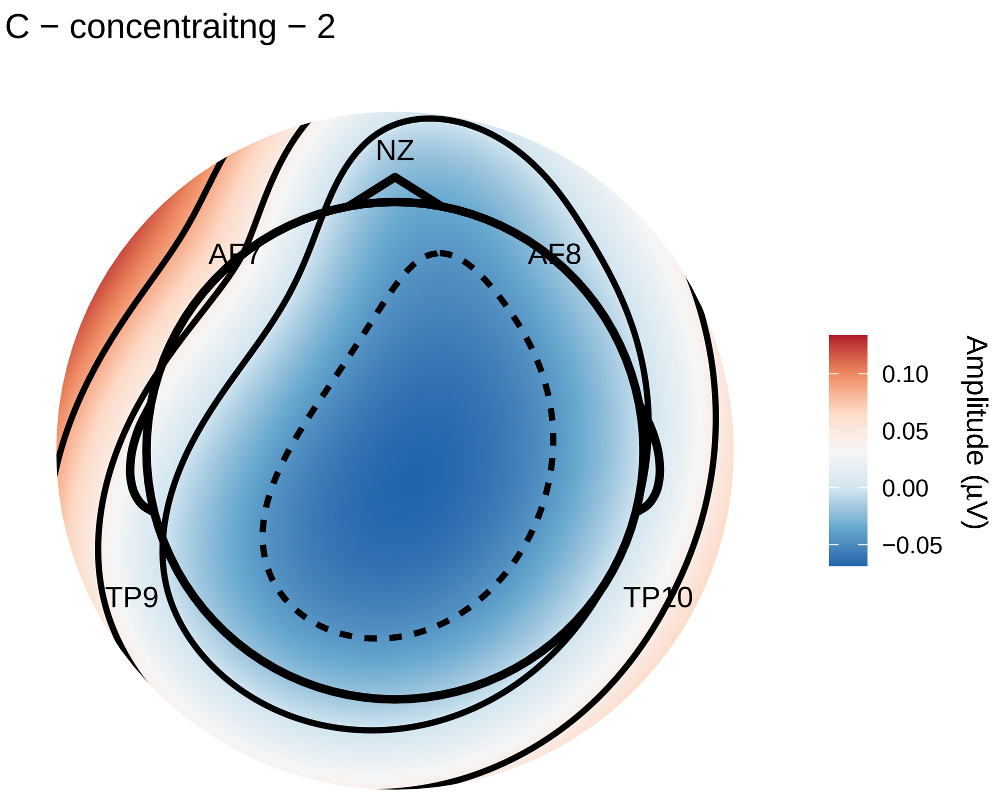
```
show_topplot(b_concentrating_2_obj, "B - concentraitng - 2")
```



```r
show_topplot(c_concentrating_1_obj, "C - concentraitng - 1")
```

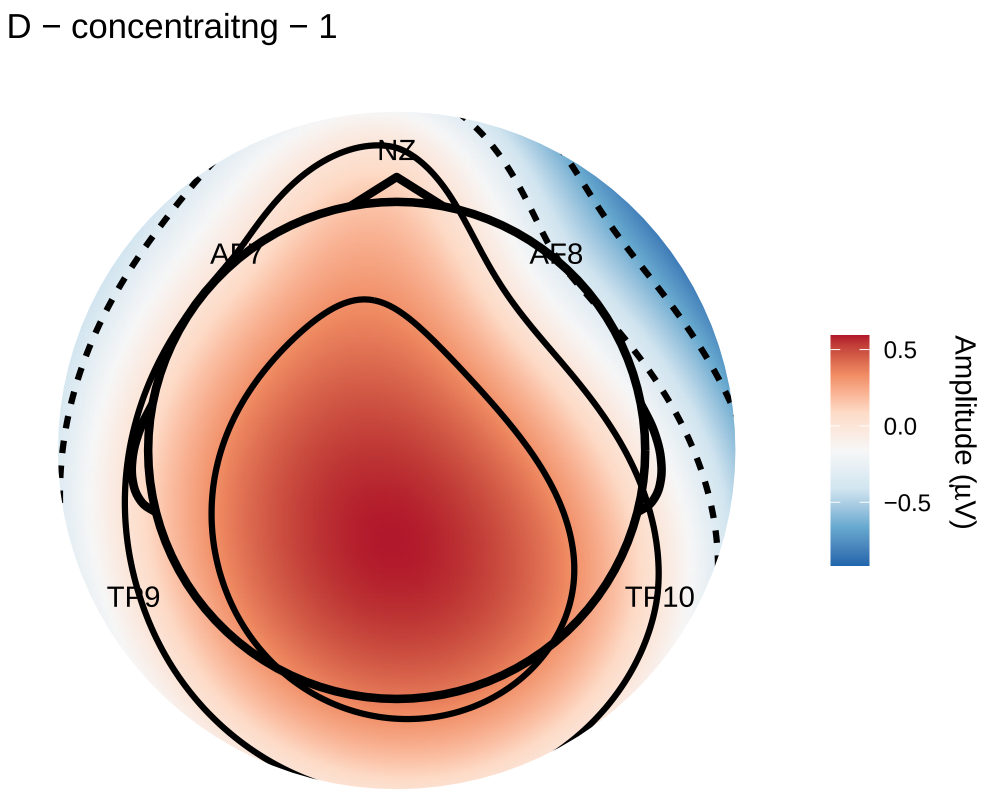


```r
show_topplot(c_concentrating_2_obj, "C - concentraitng - 2")
```

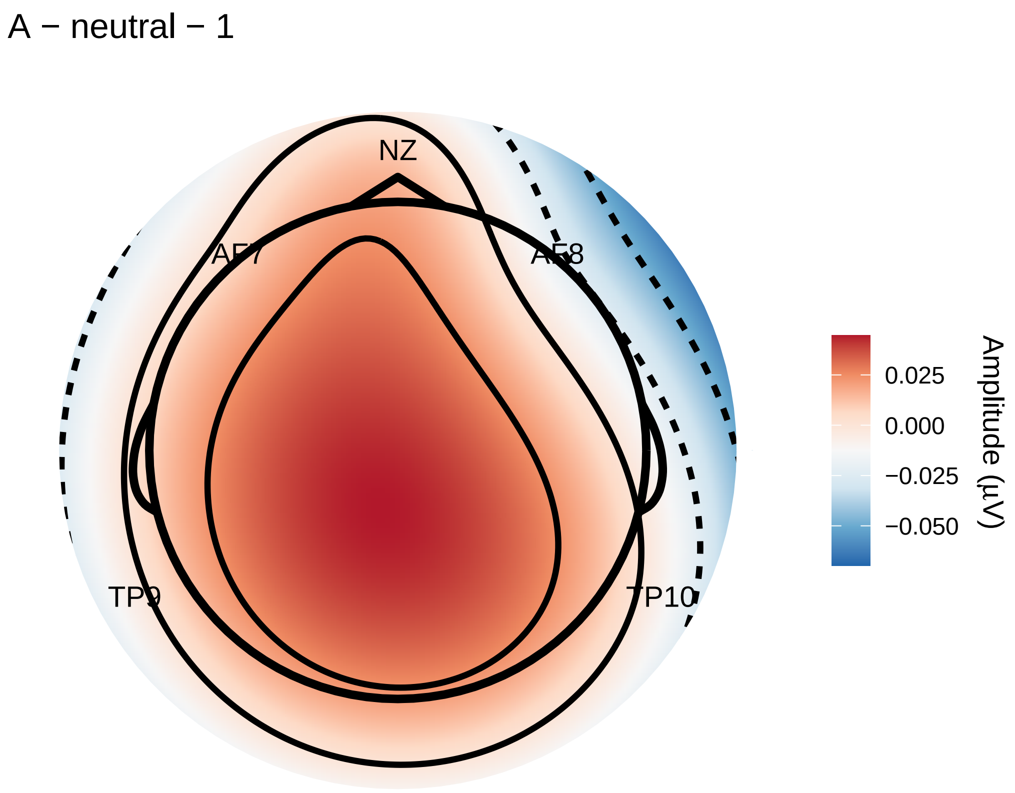


C − concentraitng − 2

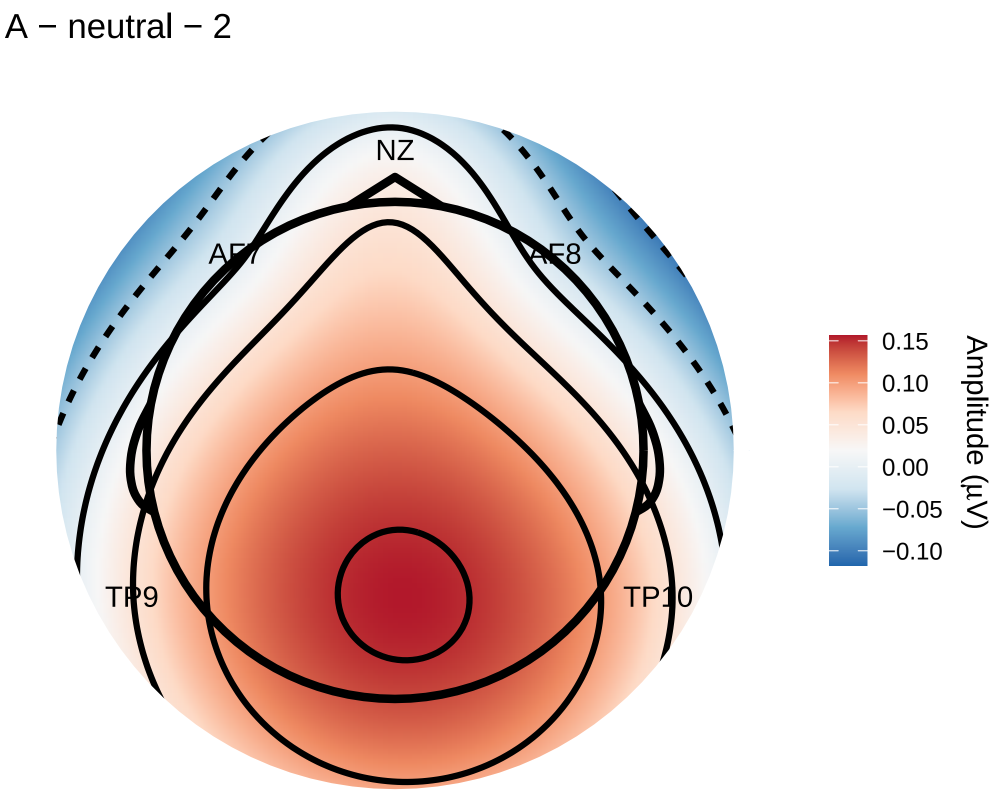
```r
show_topplot(d_concentrating_1_obj, "D - concentraitng - 1")
```



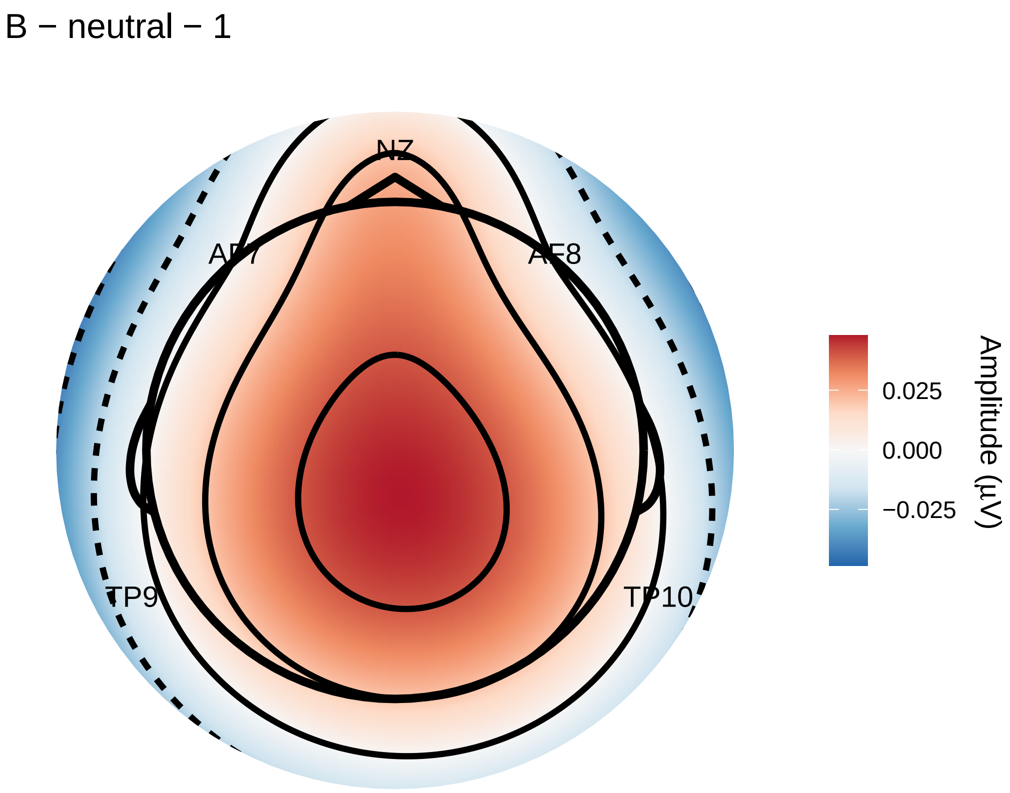
```
show_topplot(a_neutral_1_obj, "A - neutral - 1")
```



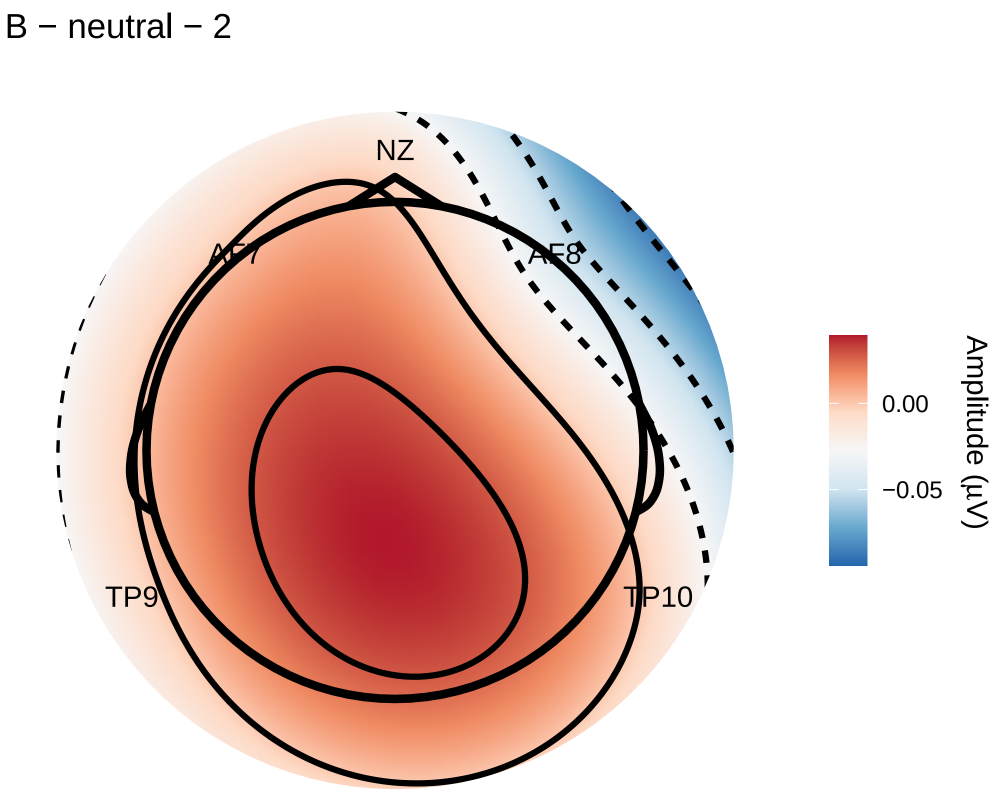
```
show_topplot(a_neutral_2_obj, "A - neutral - 2")
```



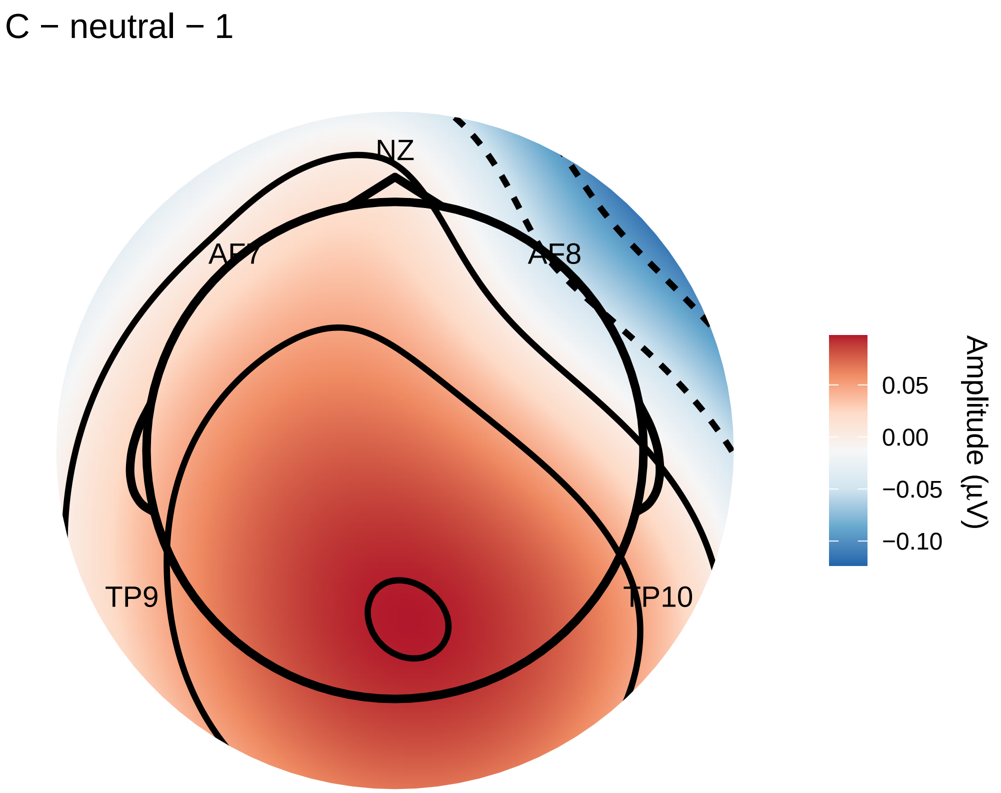
```
show_topplot(b_neutral_1_obj, "B - neutral - 1")
```



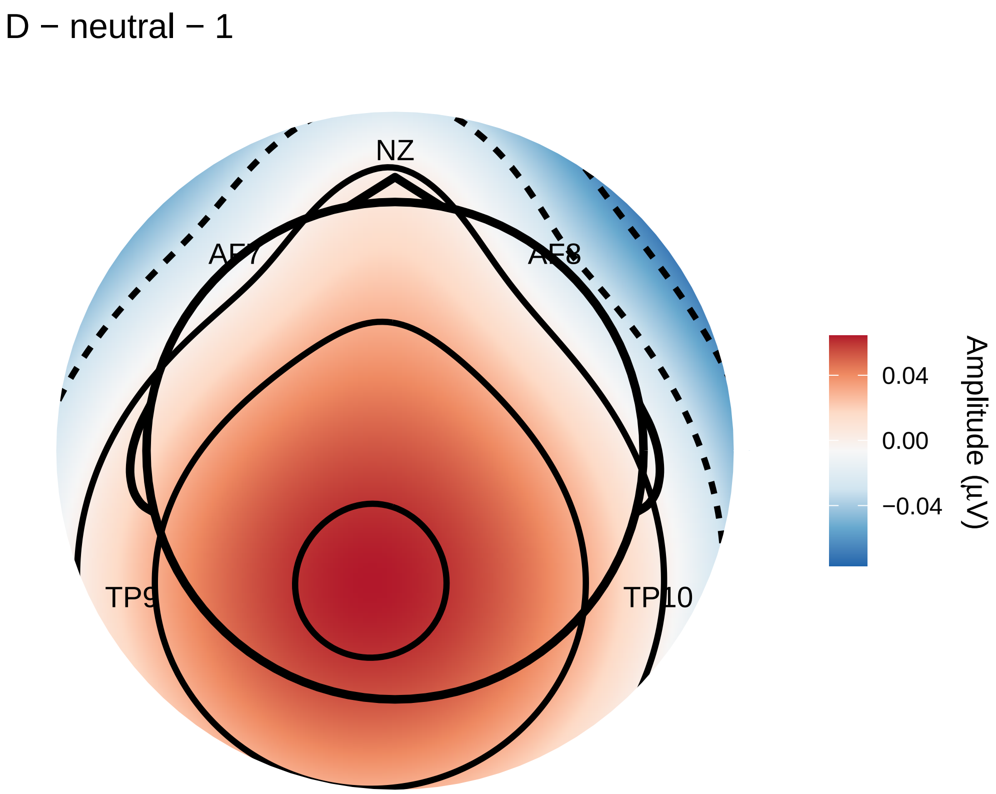
```r
show_topplot(b_neutral_2_obj, "B - neutral - 2")
```



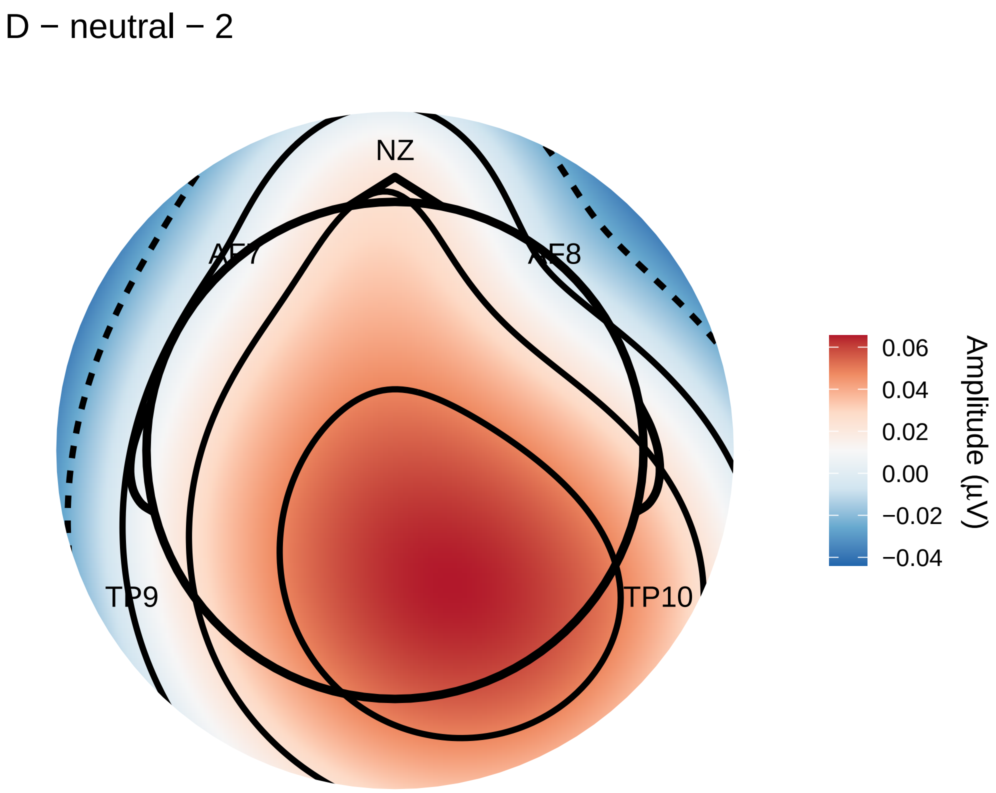
```r
show_topplot(c_neutral_1_obj, "C - neutral - 1")
```



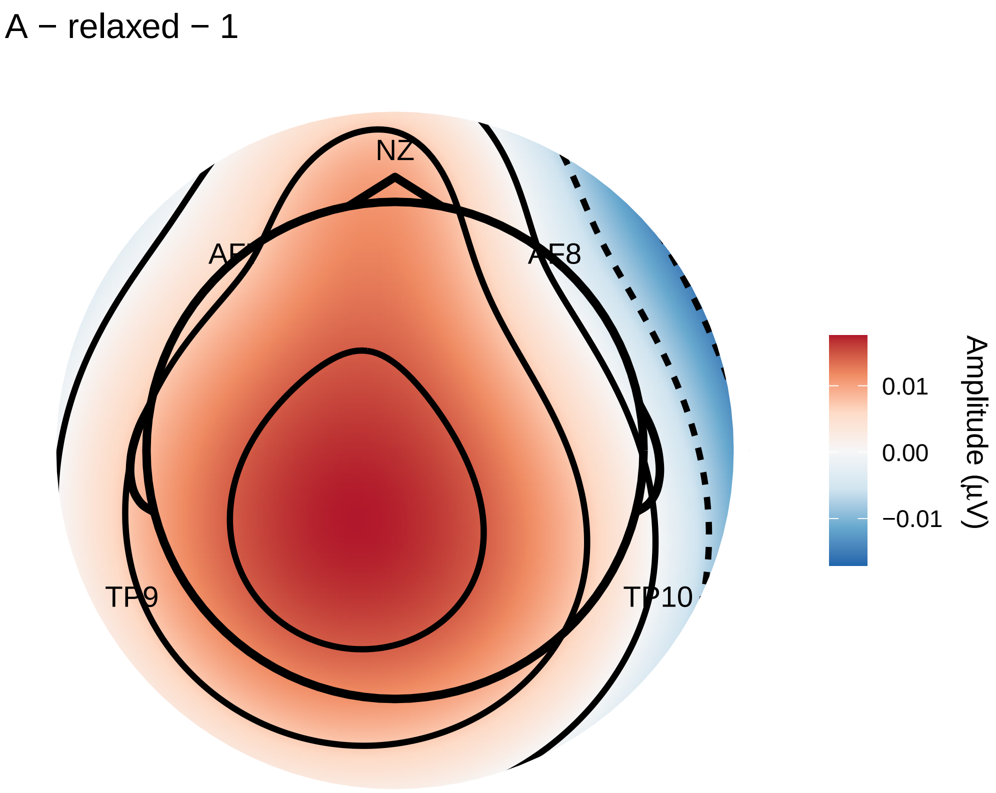
```
show_topplot(d_neutral_1_obj, "D - neutral - 1")
```



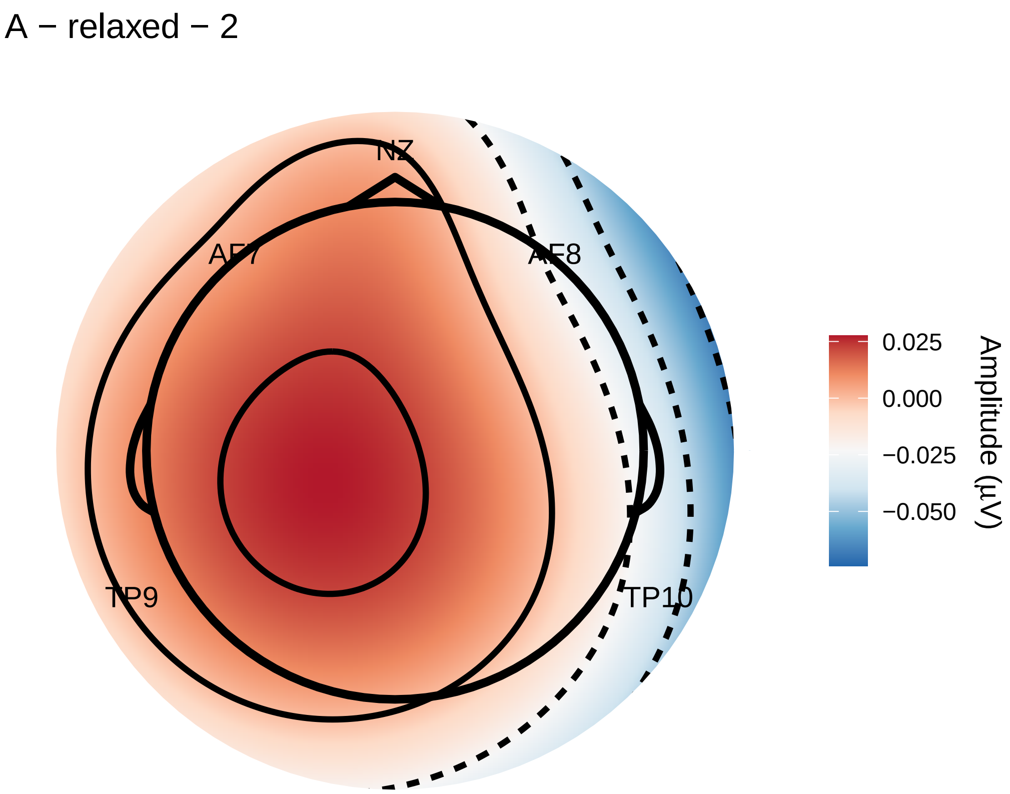
```r
show_topplot(d_neutral_2_obj, "D - neutral - 2")
```



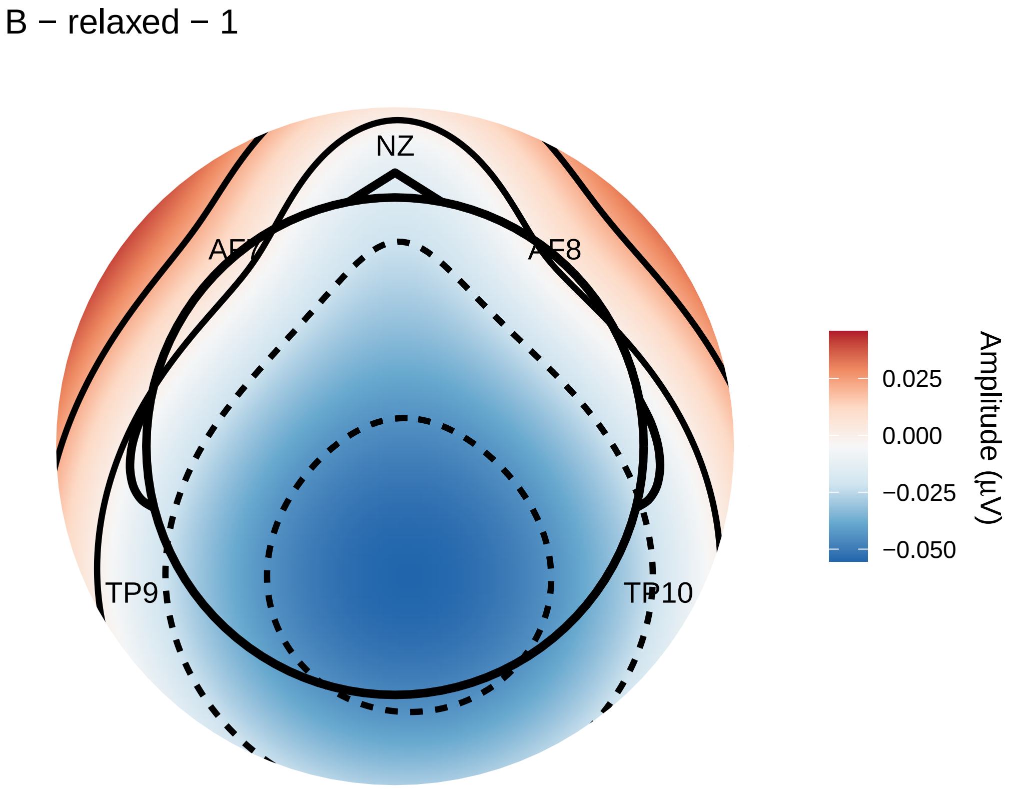
```
show_topplot(a_relaxed_1_obj, "A - relaxed - 1")
```



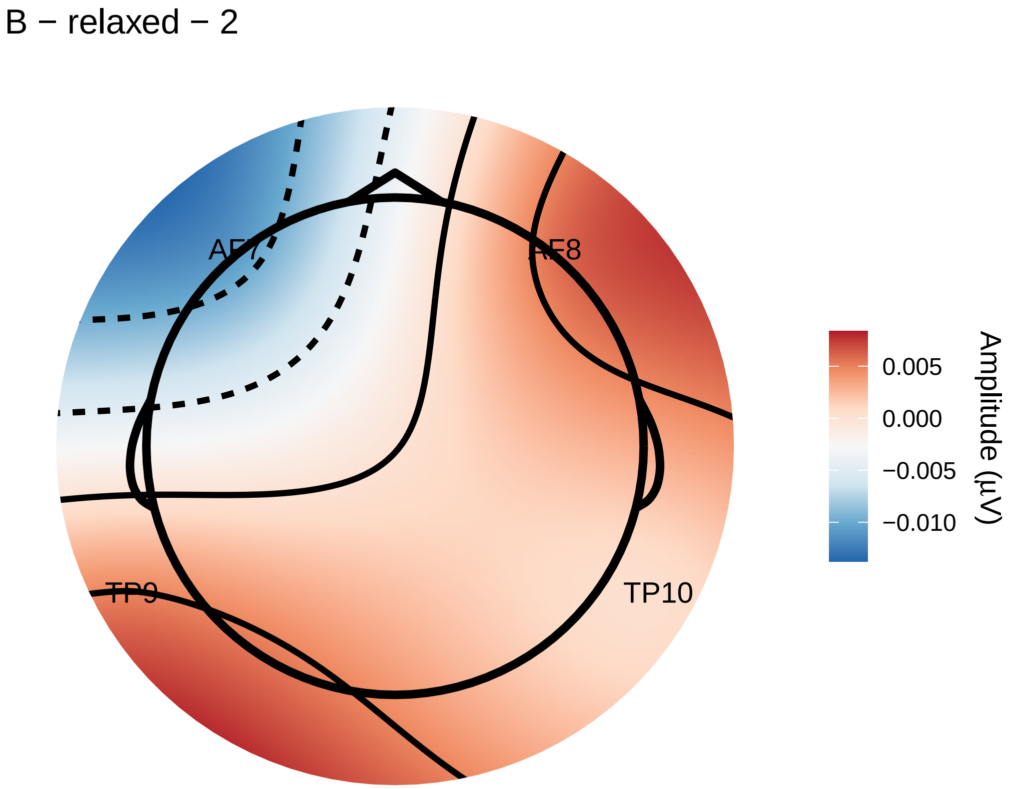
```r
show_topplot(a_relaxed_2_obj, "A - relaxed - 2")
```



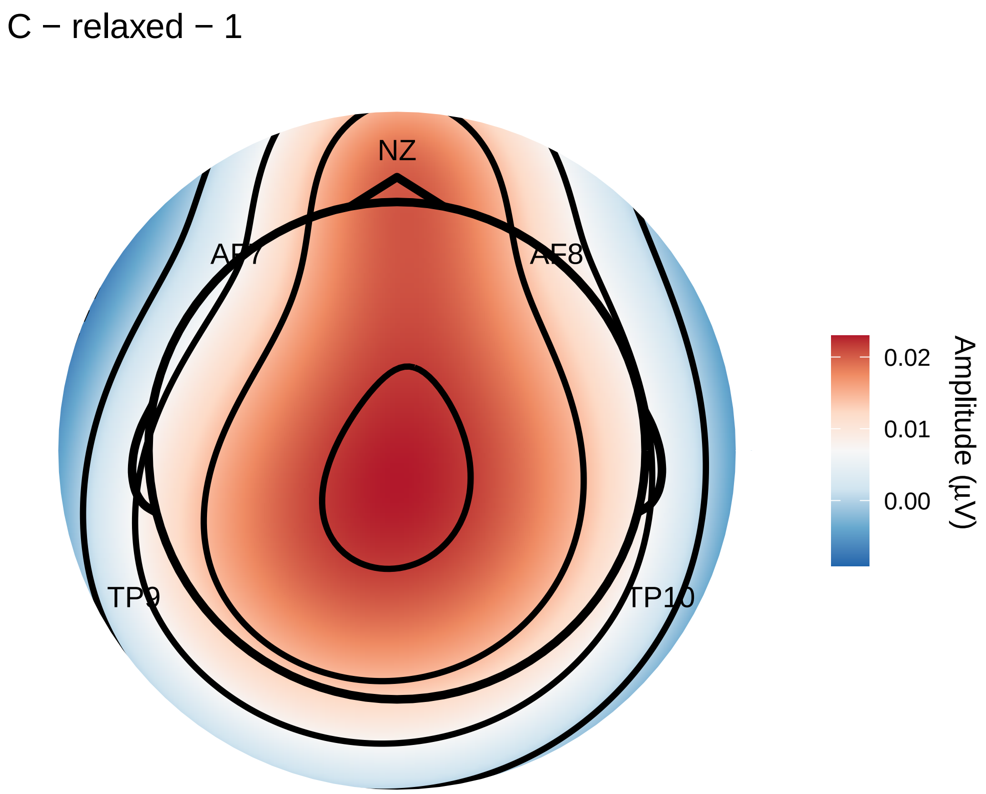
```r
show_topplot(b_relaxed_1_obj, "B - relaxed - 1")
```



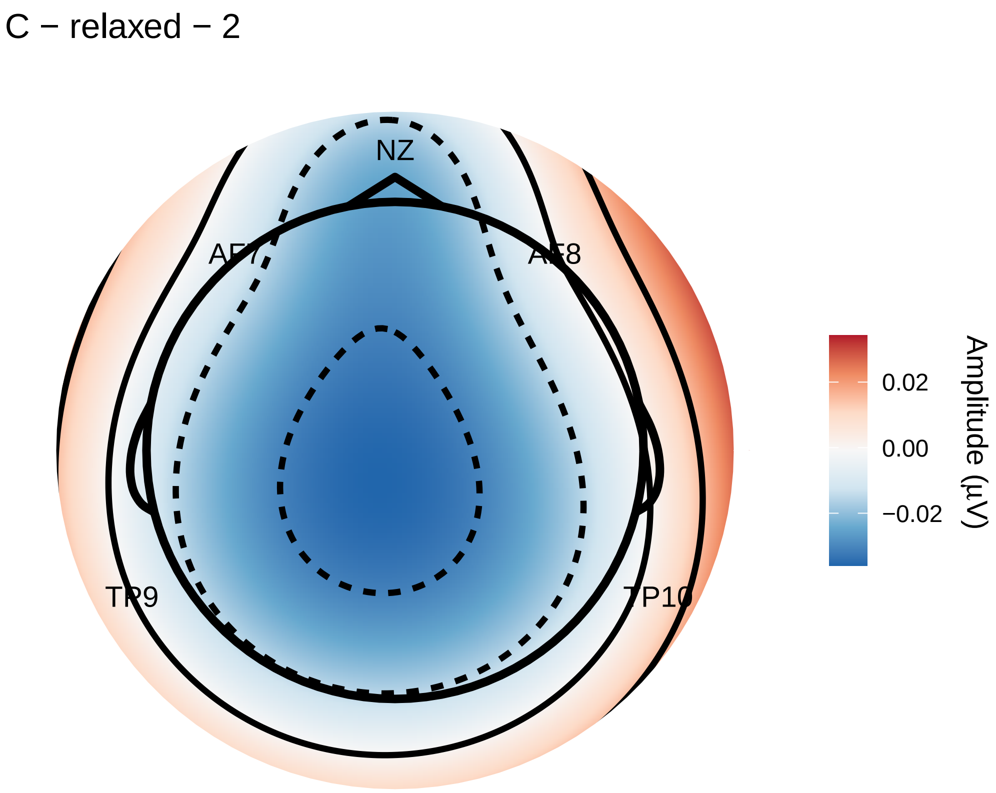
```r
show_topplot(b_relaxed_2_obj, "B - relaxed - 2")
```



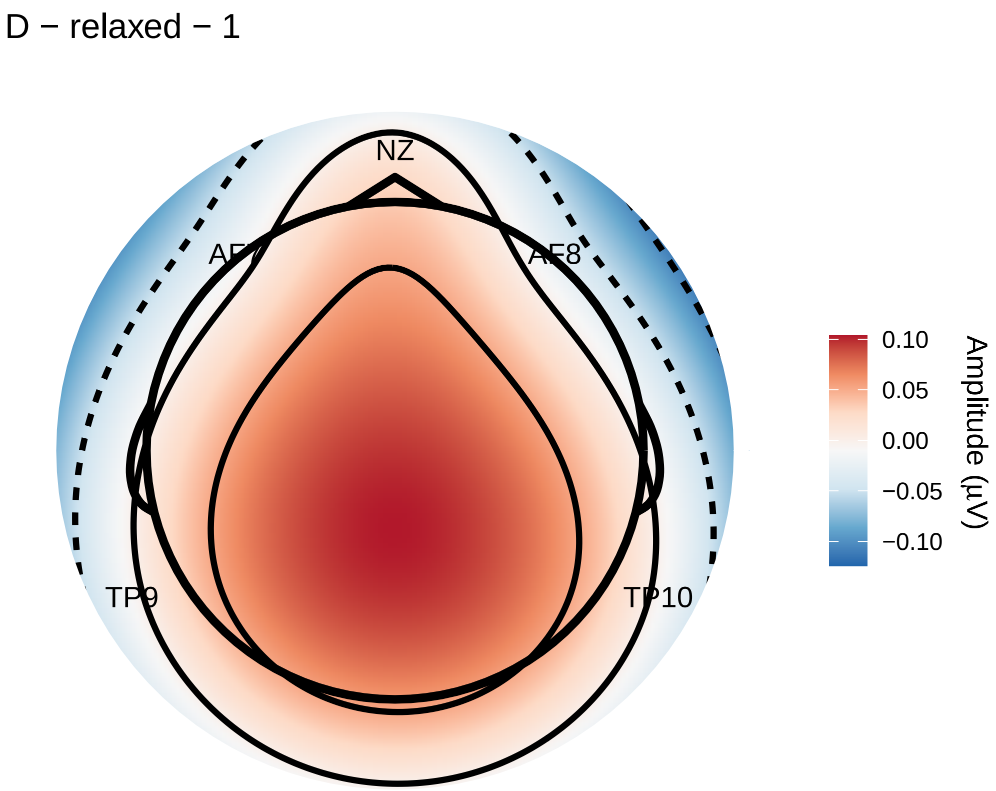
```
show_topplot(c_relaxed_1_obj, "C - relaxed - 1")
```



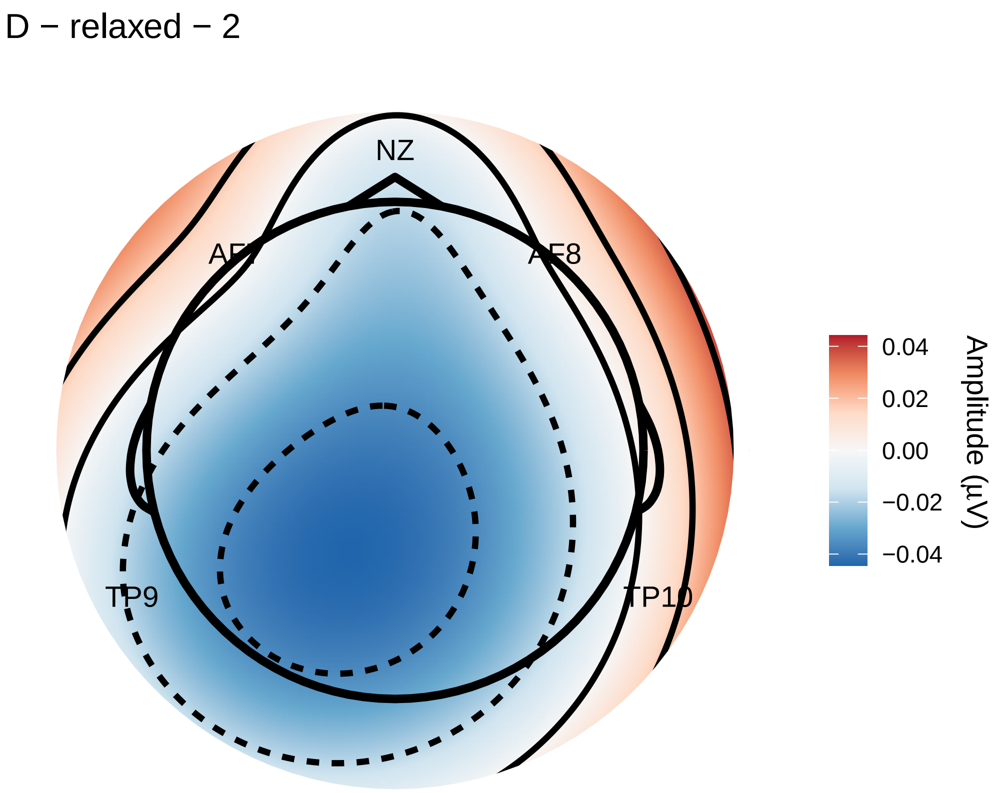
```r
show_topplot(c_relaxed_2_obj, "C - relaxed - 2")
```



```r
show_topplot(d_relaxed_1_obj, "D - relaxed - 1")
```



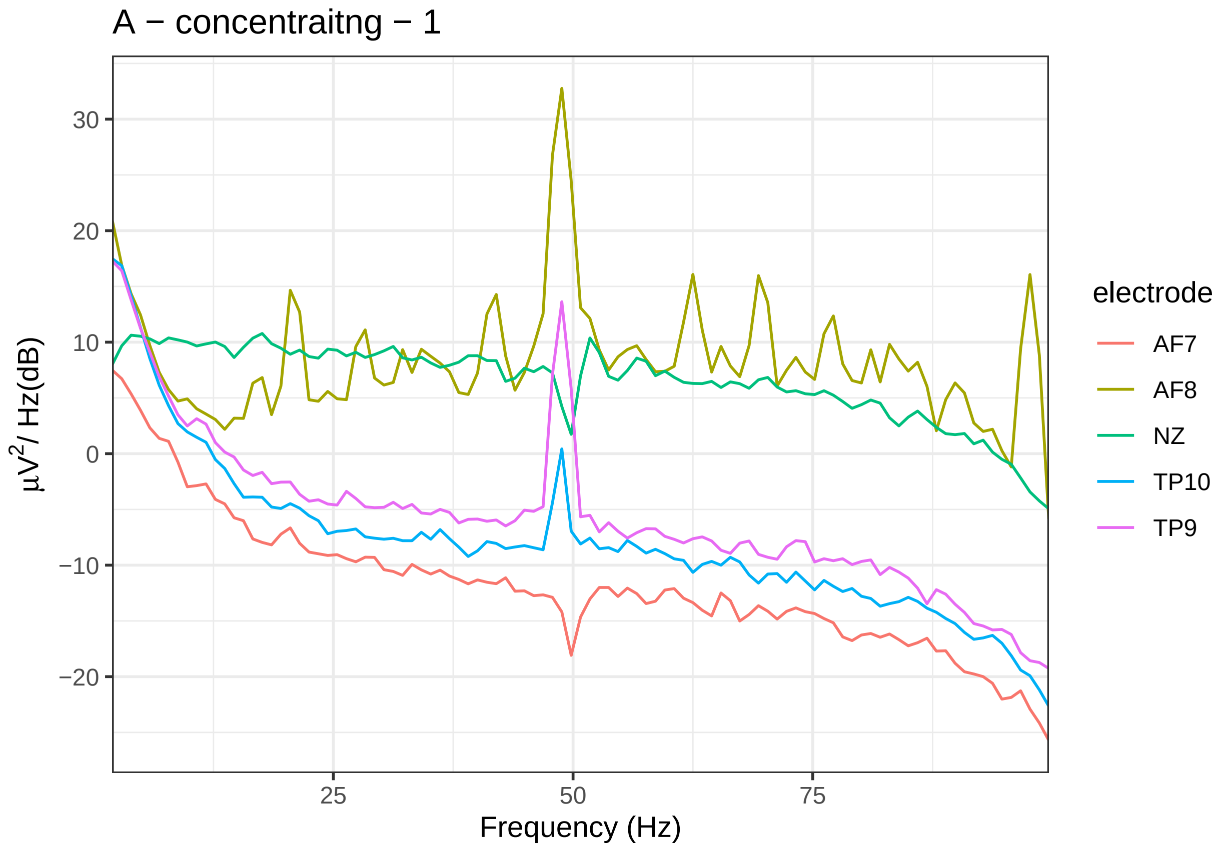
```
show_topplot(d_relaxed_2_obj, "D - relaxed - 2")
```



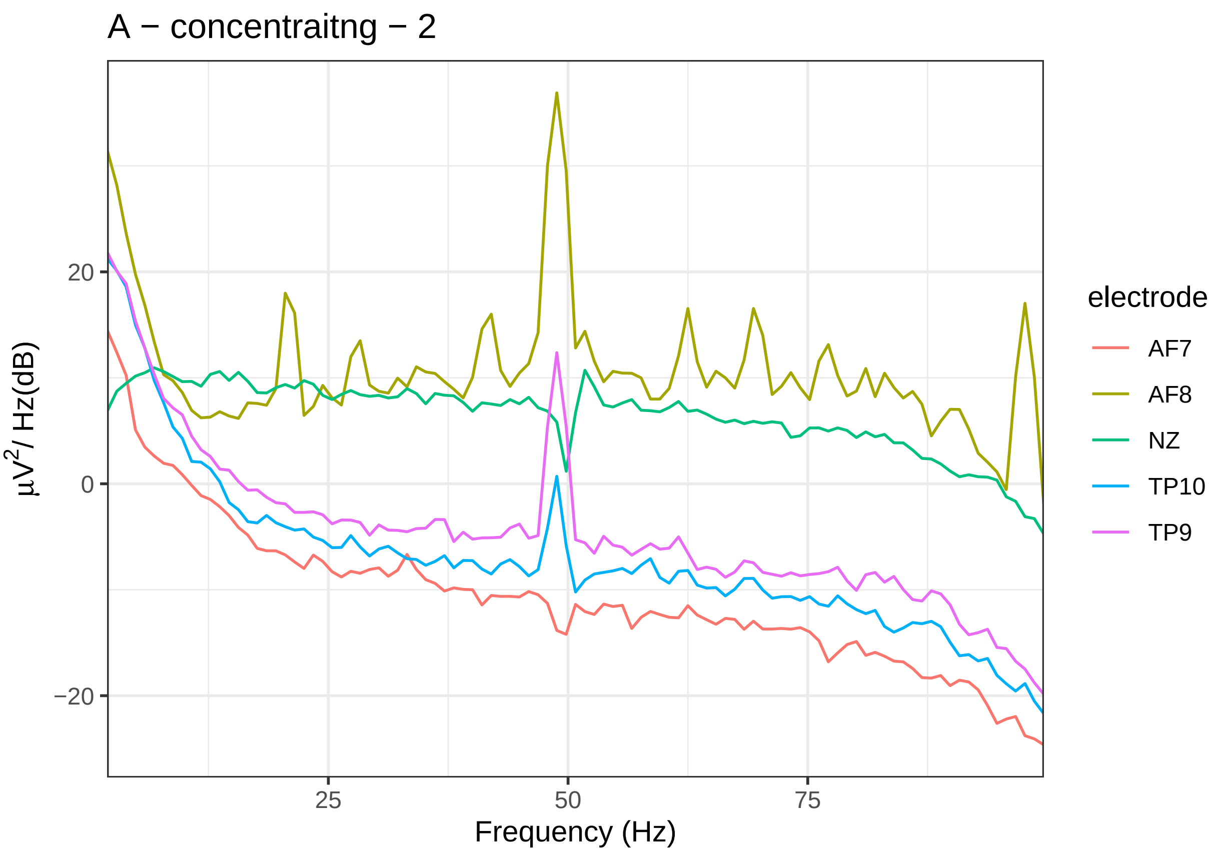
Frequency Analysis (PSD)

To determine contribution of different brain waves, we calculate Power Spectral Density. To obtain less noisy results we use Welch's method instead of Fast Fourier Transform.

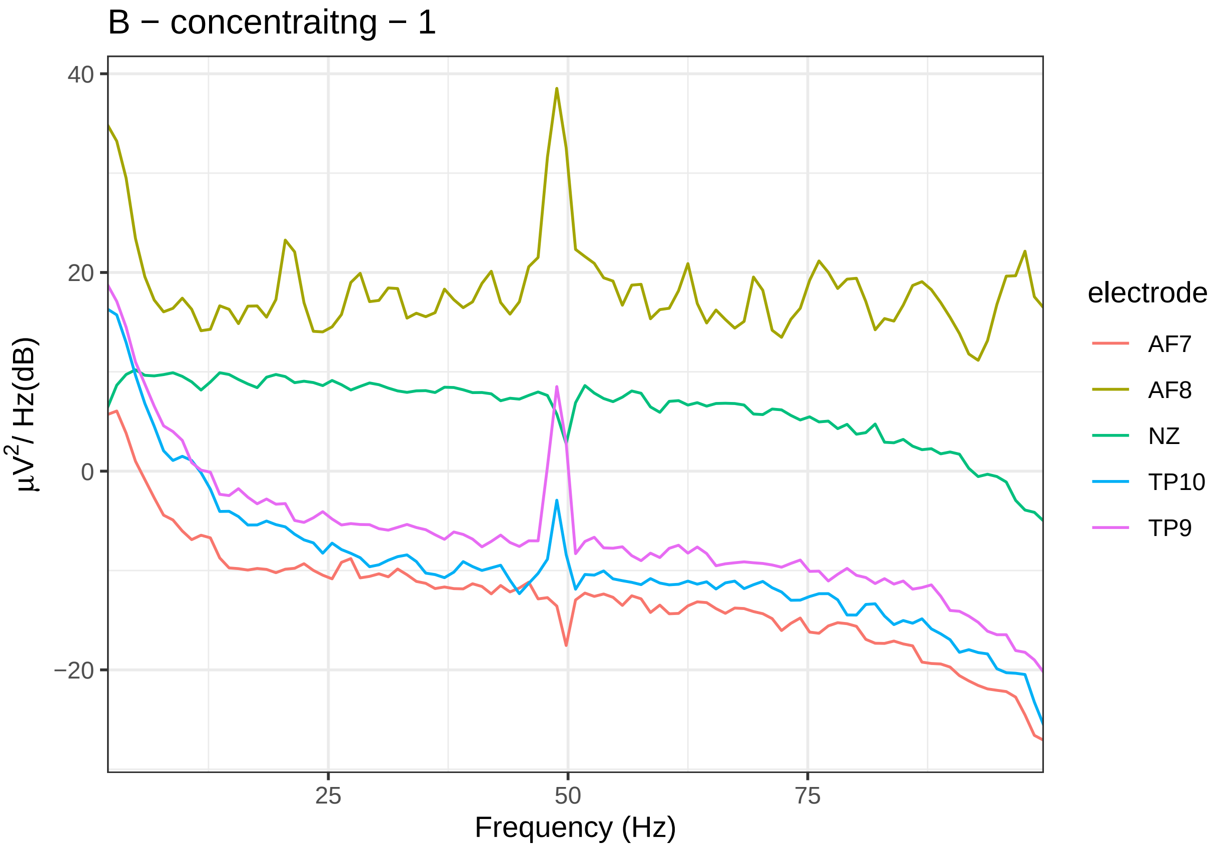
```r
show_psd <- function(eeg_obj, title) {
  return (plot_psd(eeg_obj, freq_range = c(1, 100), ) + ggtitle(title))
}

show_psd(a_concentrating_1_obj, "A - concentraitng - 1")
```



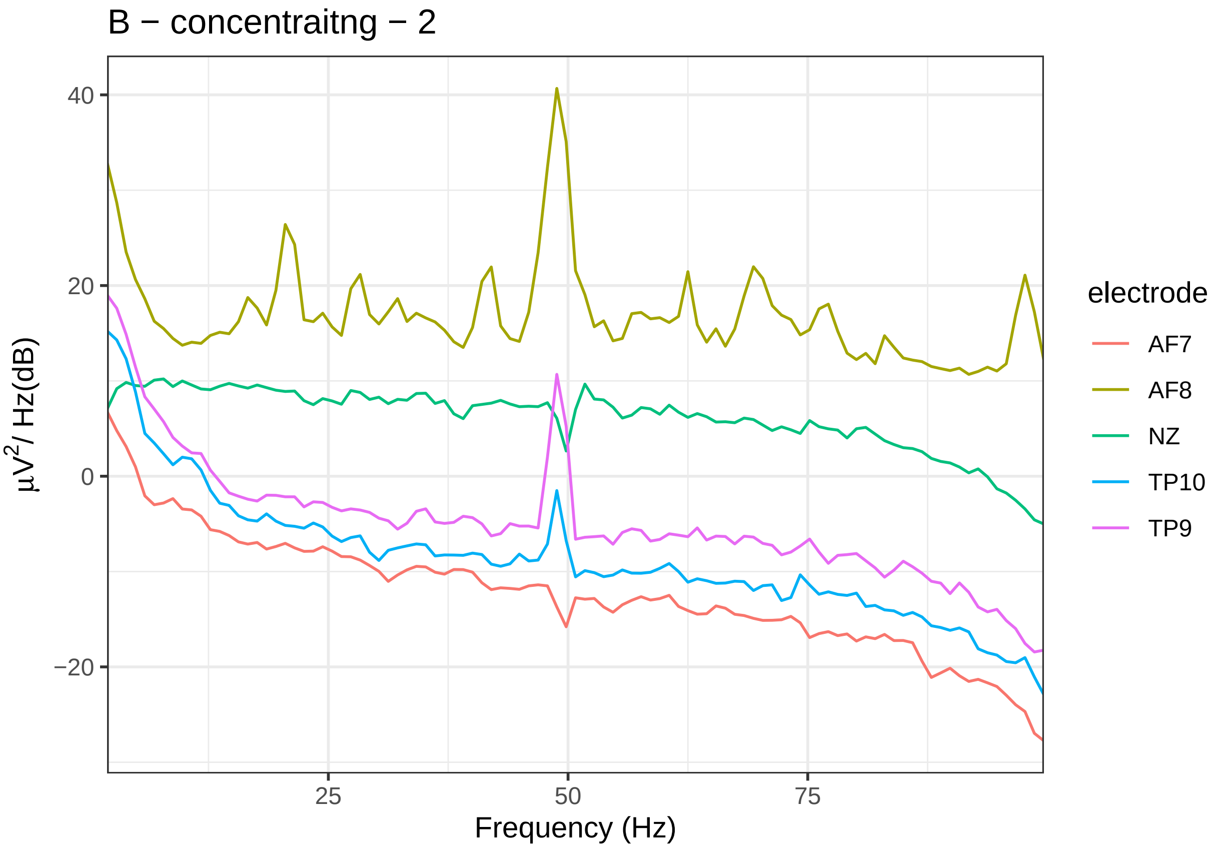
```
show_psd(a_concentrating_2_obj, "A - concentraitng - 2")
```



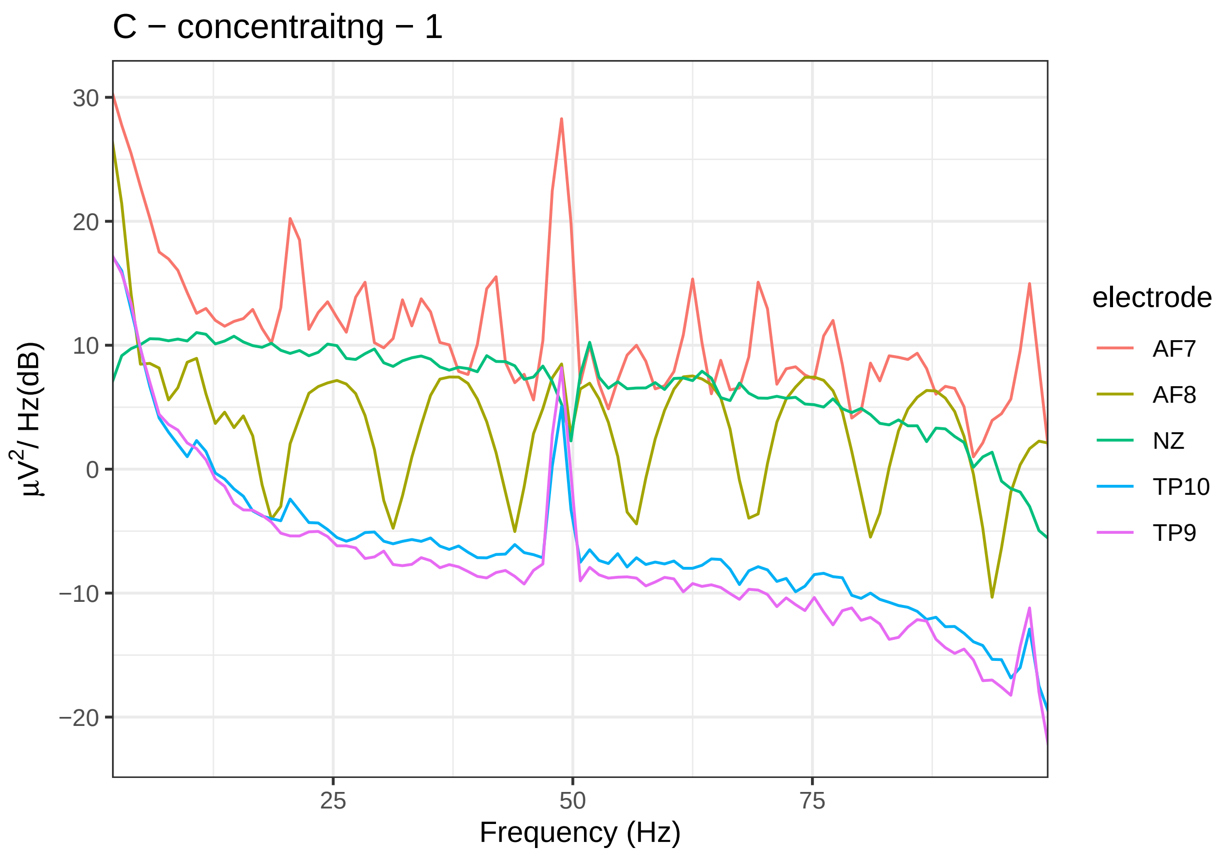
```r
show_psd(b_concentrating_1_obj, "B - concentraitng - 1")
```



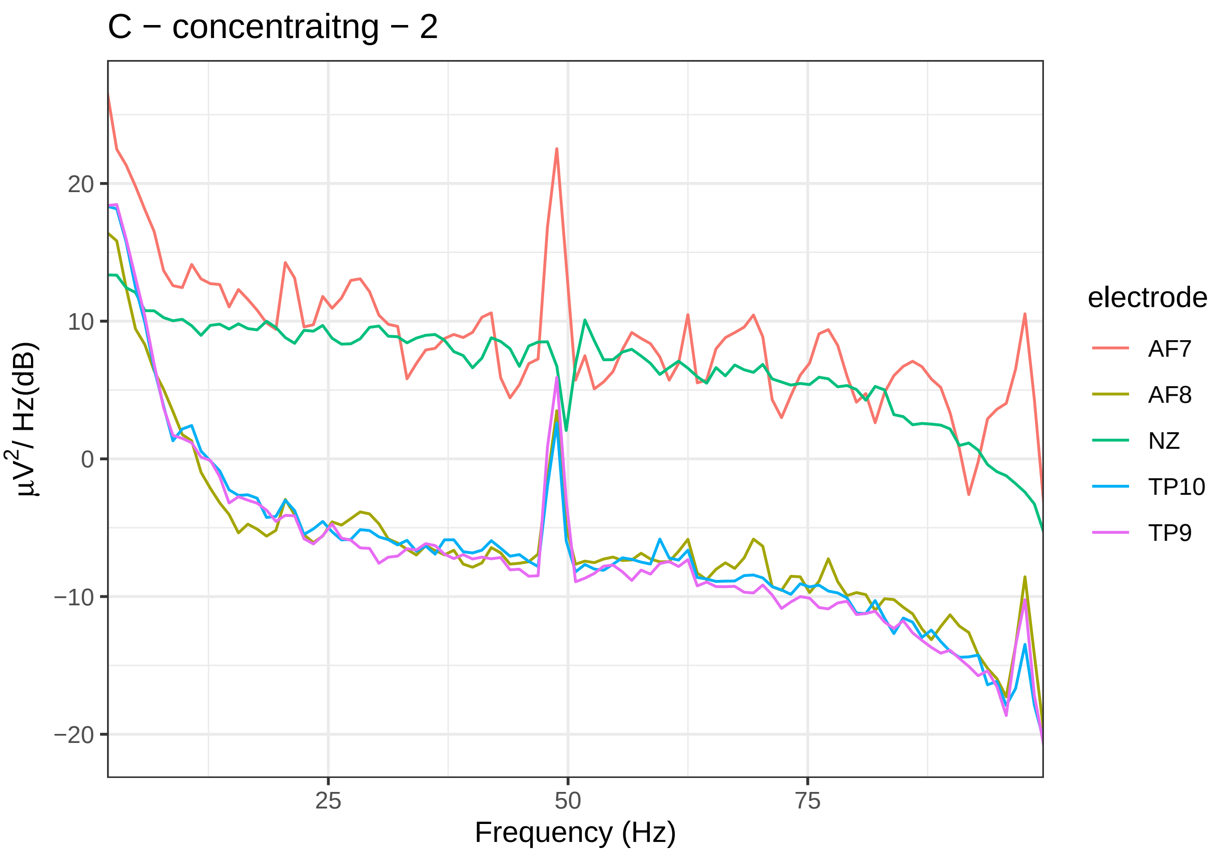
```r
show_psd(b_concentrating_2_obj, "B - concentraitng - 2")
```



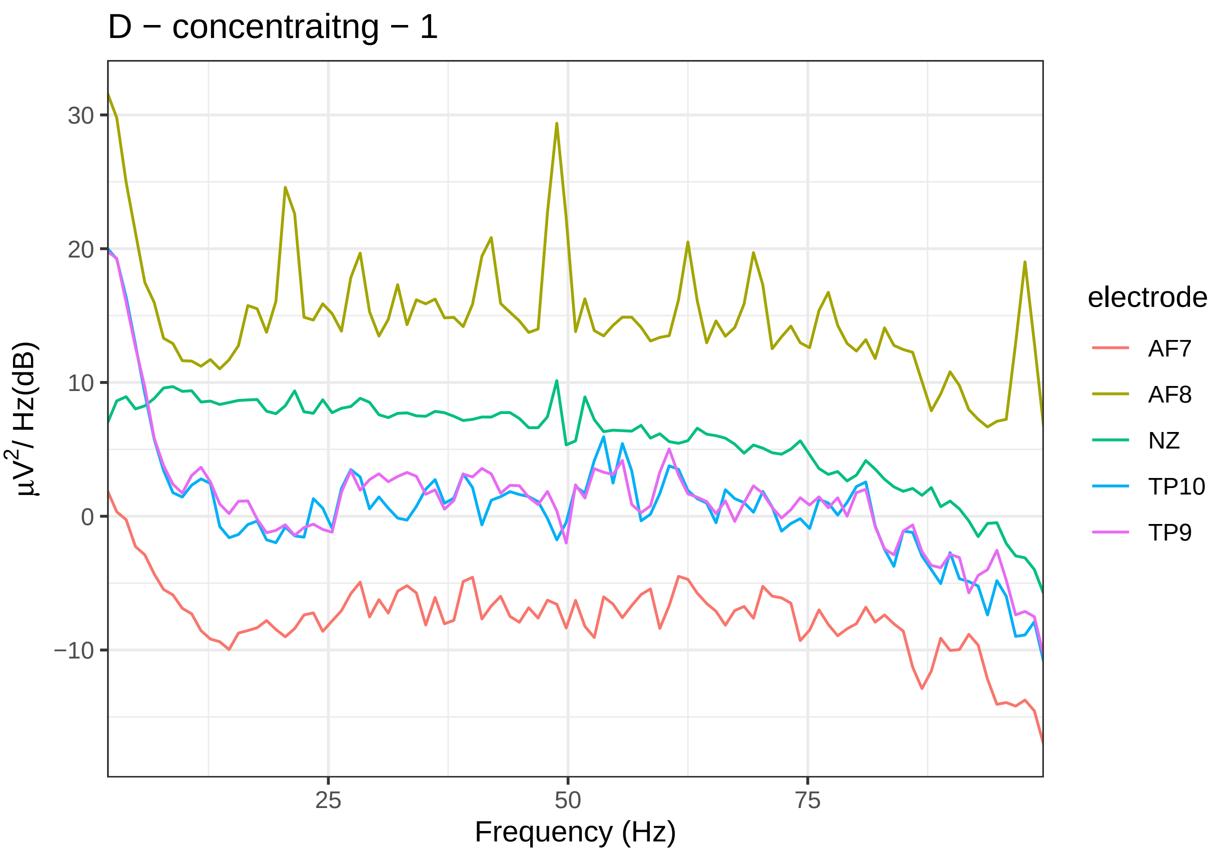
```
show_psd(c_concentrating_1_obj, "C - concentraitng - 1")
```



```r
show_psd(c_concentrating_2_obj, "C - concentraitng - 2")
```

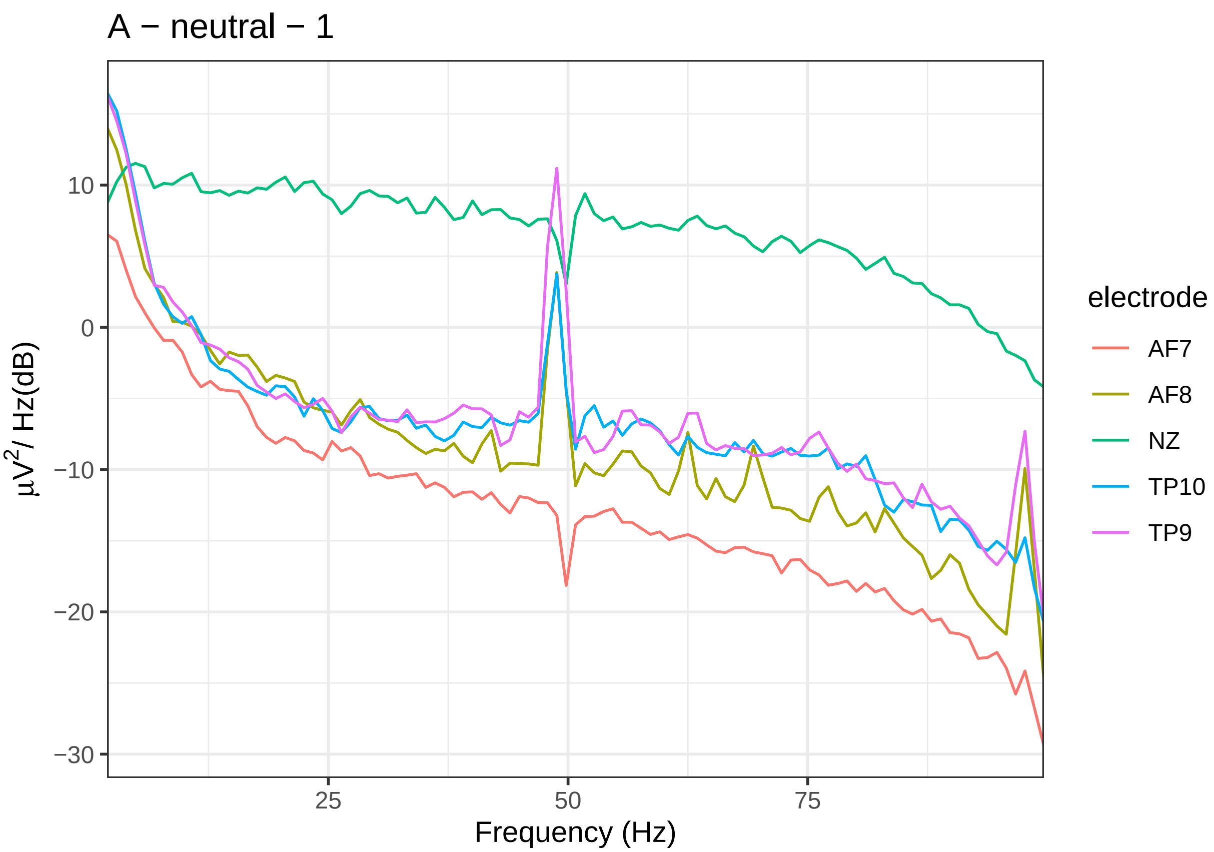


```
show_psd(d_concentrating_1_obj, "D - concentraitng - 1")
```

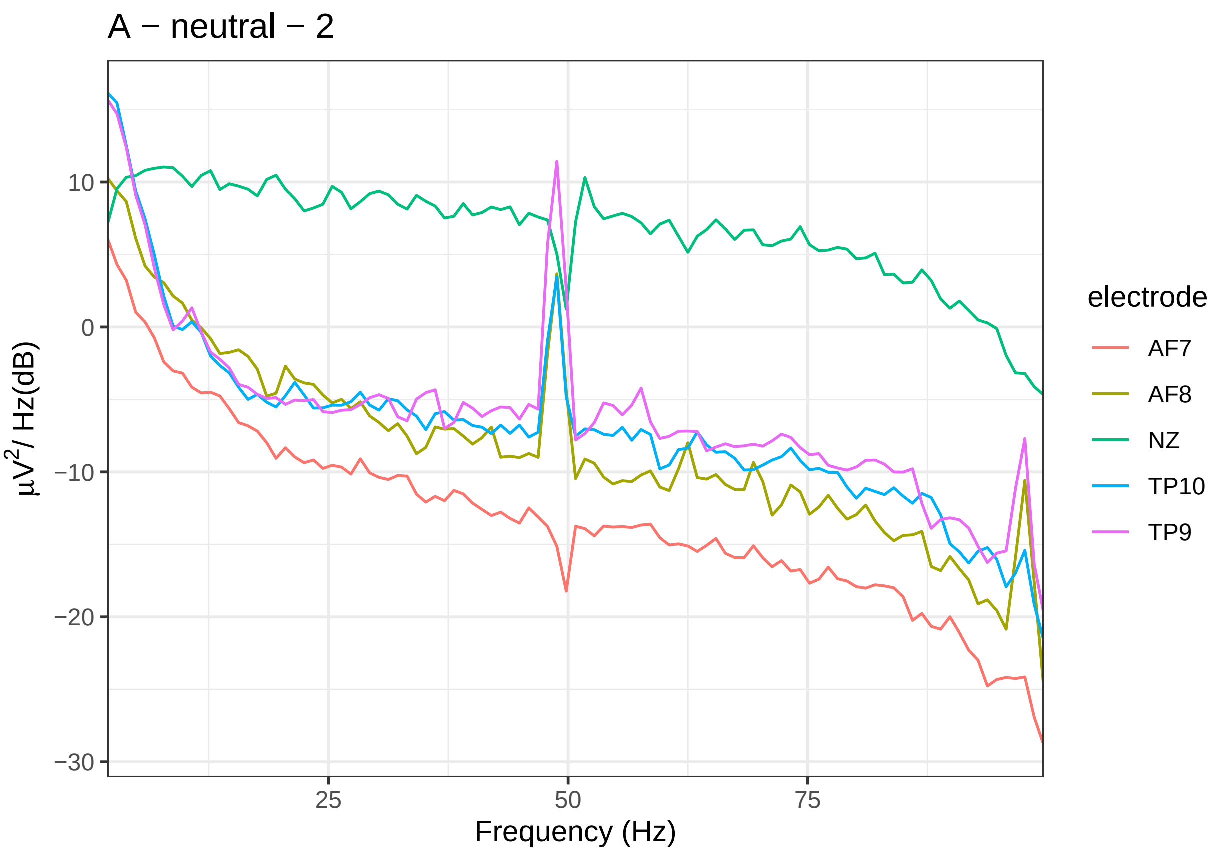


```r
#show_psd(d_concentrating_2_obj, "D - concentraitng - 2")
```

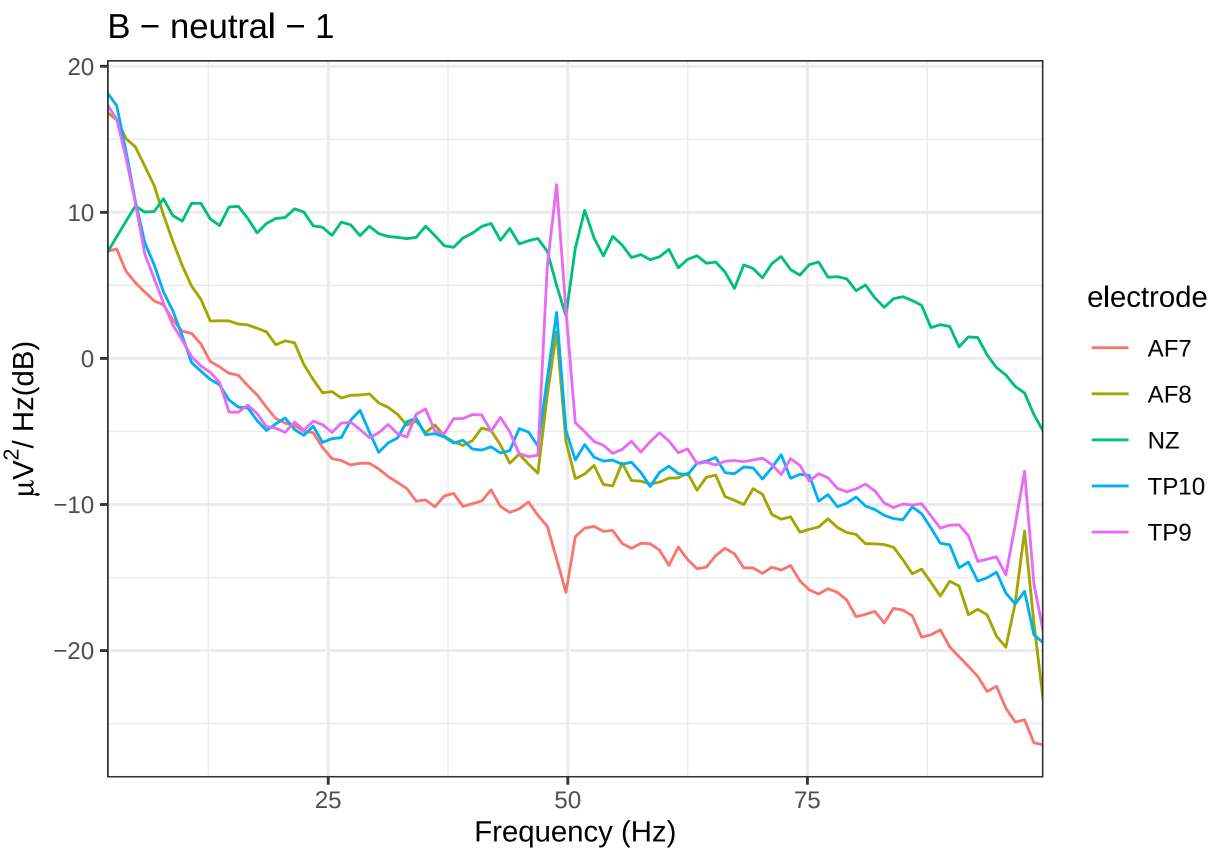
```r
show_psd(a_neutral_1_obj, "A - neutral - 1")
```



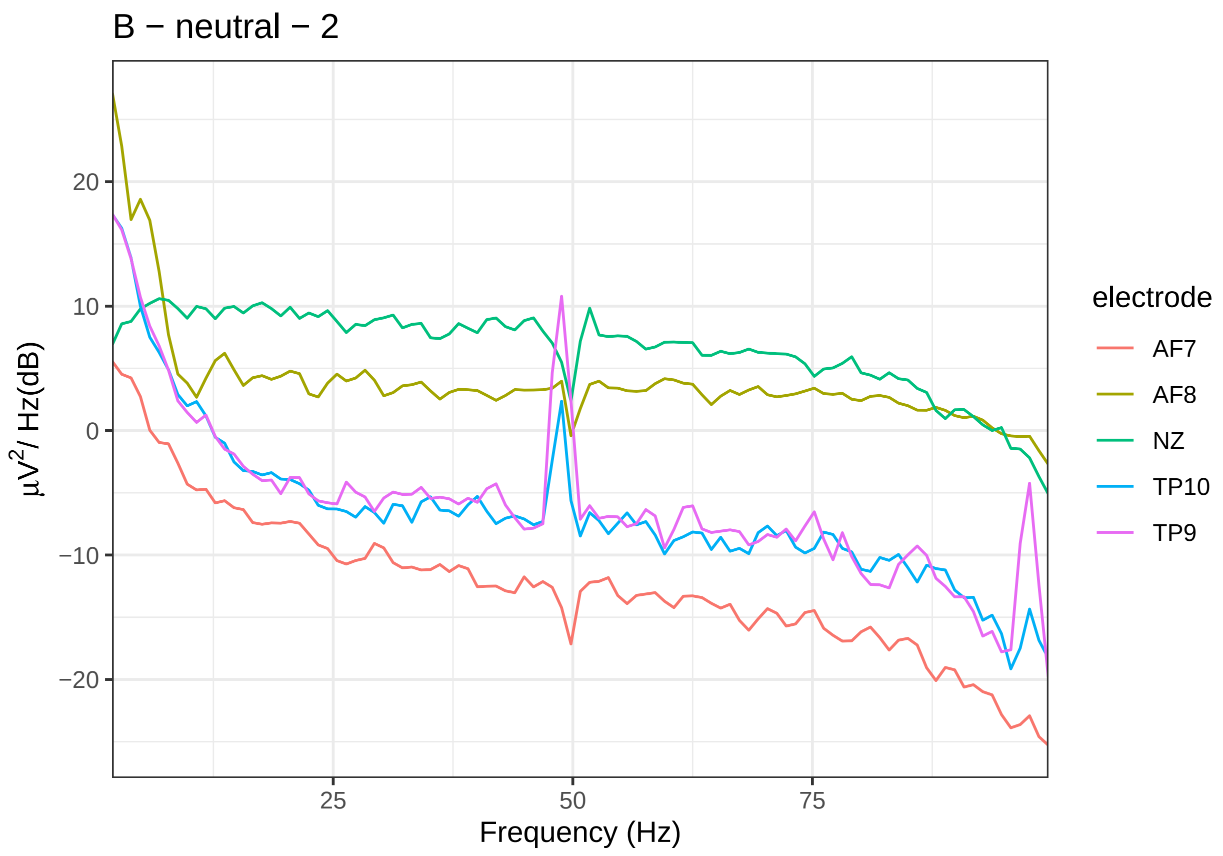
```
show_psd(a_neutral_2_obj, "A - neutral - 2")
```



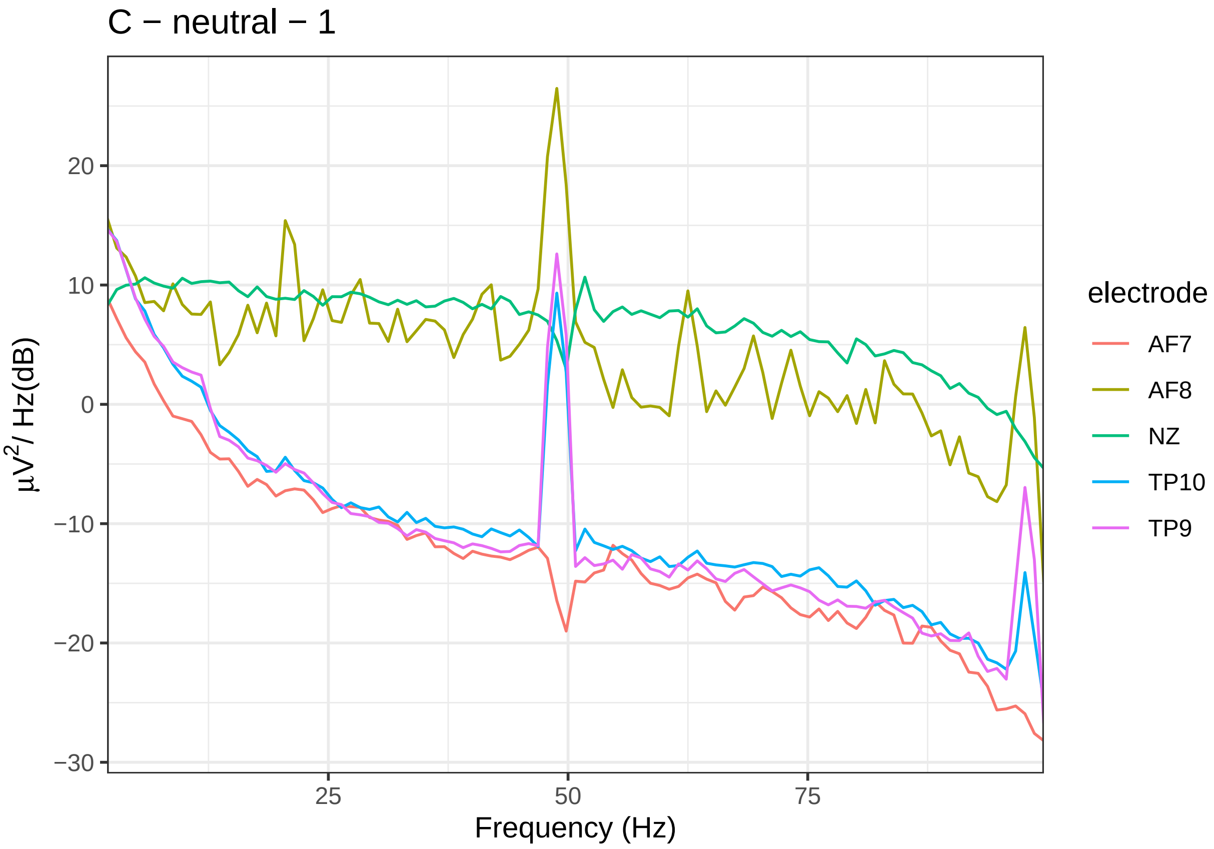
```
show_psd(b_neutral_1_obj, "B - neutral - 1")
```



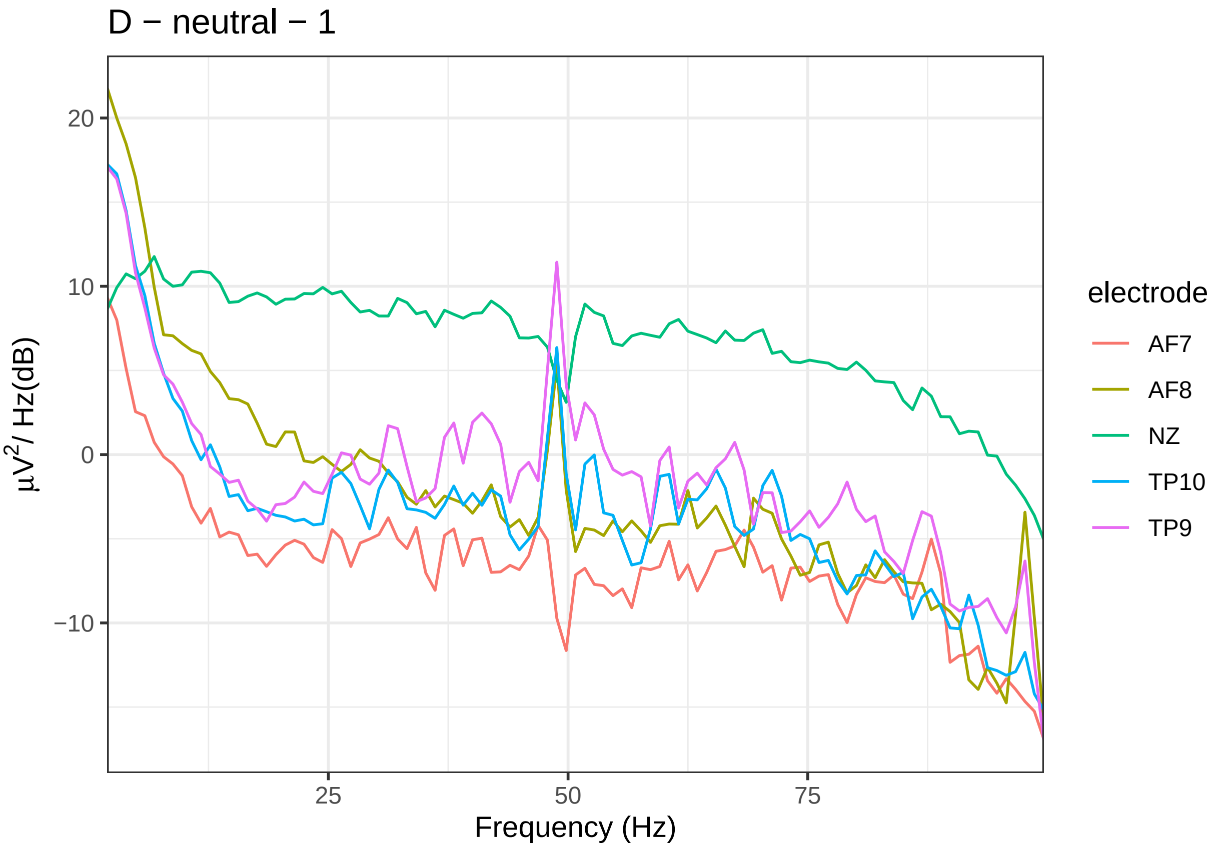
```r
show_psd(b_neutral_2_obj, "B - neutral - 2")
```



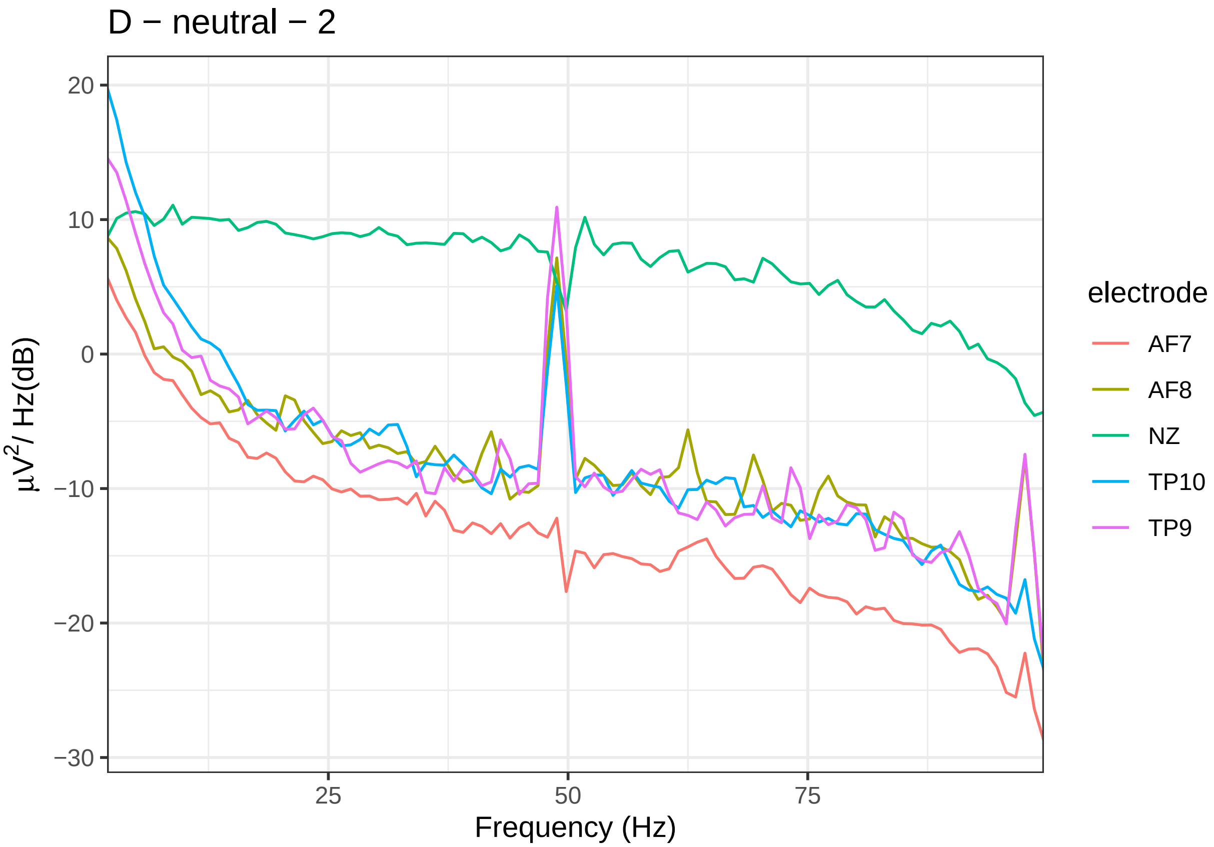
```
show_psd(c_neutral_1_obj, "C - neutral - 1")
```



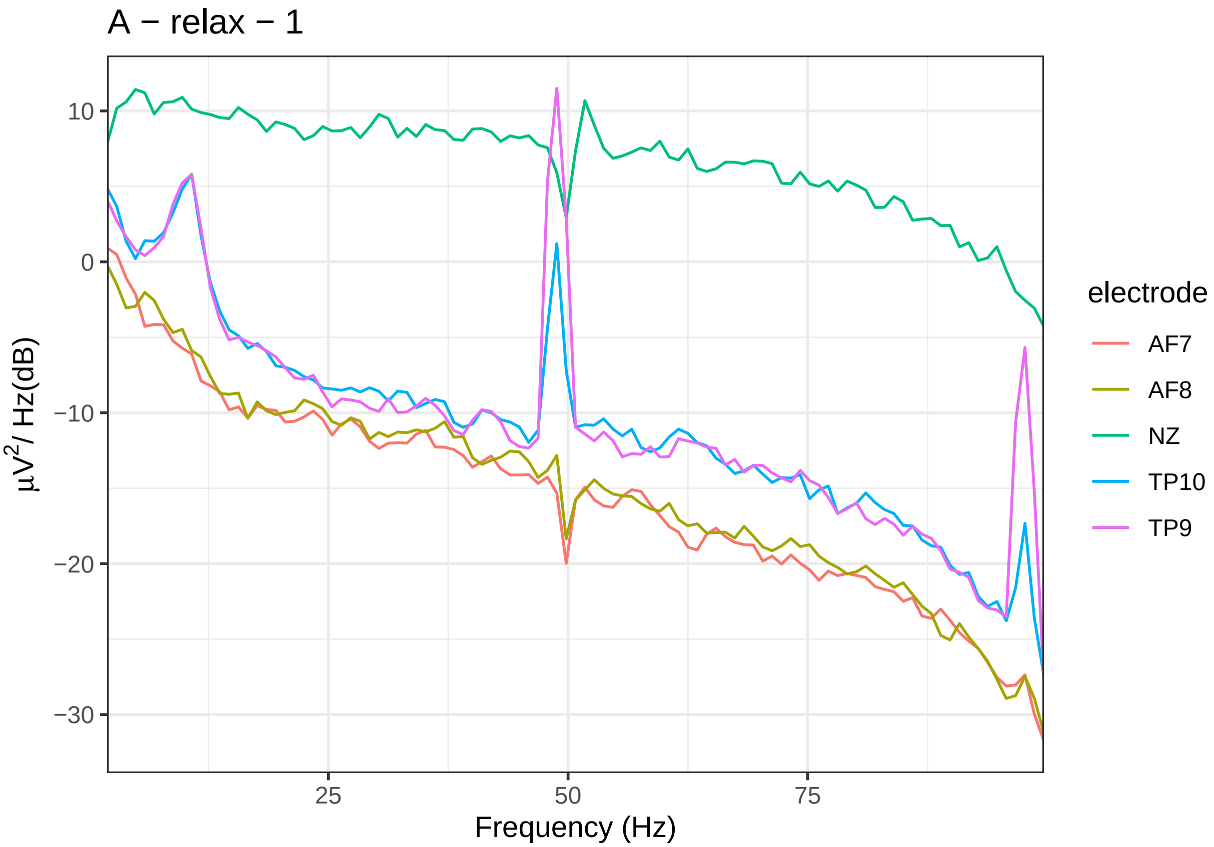
```
show_psd(d_neutral_1_obj, "D - neutral - 1")
```



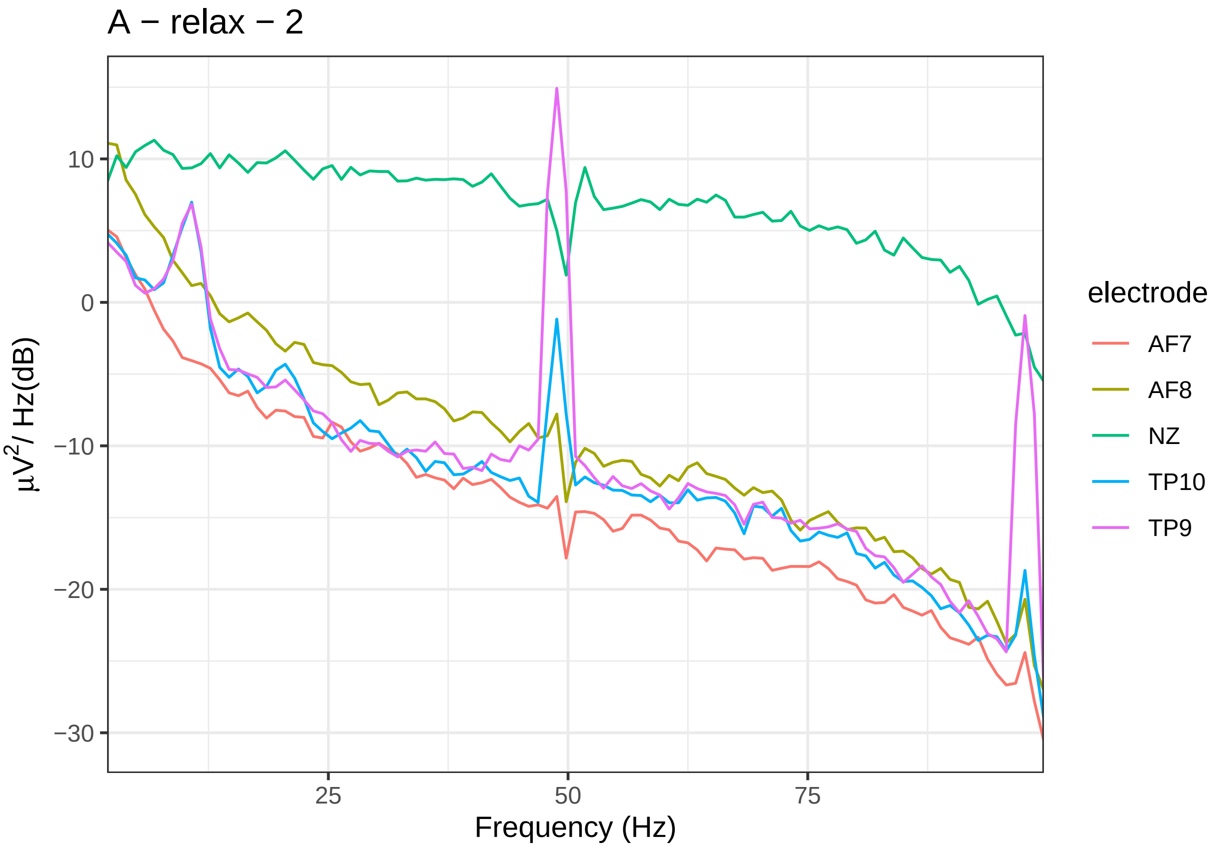
```
show_psd(d_neutral_2_obj, "D - neutral - 2")
```



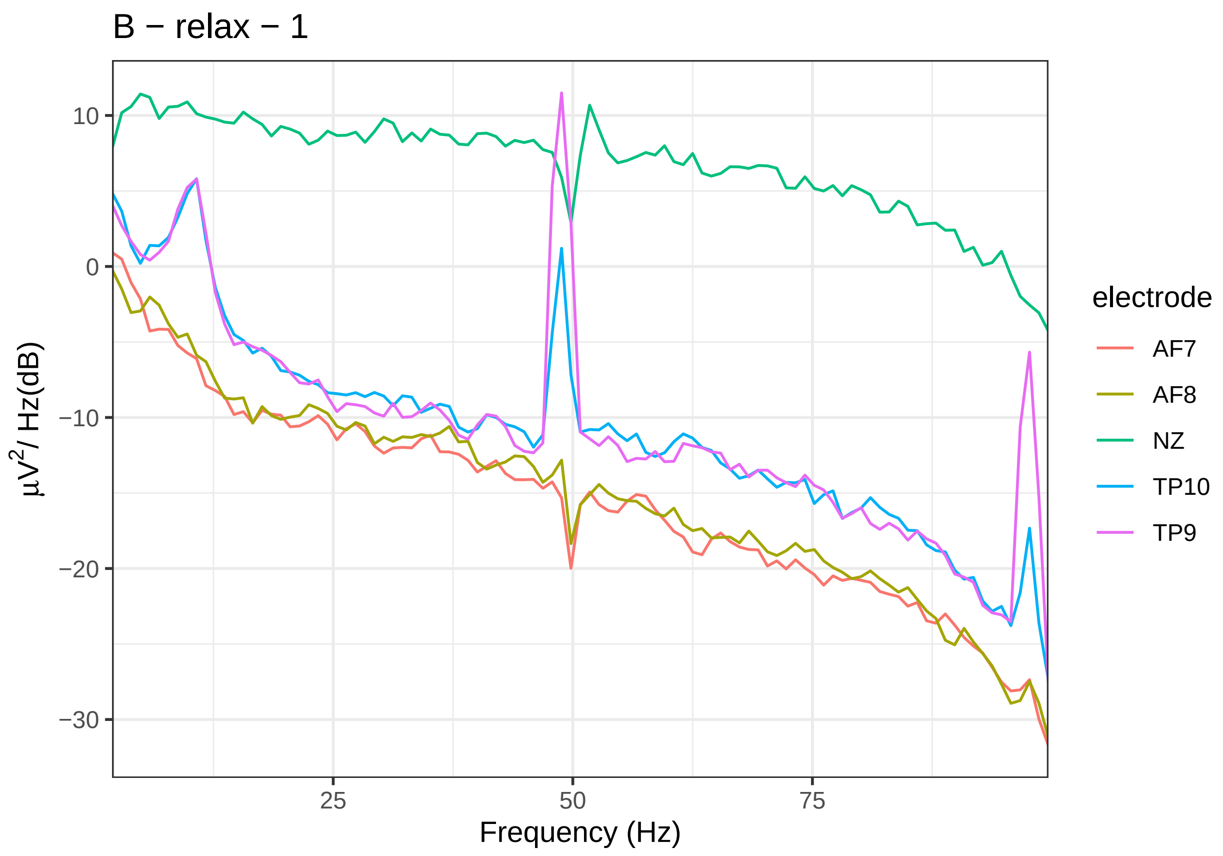
```r
show_psd(a_relaxed_1_obj, "A - relax - 1")
```



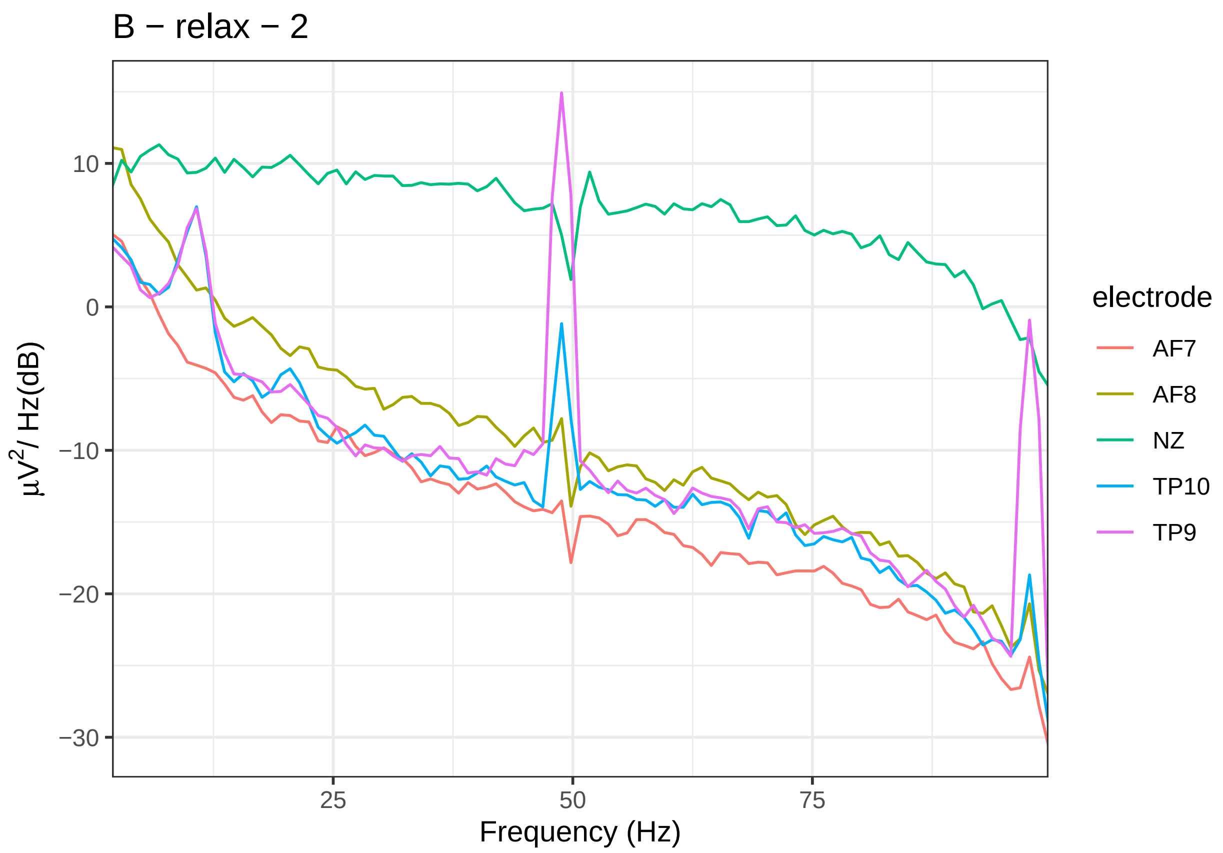
```r
show_psd(a_relaxed_2_obj, "A - relax - 2")
```



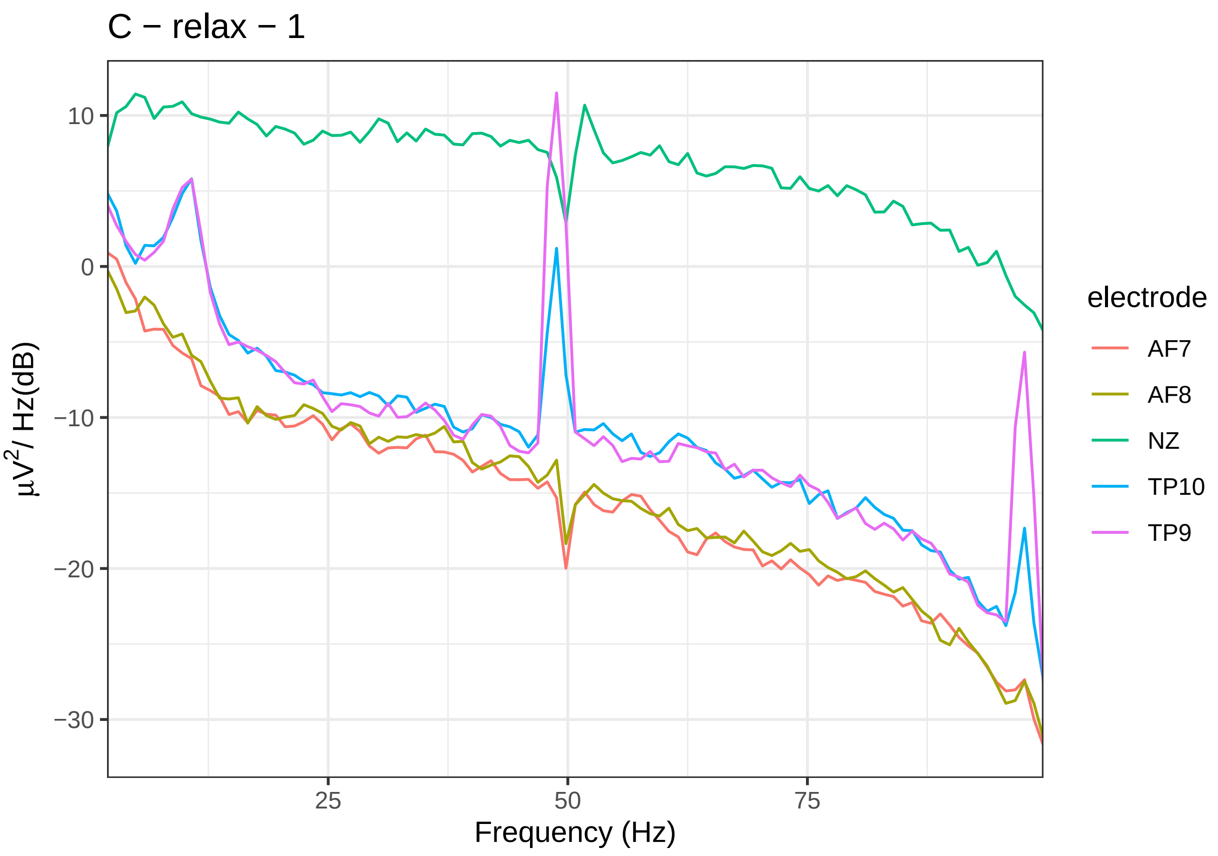
```
show_psd(a_relaxed_1_obj, "B - relax - 1")
```



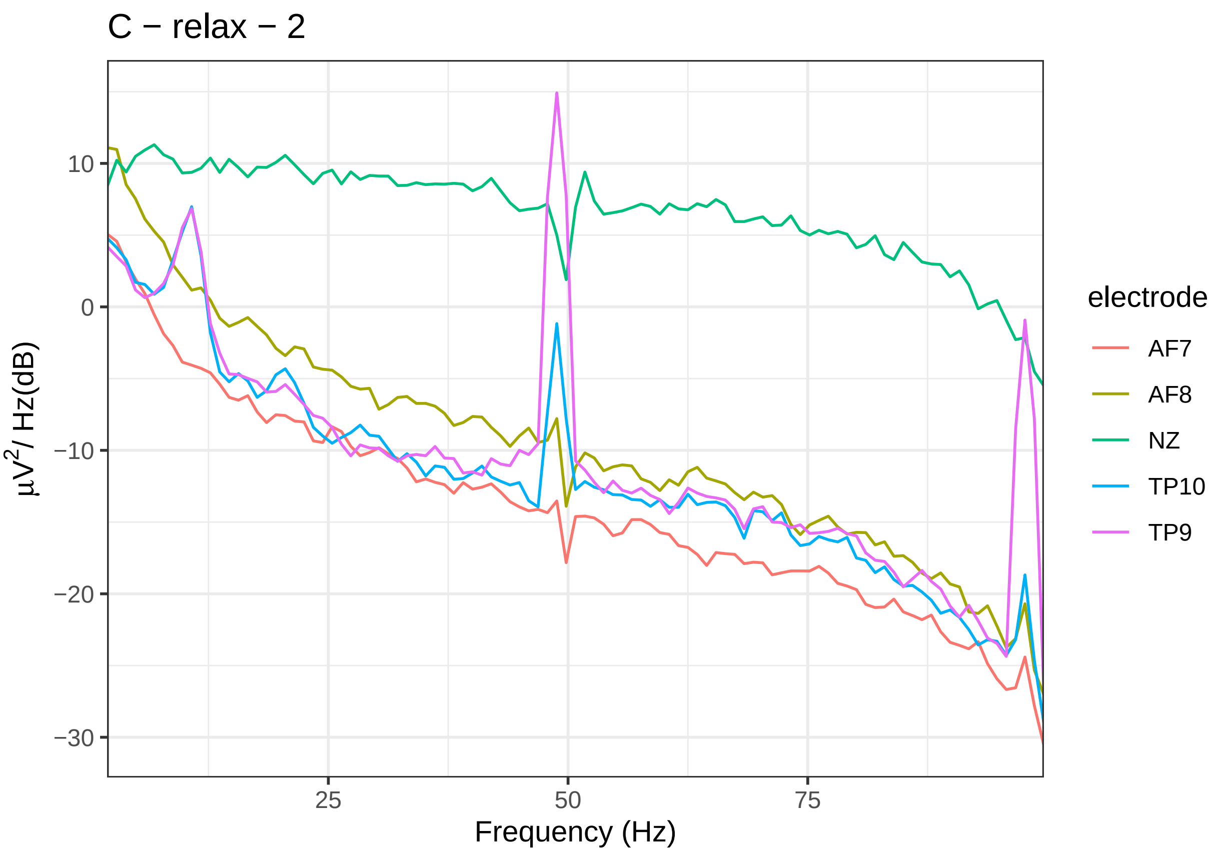
```
show_psd(a_relaxed_2_obj, "B - relax - 2")
```



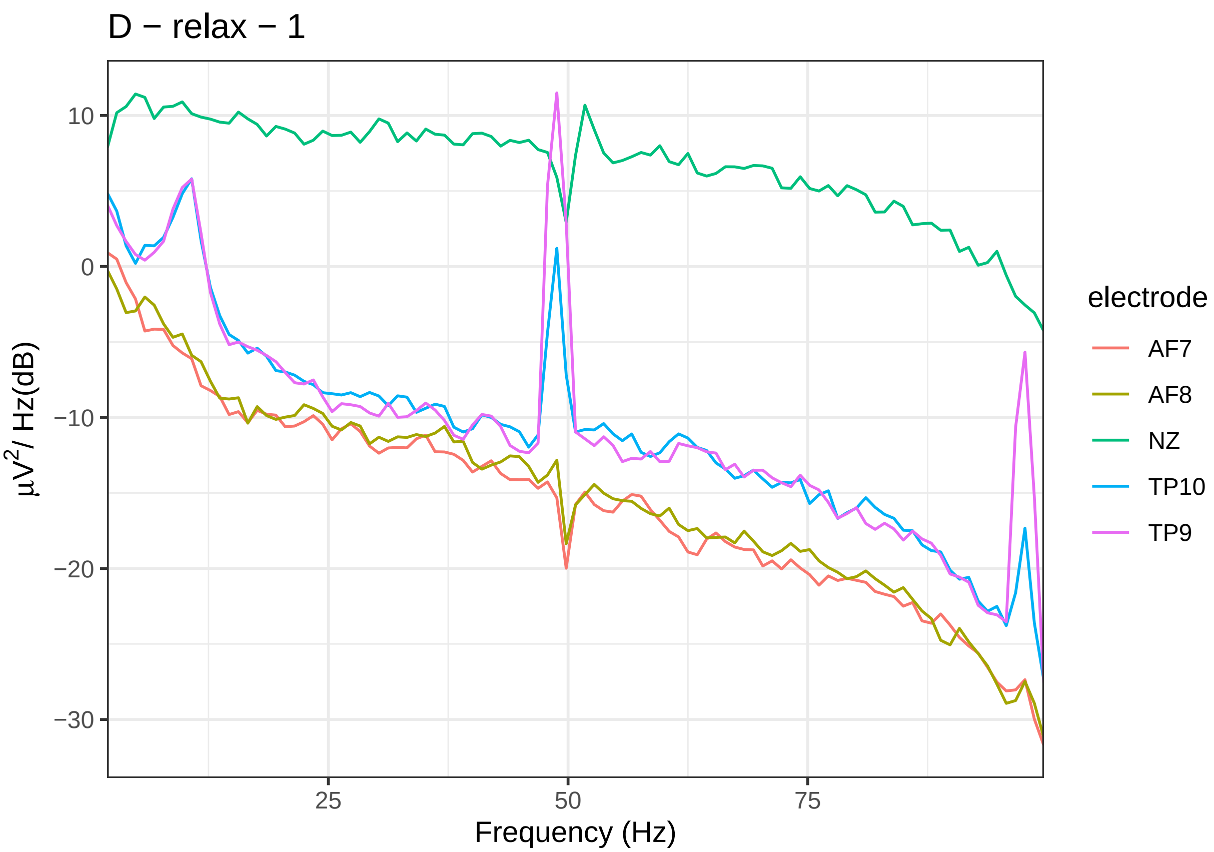
```
show_psd(a_relaxed_1_obj, "C - relax - 1")
```



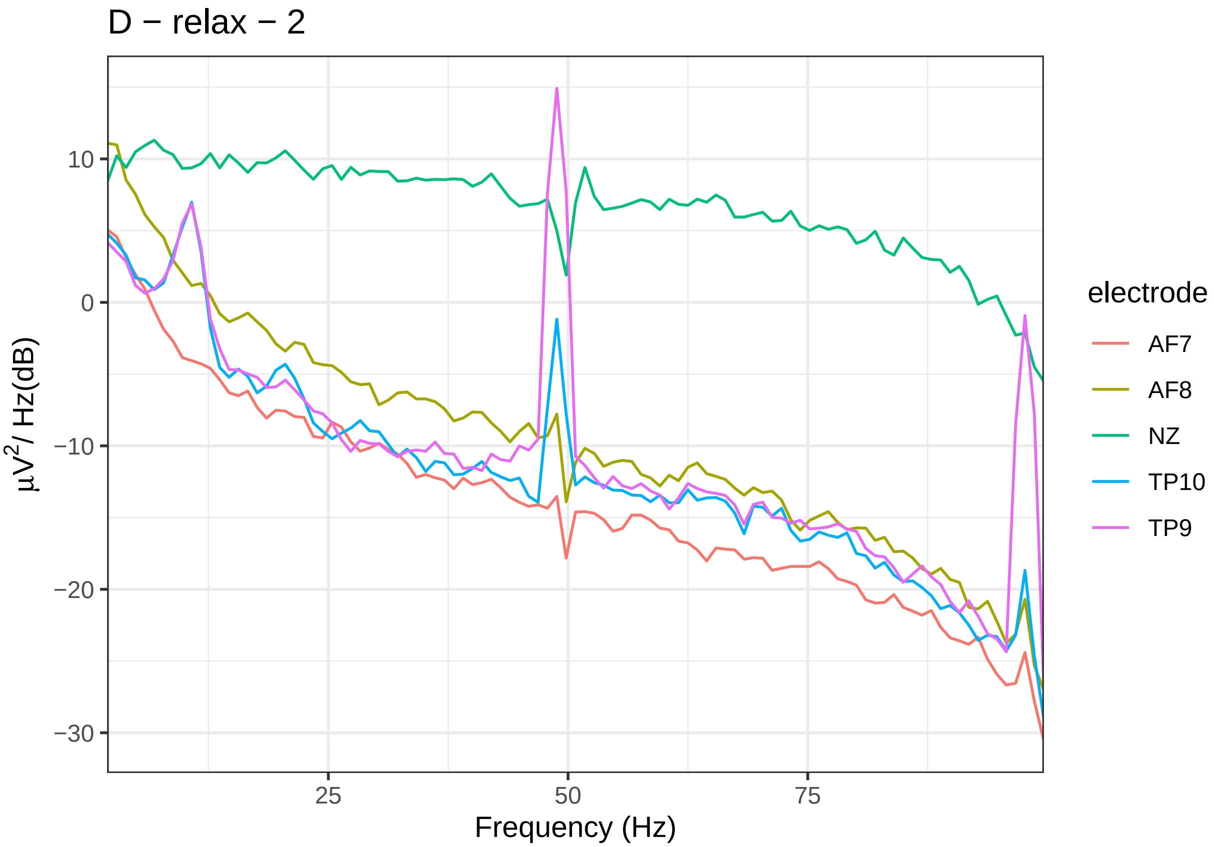
```
show_psd(a_relaxed_2_obj, "C - relax - 2")
```



```
show_psd(a_relaxed_1_obj, "D - relax - 1")
```



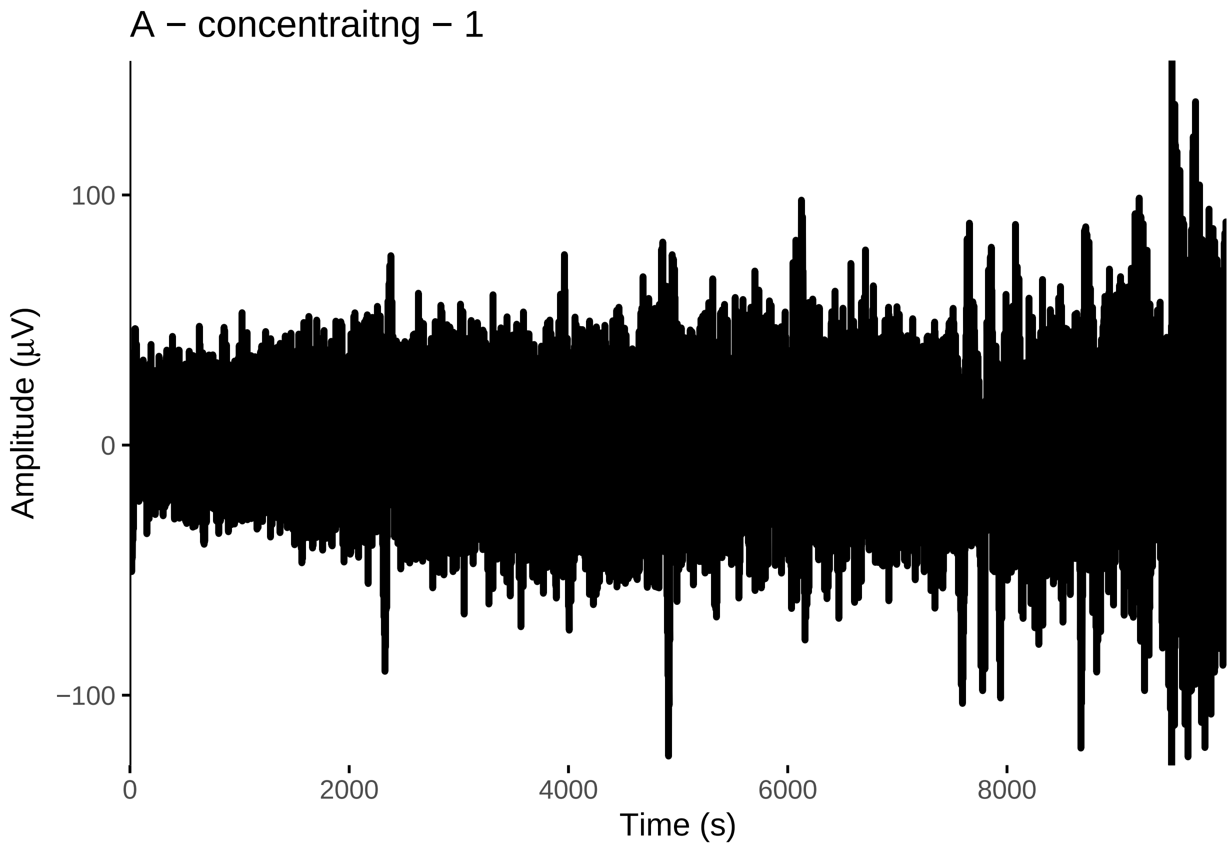
```
show_psd(a_relaxed_2_obj, "D - relax - 2")
```



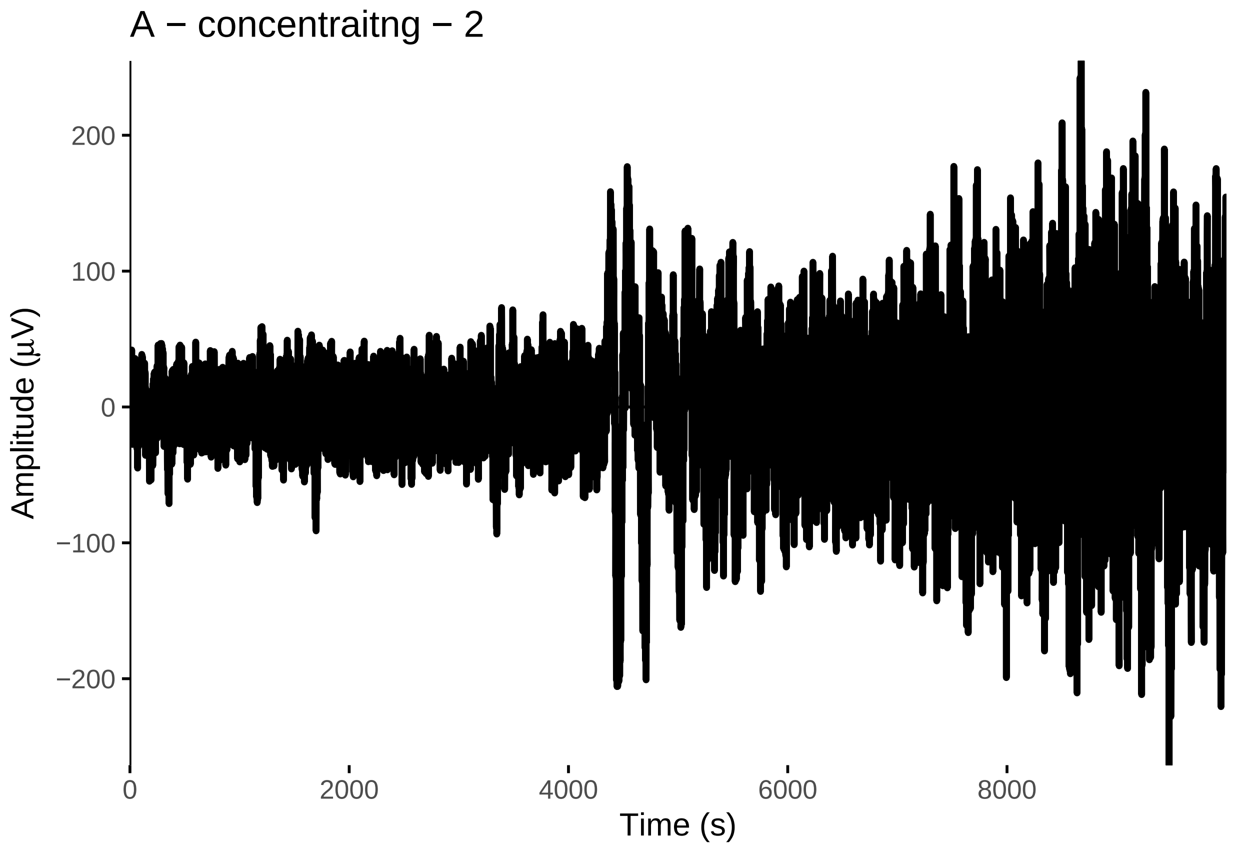
We noticed that Right.AUX recordings doesn't help in pattern recognition (values always oscillates around similar power for a given frequencies, despite the mental state). That's why for averaged frequency-time analysis we drop this channel.

Below we clearly see, that during concentration brain waves have higher amplitudes. The lowest brain activity is during relaxation.

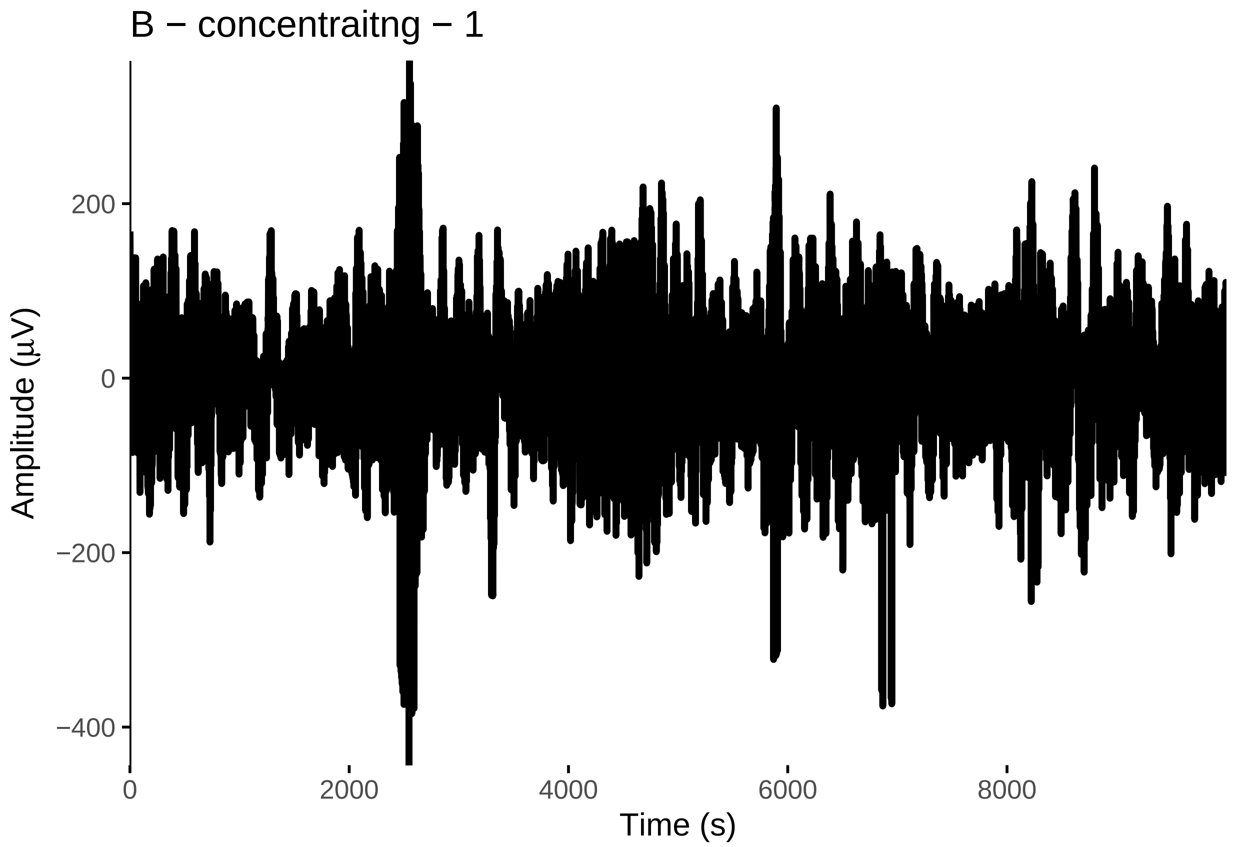
```
show_timecourse <- function(eeg_obj, title) {
  return (plot_timecourse(eeg_obj, electrode = c("AF7", "AF8", "TP10", "TP10")) + ggtitle(title))
}

show_timecourse(a_concentrating_1_obj, "A - concentraitng - 1")
```



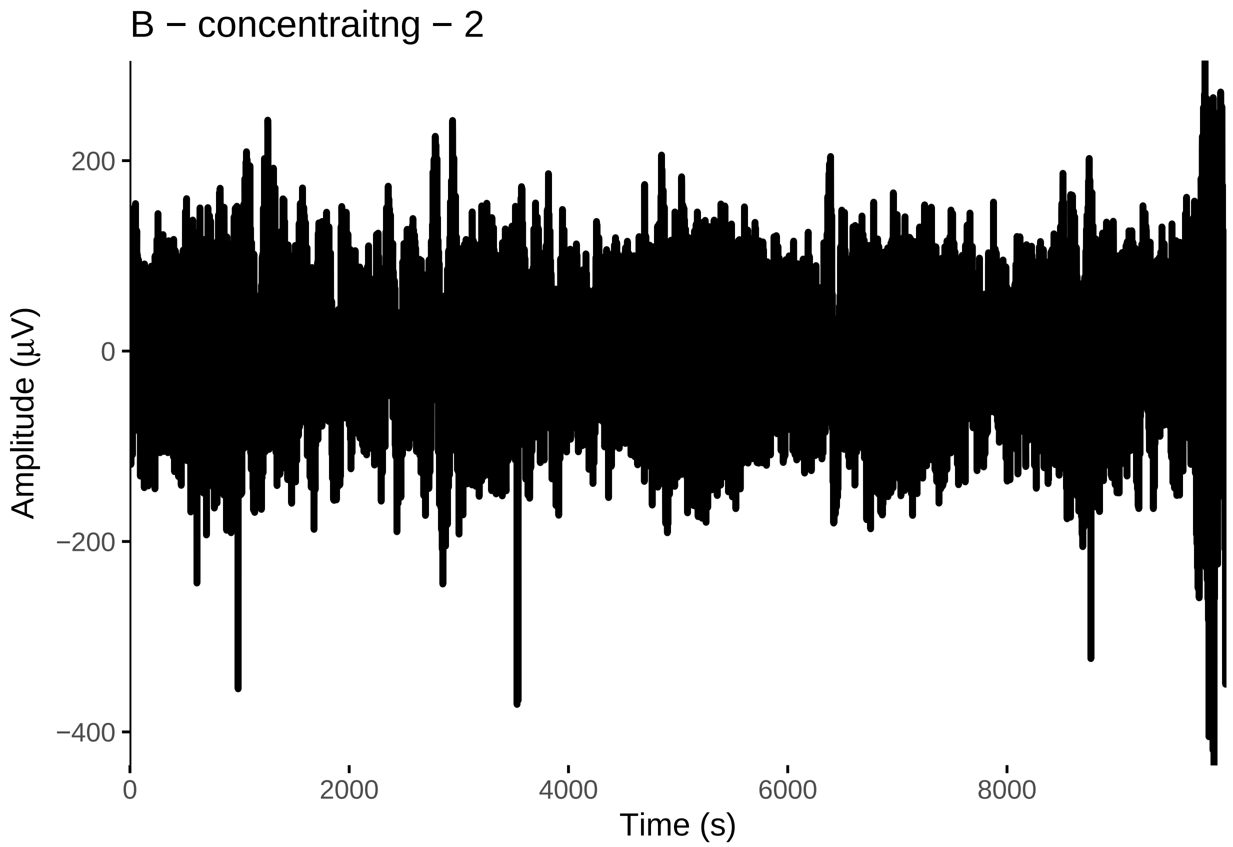
```
show_timecourse(a_concentrating_2_obj, "A - concentraitng - 2")
```



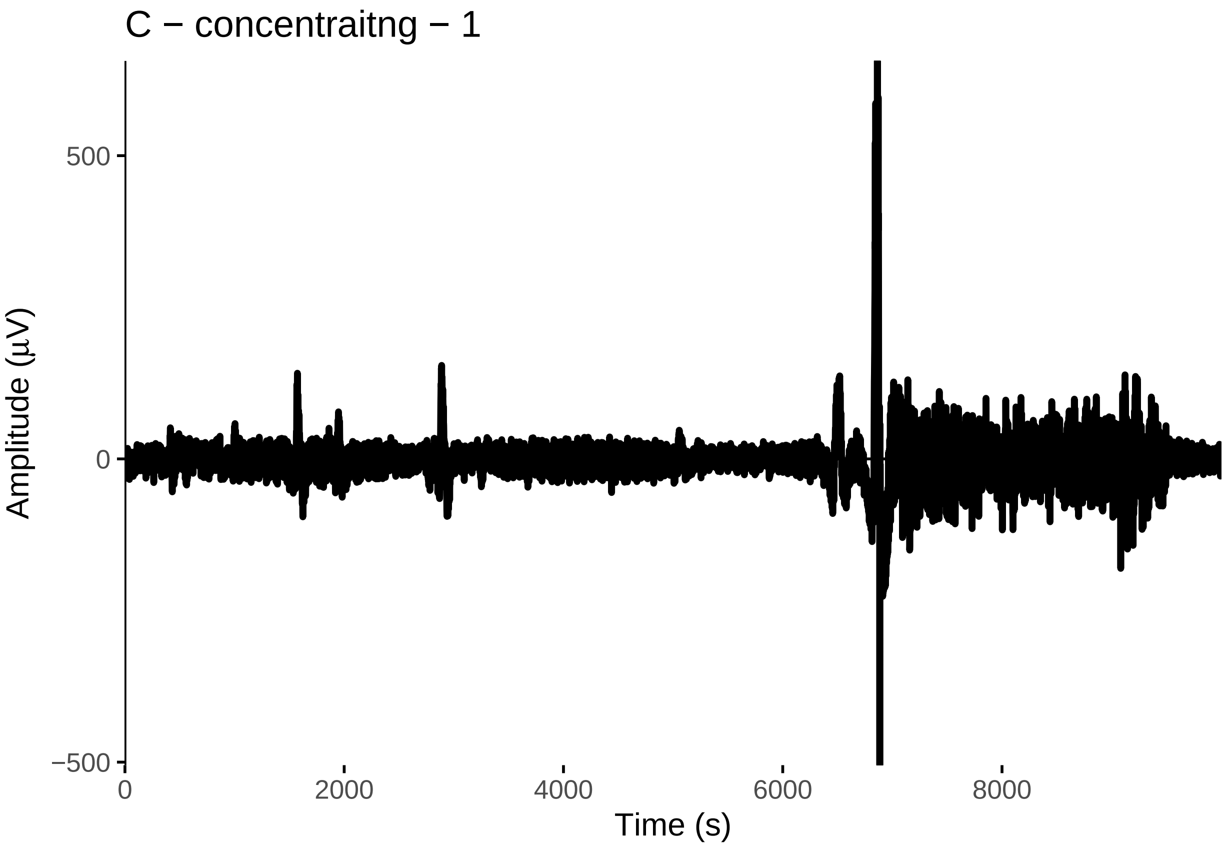
```r
show_timecourse(b_concentrating_1_obj, "B - concentraitng - 1")
```



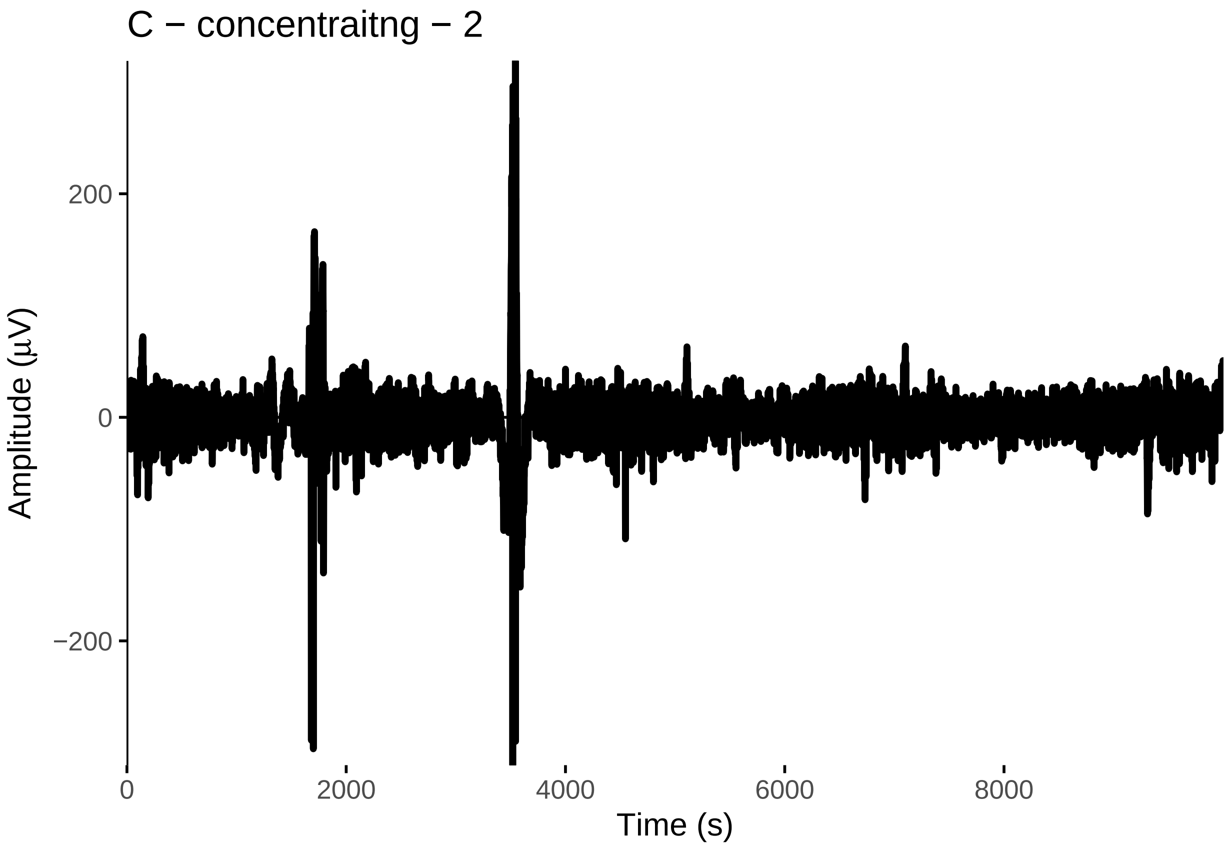
```
show_timecourse(b_concentrating_2_obj, "B - concentraitng - 2")
```



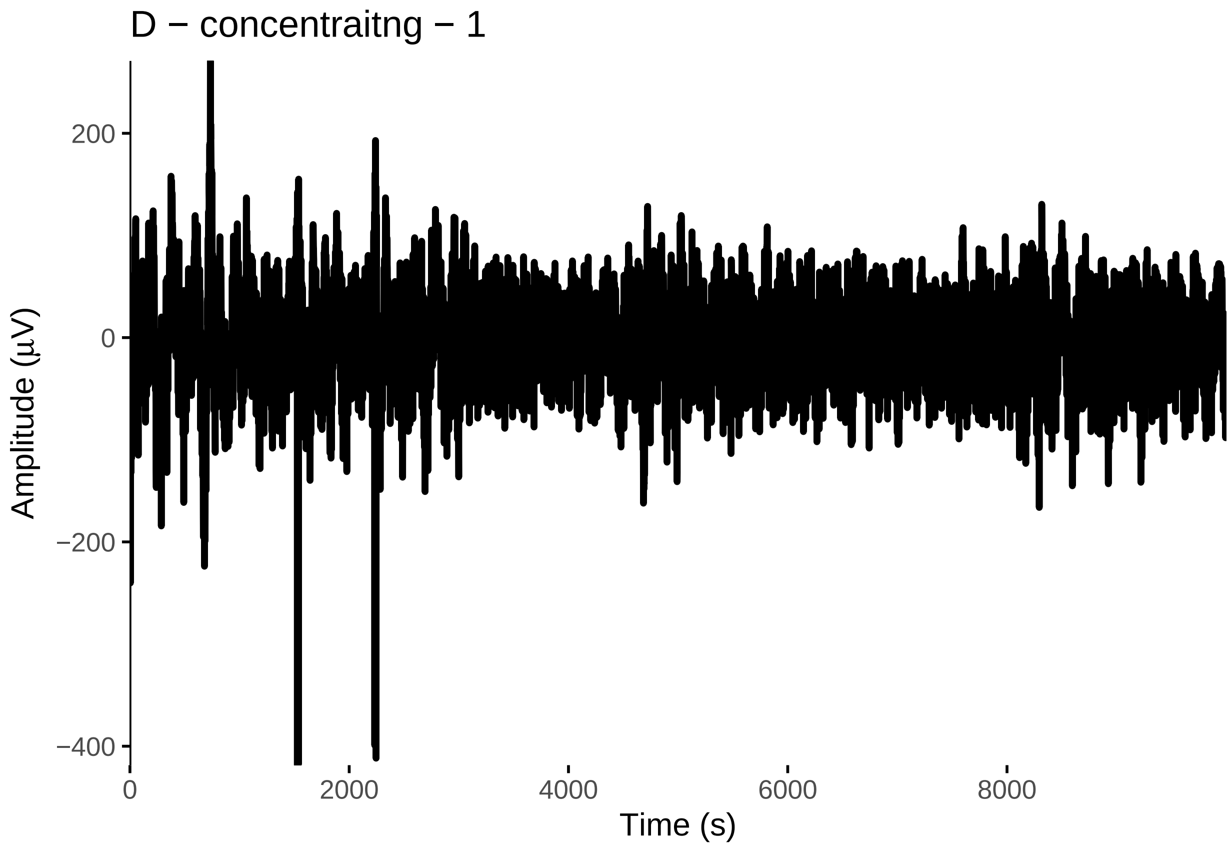
```
show_timecourse(c_concentrating_1_obj, "C - concentraitng - 1")
```



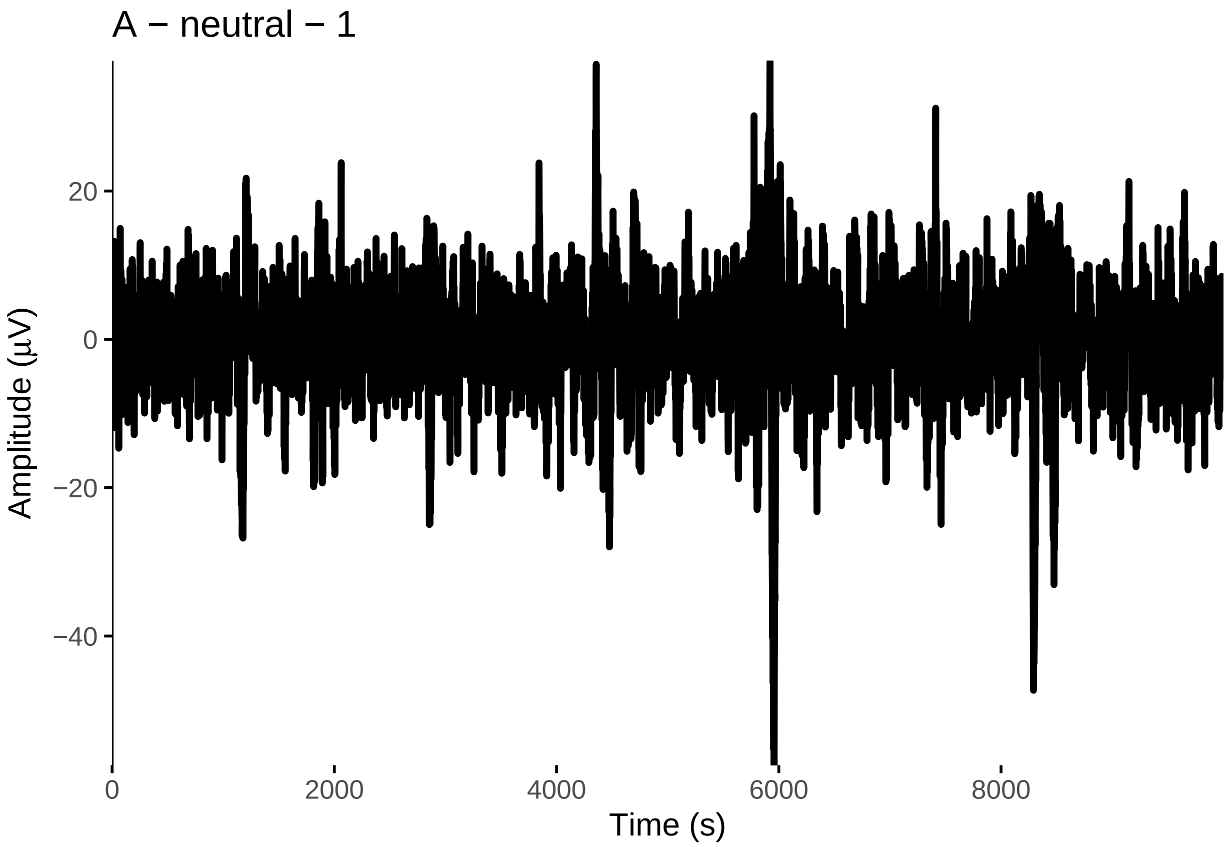
```r
show_timecourse(c_concentrating_2_obj, "C - concentraitng - 2")
```



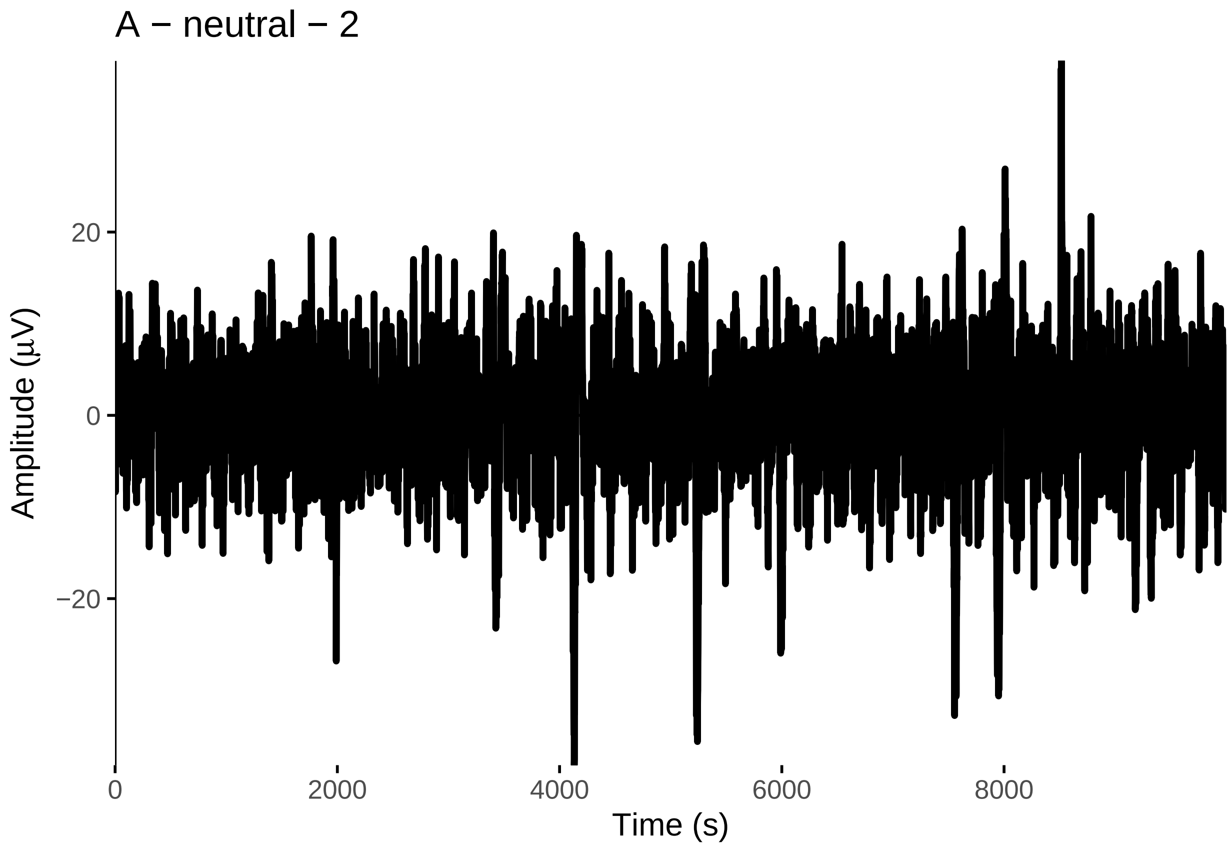
```
show_timecourse(d_concentrating_1_obj, "D - concentraitng - 1")
```



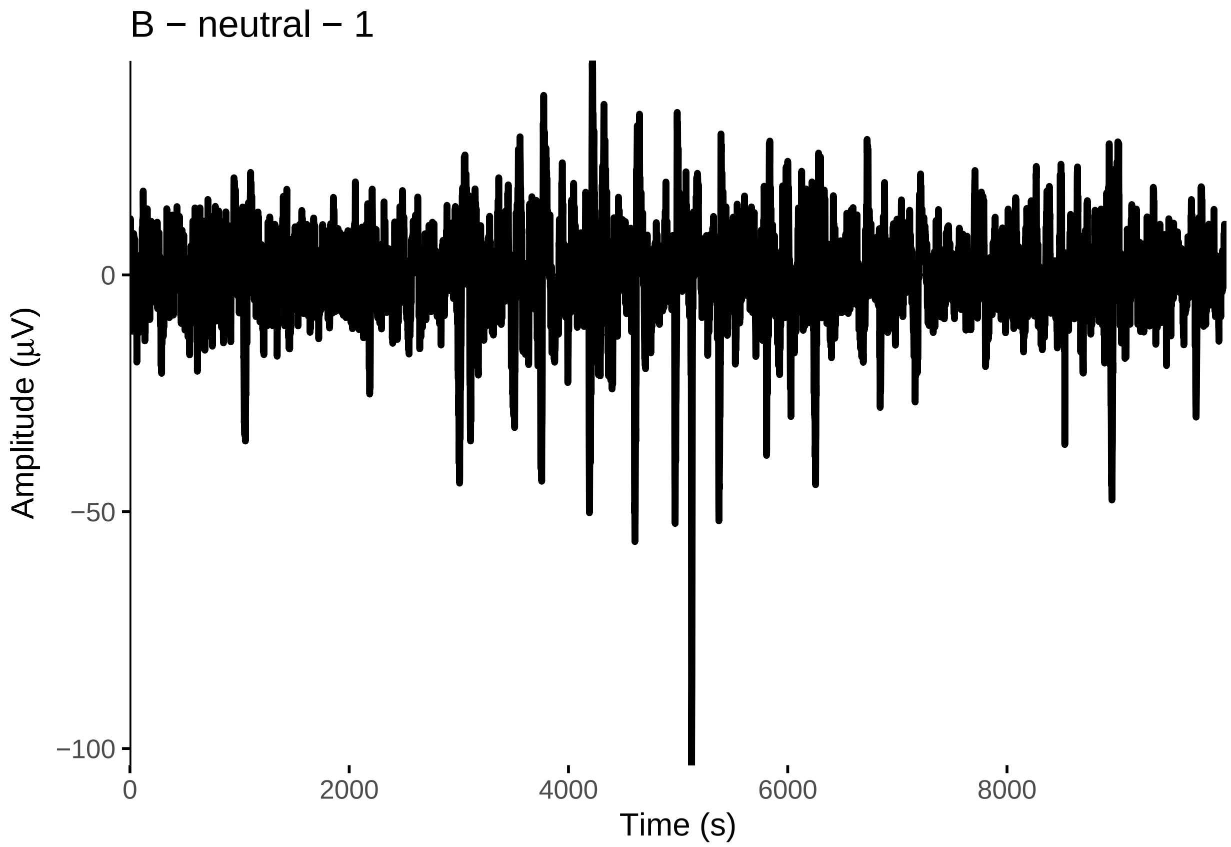
```r
show_timecourse(a_neutral_1_obj, "A - neutral - 1")
```



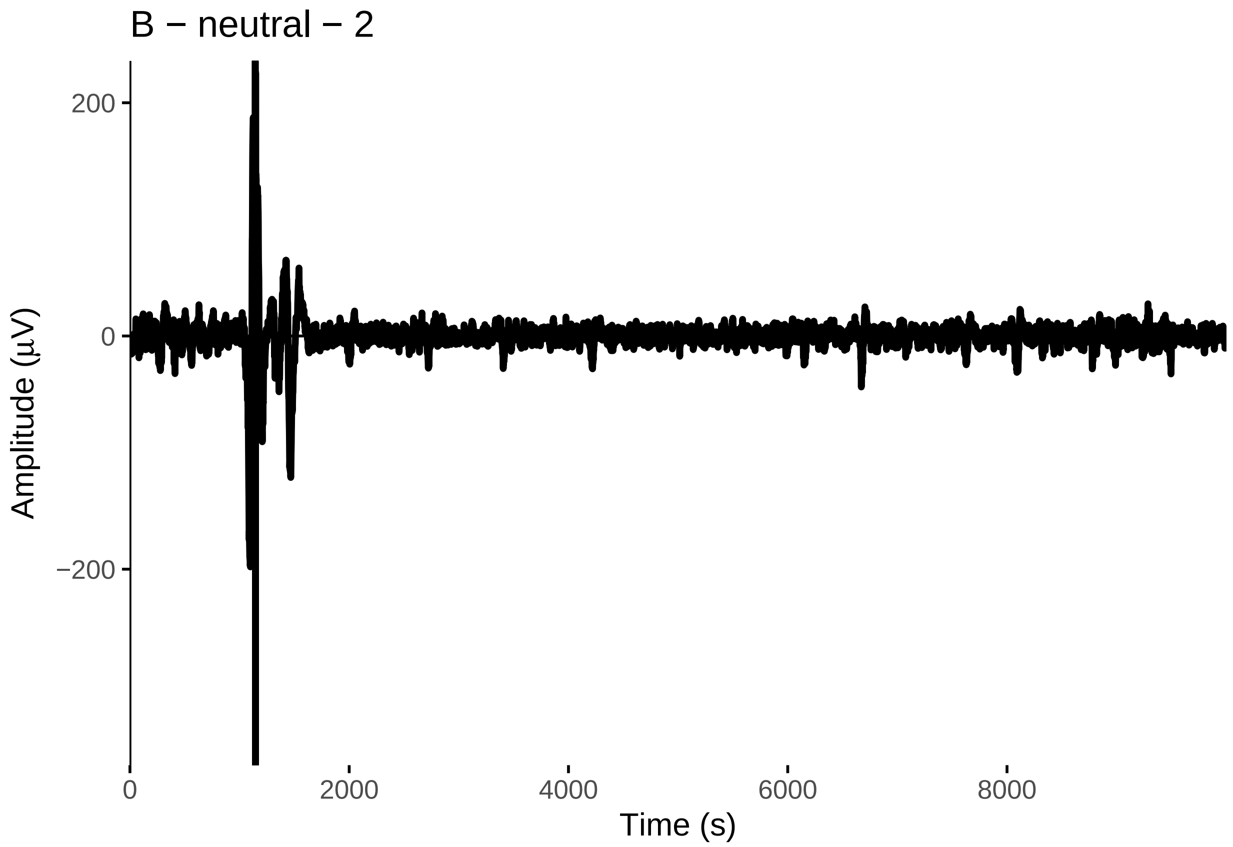
```
show_timecourse(a_neutral_2_obj, "A - neutral - 2")
```



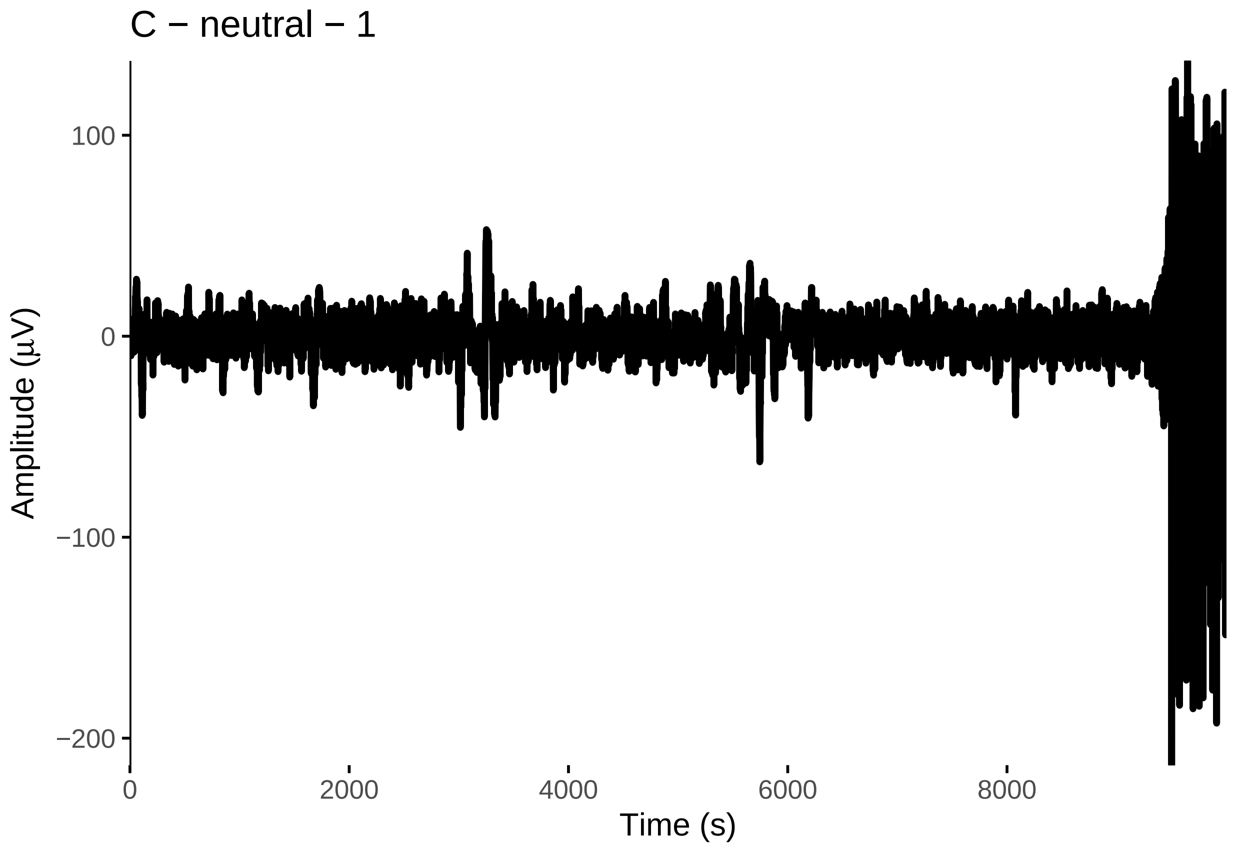
```
show_timecourse(b_neutral_1_obj, "B - neutral - 1")
```



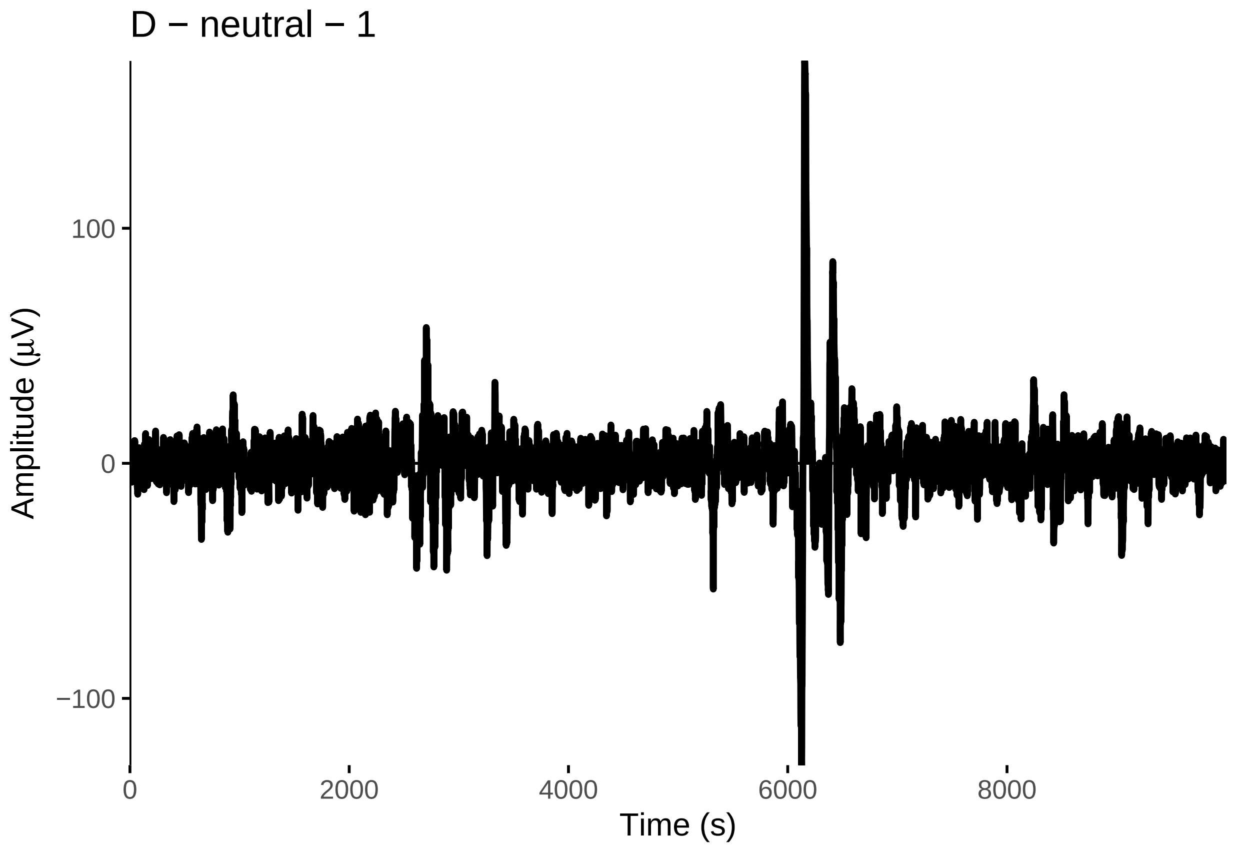
```r
show_timecourse(b_neutral_2_obj, "B - neutral - 2")
```



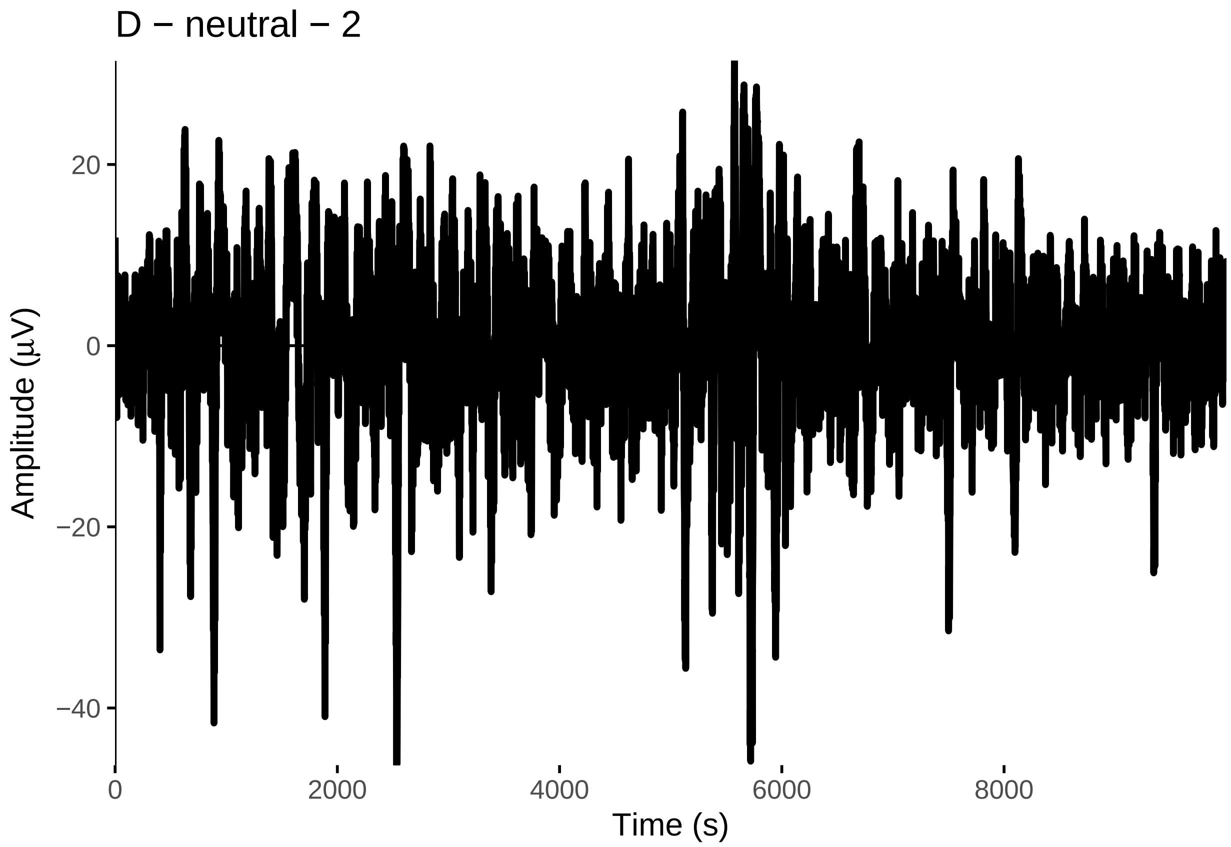
```
show_timecourse(c_neutral_1_obj, "C - neutral - 1")
```



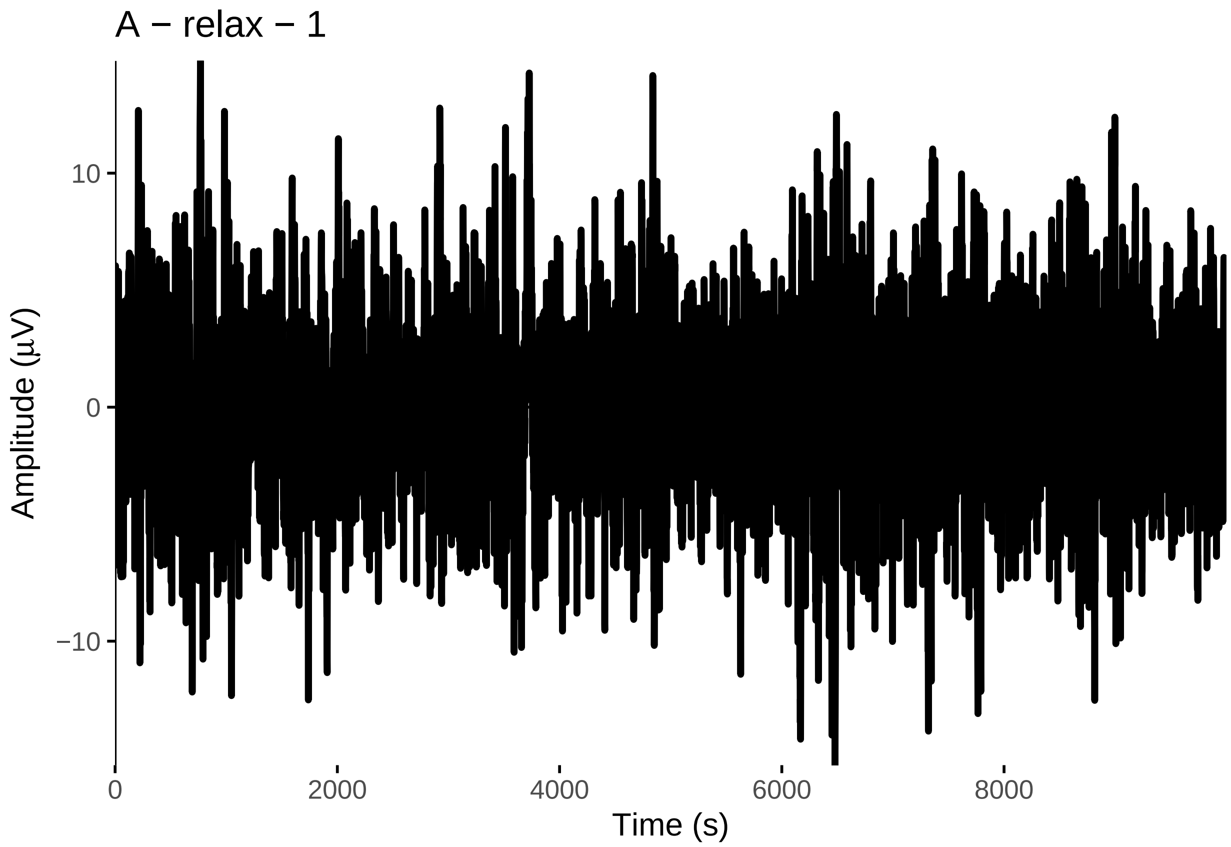
```
show_timecourse(d_neutral_1_obj, "D - neutral - 1")
```



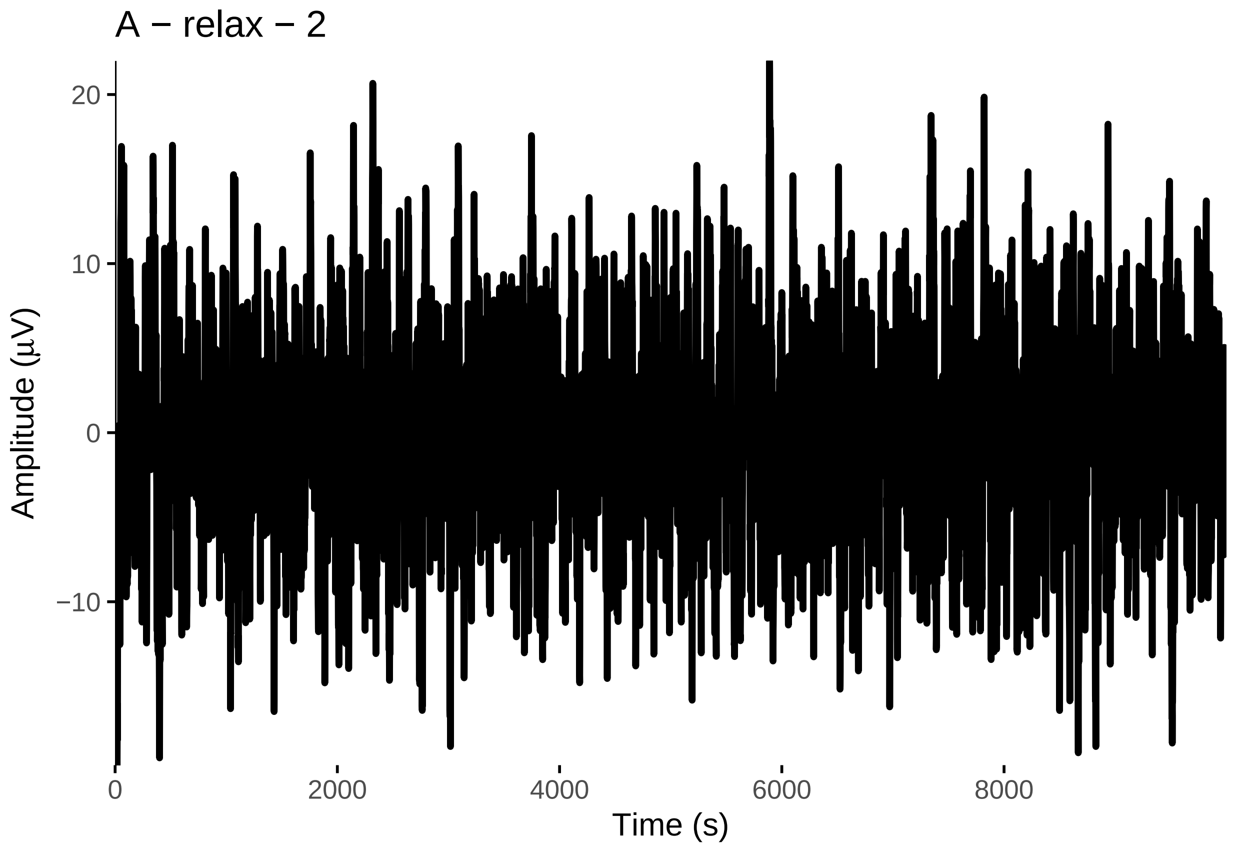
```
show_timecourse(d_neutral_2_obj, "D - neutral - 2")
```



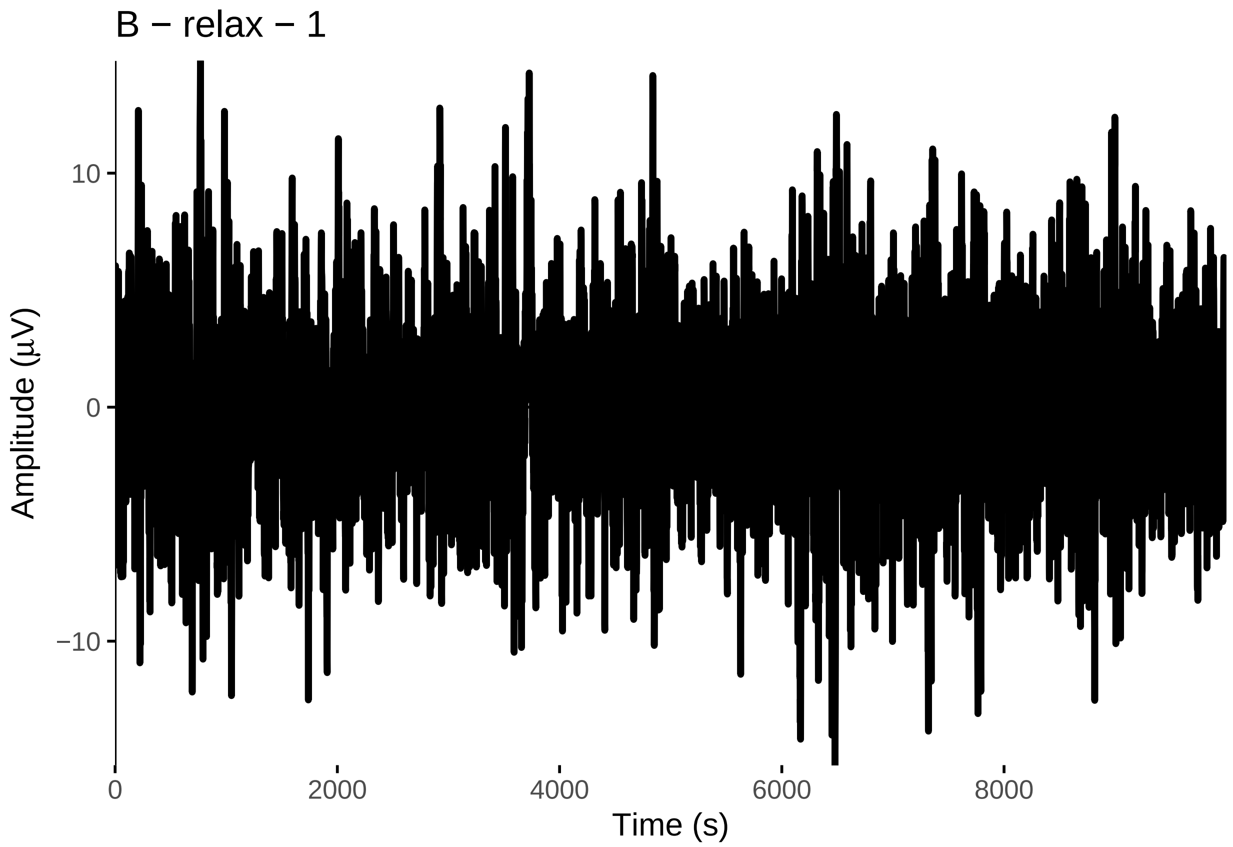
```r
show_timecourse(a_relaxed_1_obj, "A - relax - 1")
```



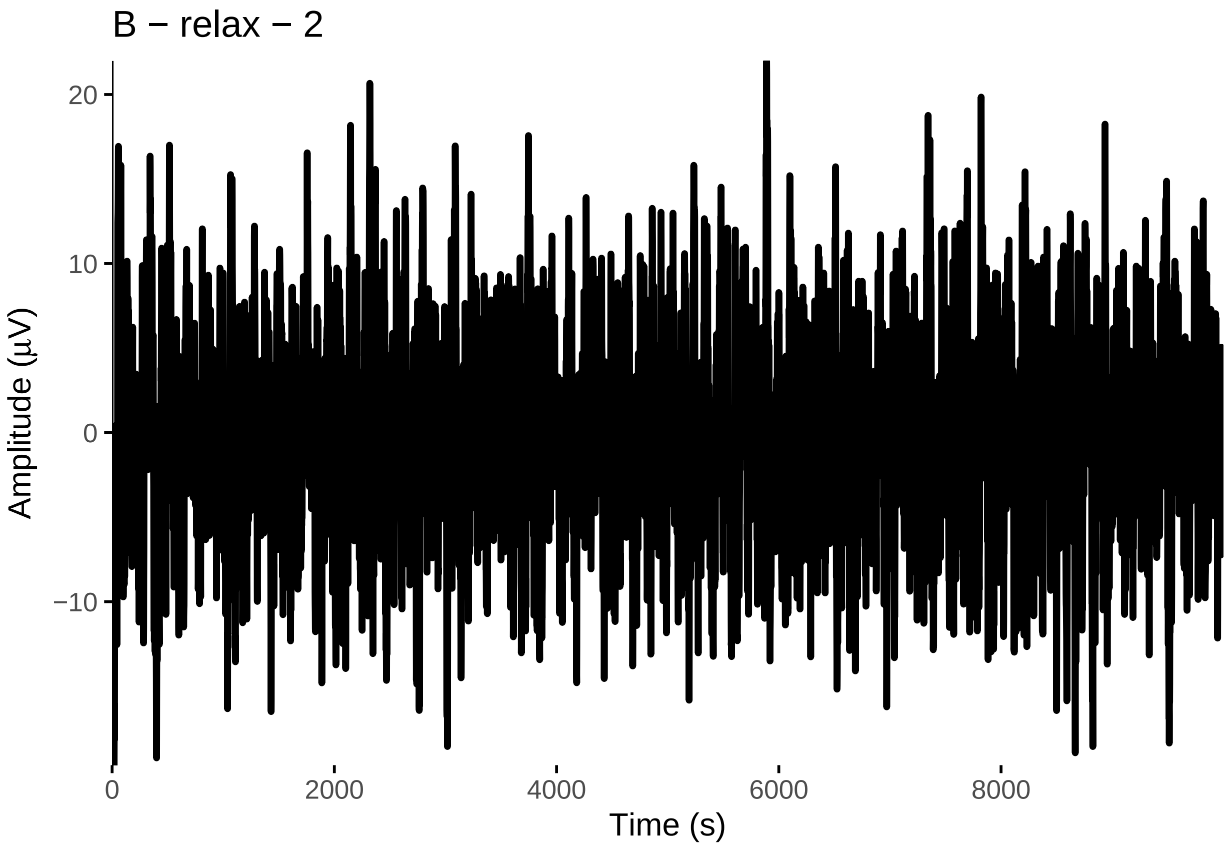
```
show_timecourse(a_relaxed_2_obj, "A - relax - 2")
```



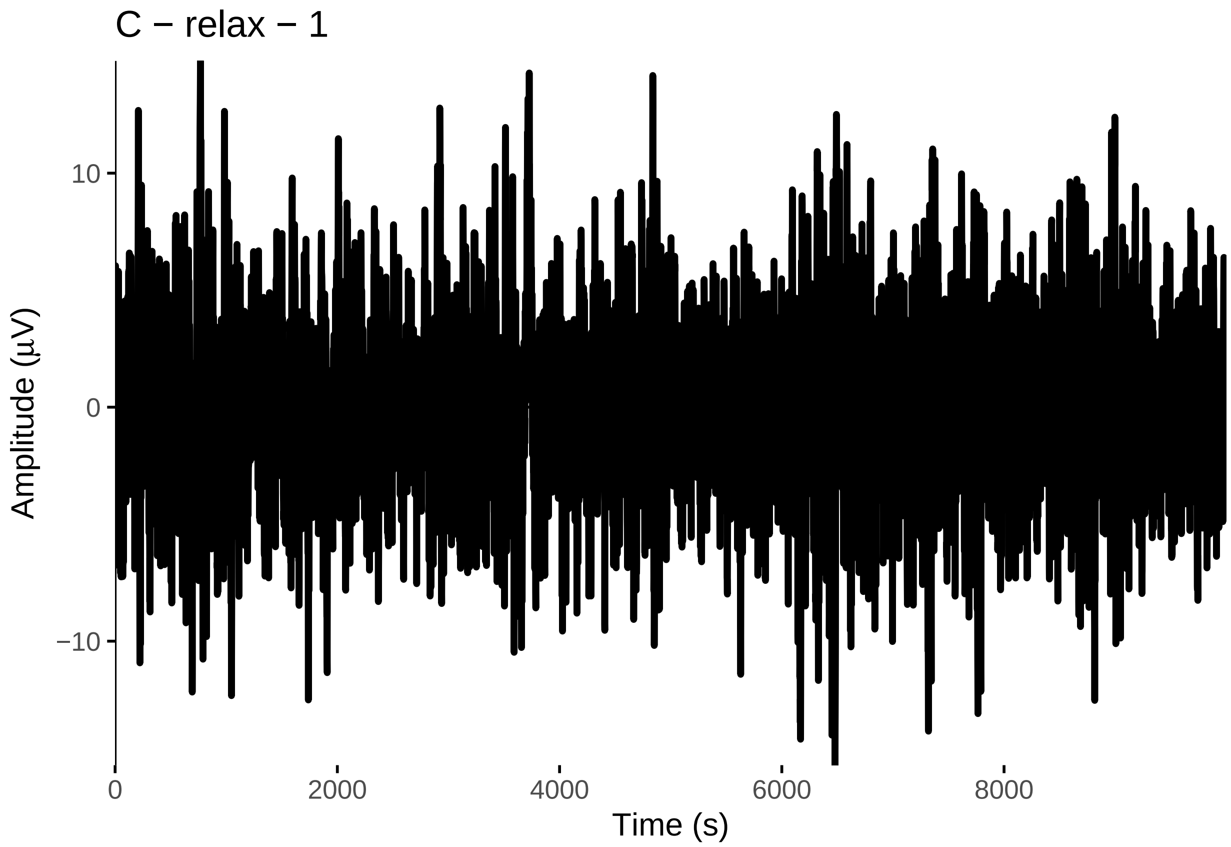
```r
show_timecourse(a_relaxed_1_obj, "B - relax - 1")
```



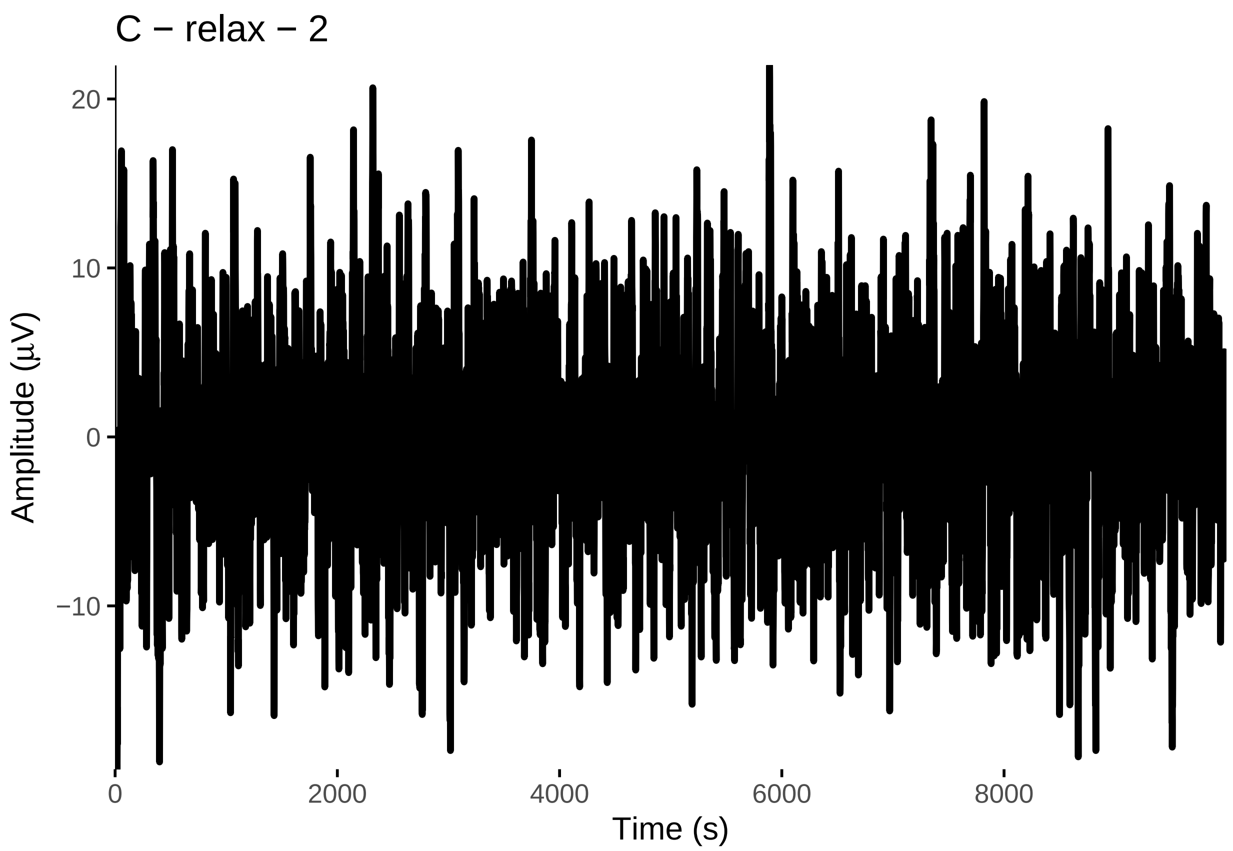
```r
show_timecourse(a_relaxed_2_obj, "B - relax - 2")
```



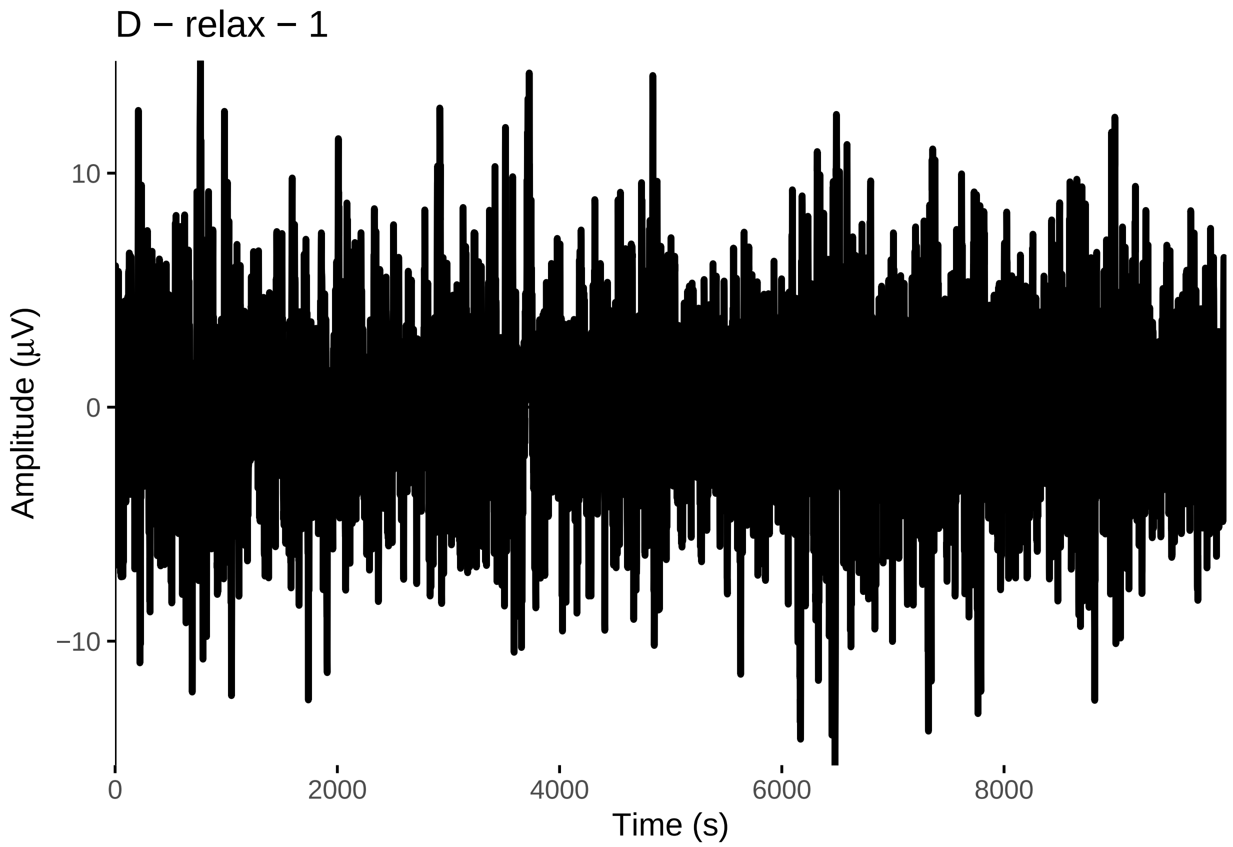
```
show_timecourse(a_relaxed_1_obj, "C - relax - 1")
```



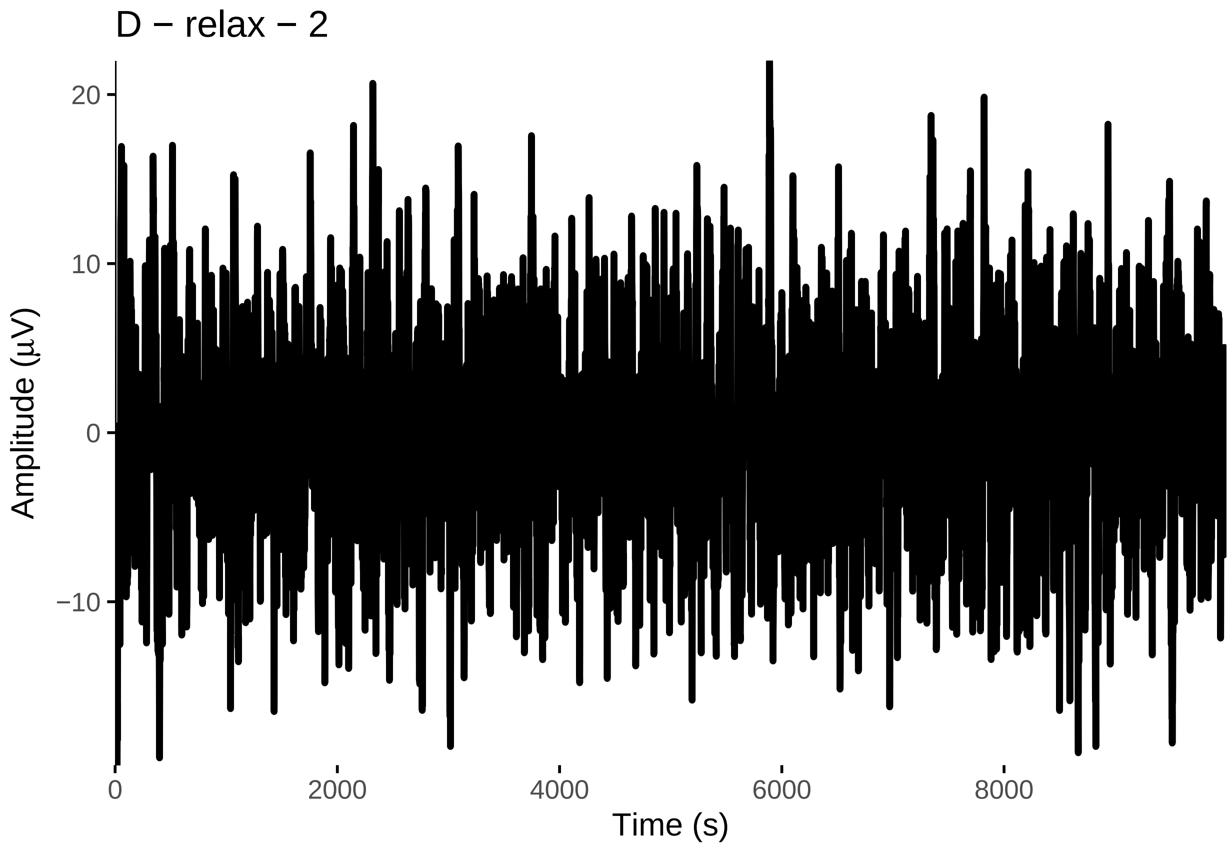
```r
show_timecourse(a_relaxed_2_obj, "C - relax - 2")
```



```
show_timecourse(a_relaxed_1_obj, "D - relax - 1")
```



```
show_timecourse(a_relaxed_2_obj, "D - relax - 2")
```



Feature extraction

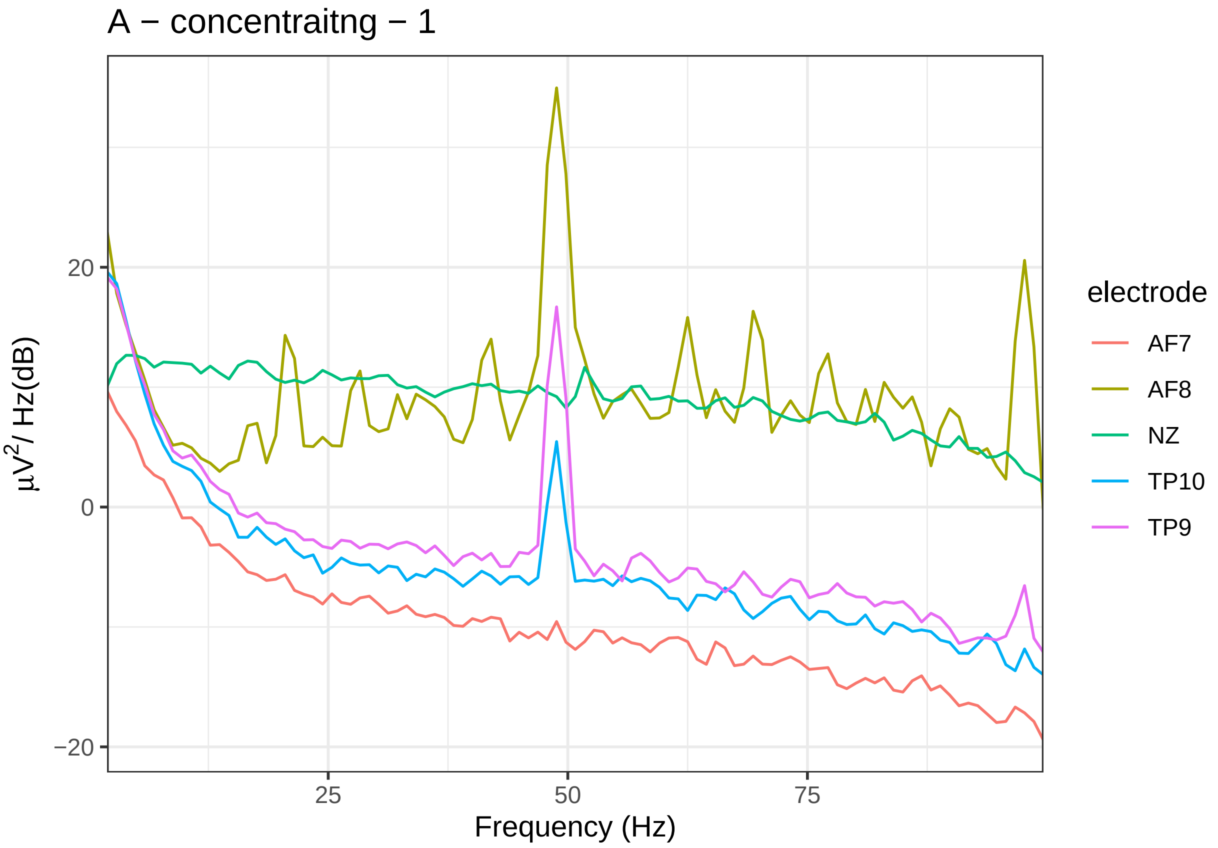
In order to better identify patterns or characteristics in the EEG data that are associated with specific mental states, we apply difference between EEG data during different mental states and a baseline (averaged neutral) state to extract features that represent the differences in brain activity across these states.

```
a_base = (a_neutral_1 + a_neutral_2) / 2
a_concentrating_1_obj <- wrap(a_concentrating_1 - a_base)
a_concentrating_2_obj <- wrap(a_concentrating_2 - a_base)
a_neutral_1_obj <- wrap(a_neutral_1 - a_base)
a_neutral_2_obj <- wrap(a_neutral_2 - a_base)
a_relaxed_1_obj <- wrap(a_relaxed_1 - a_base)
a_relaxed_2_obj <- wrap(a_relaxed_2 - a_base)

b_base = (b_neutral_1 + b_neutral_2) / 2
b_concentrating_1_obj <- wrap(b_concentrating_1 - b_base)
b_concentrating_2_obj <- wrap(b_concentrating_2 - b_base)
b_neutral_1_obj <- wrap(b_neutral_1 - b_base)
b_neutral_2_obj <- wrap(b_neutral_2 - b_base)
b_relaxed_1_obj <- wrap(b_relaxed_1 - b_base)
b_relaxed_2_obj <- wrap(b_relaxed_2 - b_base)

c_base = c_neutral_1
c_concentrating_1_obj <- wrap(c_concentrating_1 - c_base)
c_concentrating_2_obj <- wrap(c_concentrating_2 - c_base)
```

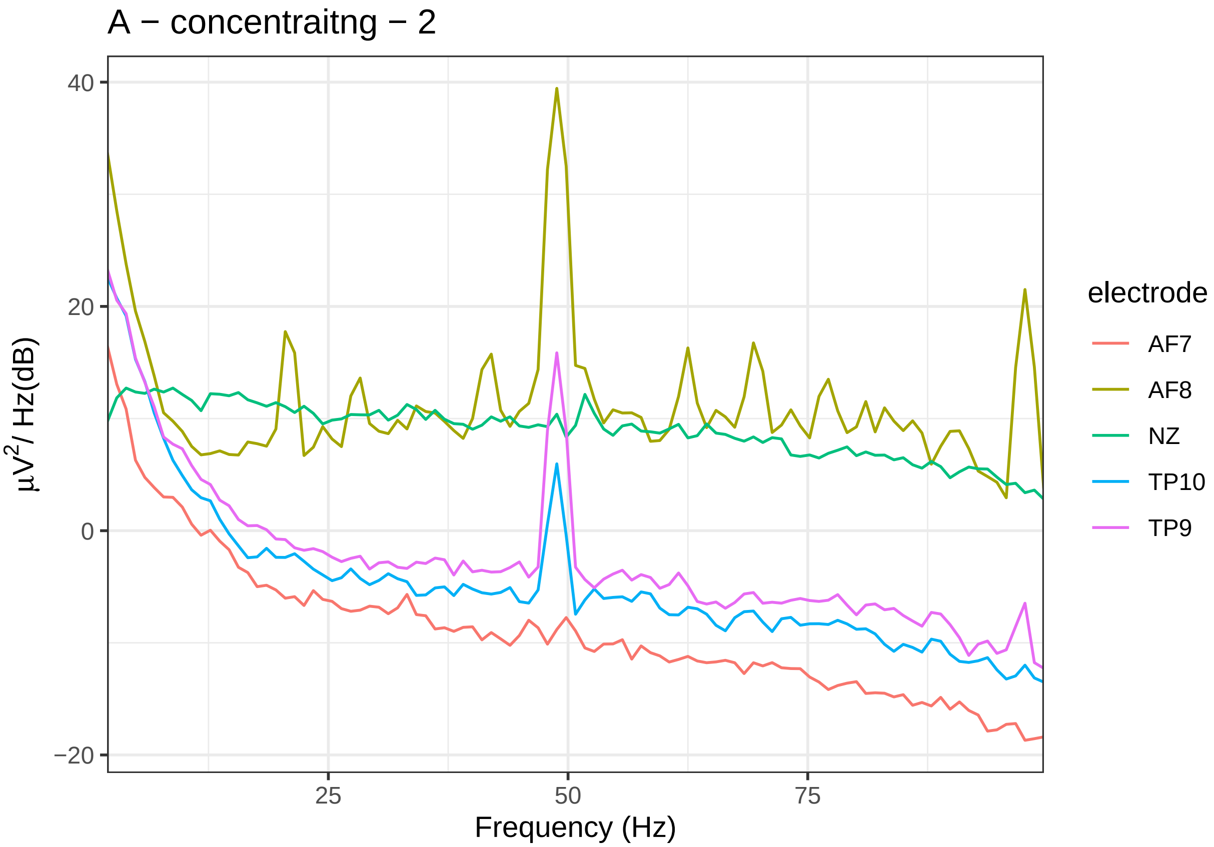
```
c_neutral_1_obj <- wrap(c_neutral_1 - c_base)
#c_neutral_2_obj <- wrap(c_neutral_2)
c_relaxed_1_obj <- wrap(c_relaxed_1 - c_base)
c_relaxed_2_obj <- wrap(c_relaxed_2 - c_base)

d_base = (d_neutral_1 + d_neutral_2) / 2
d_concentrating_1_obj <- wrap(d_concentrating_1 - d_base)
d_neutral_1_obj <- wrap(d_neutral_1 - d_base)
d_neutral_2_obj <- wrap(d_neutral_2 - d_base)
d_relaxed_1_obj <- wrap(d_relaxed_1 - d_base)
d_relaxed_2_obj <- wrap(d_relaxed_2 - d_base)
```

After applying the baseline results are more distinct for different states. For concentration power is distributed evenly, whereas for relaxation, the plot is left-skewed.

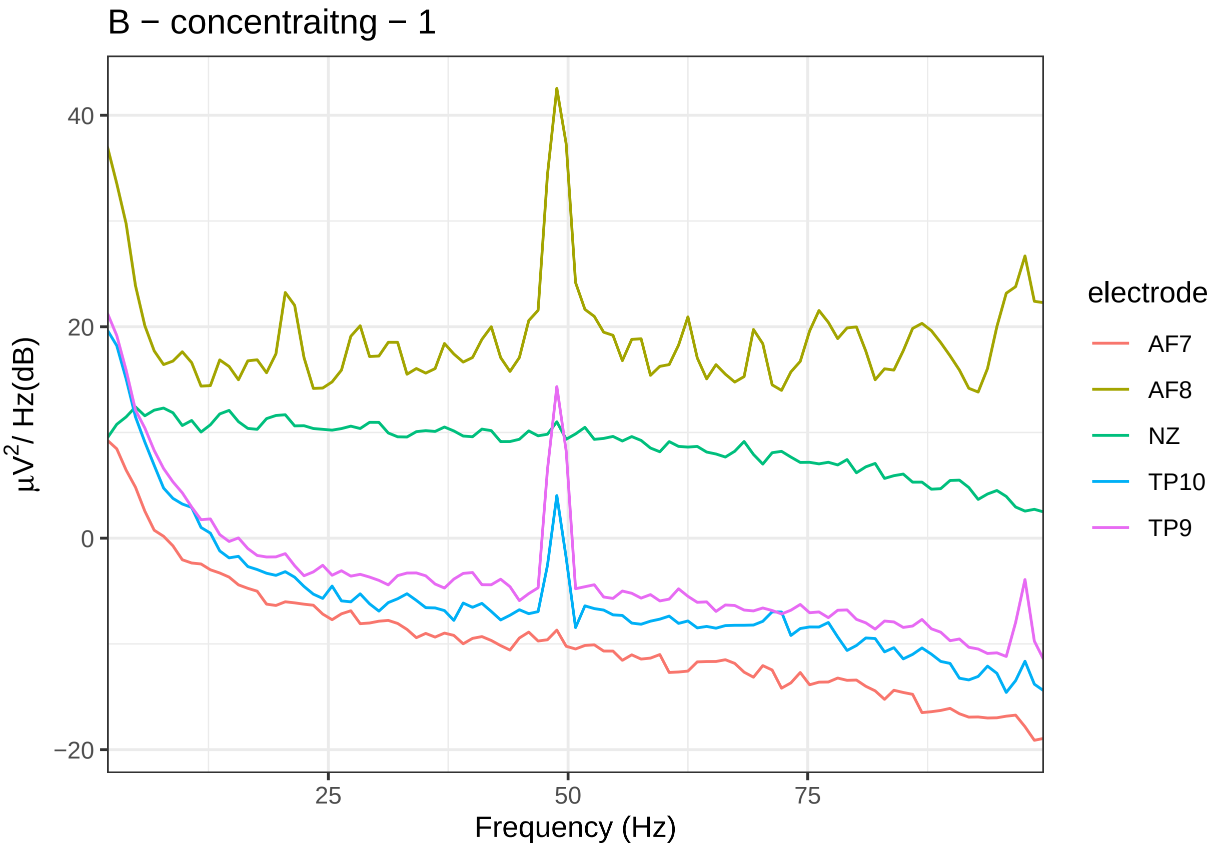
```
show_psd <- function(eeg_obj, title) {
  return (plot_psd(eeg_obj, freq_range = c(1, 100), ) + ggtitle(title))
}

show_psd(a_concentrating_1_obj, "A - concentraitng - 1")
```



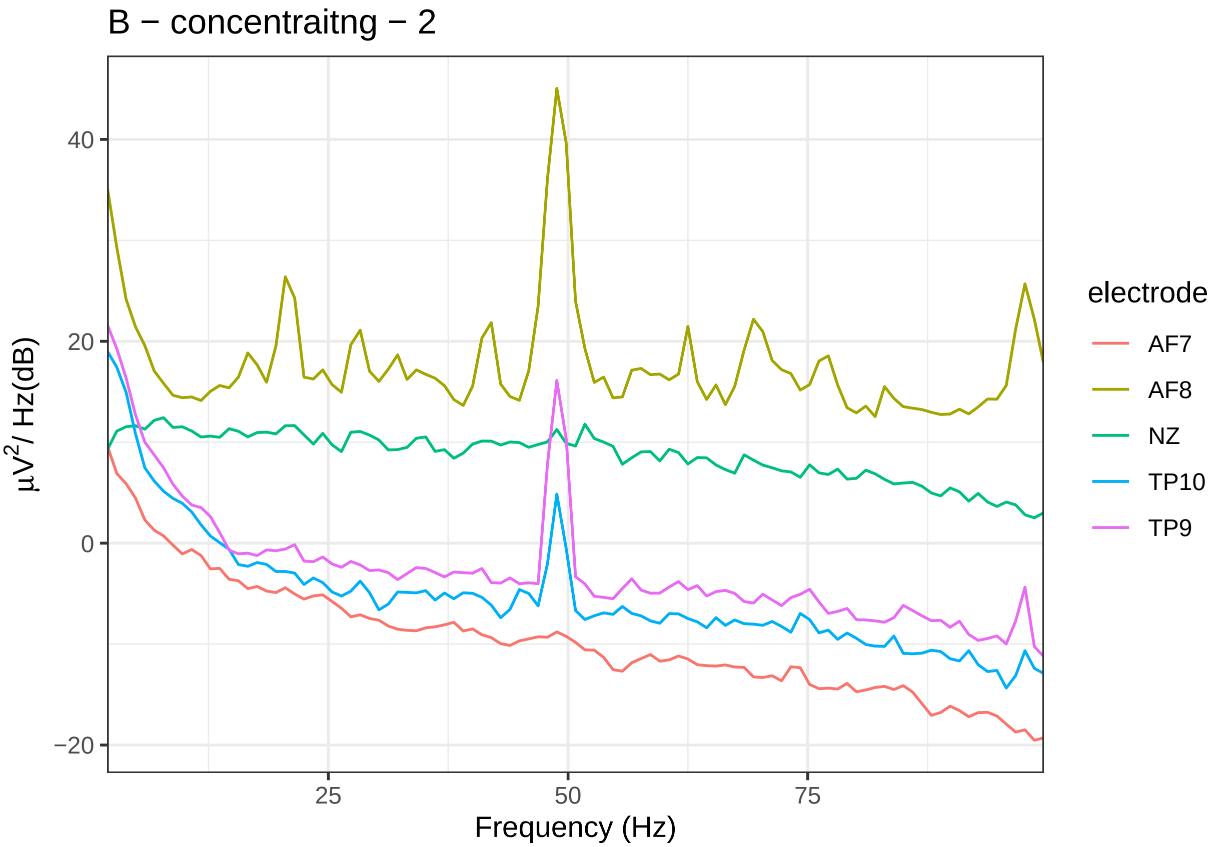
```
show_psd(a_concentrating_2_obj, "A - concentraitng - 2")
```



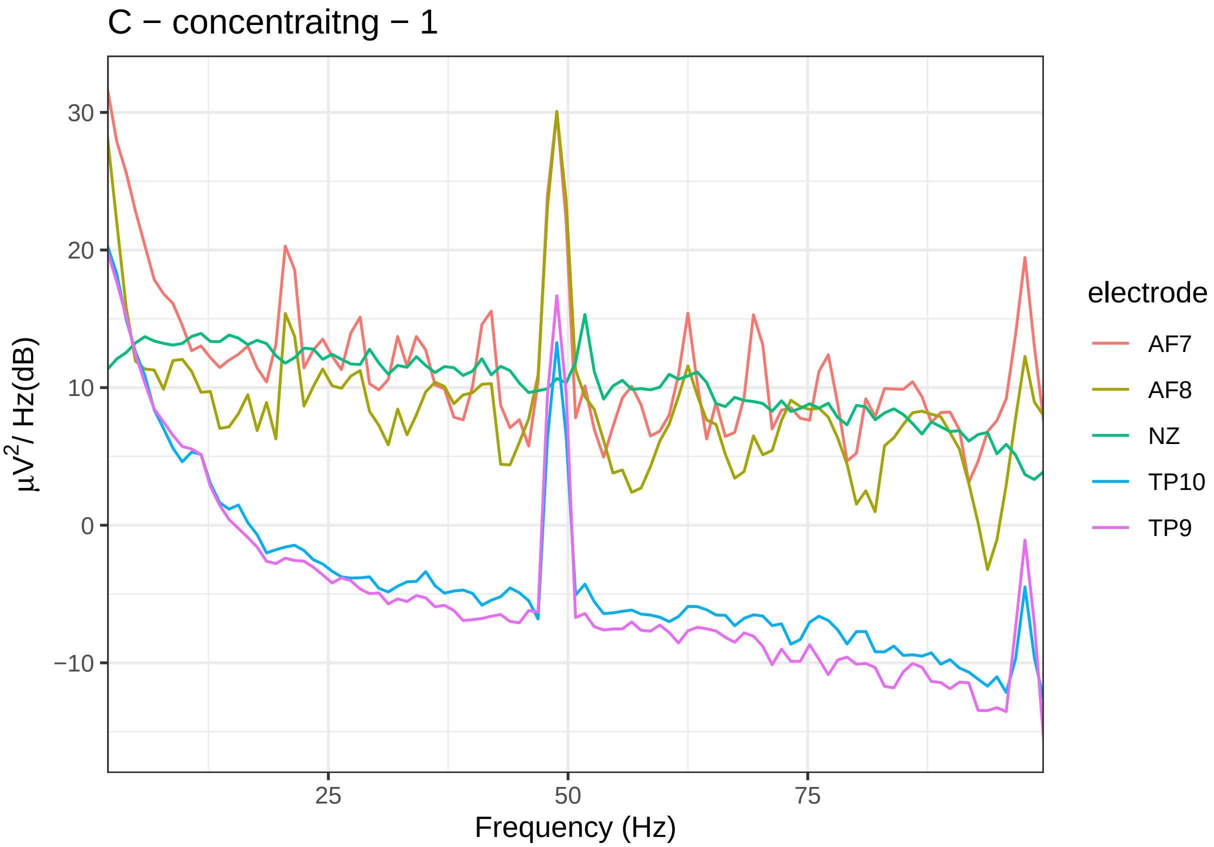
```
show_psd(b_concentrating_1_obj, "B - concentraitng - 1")
```



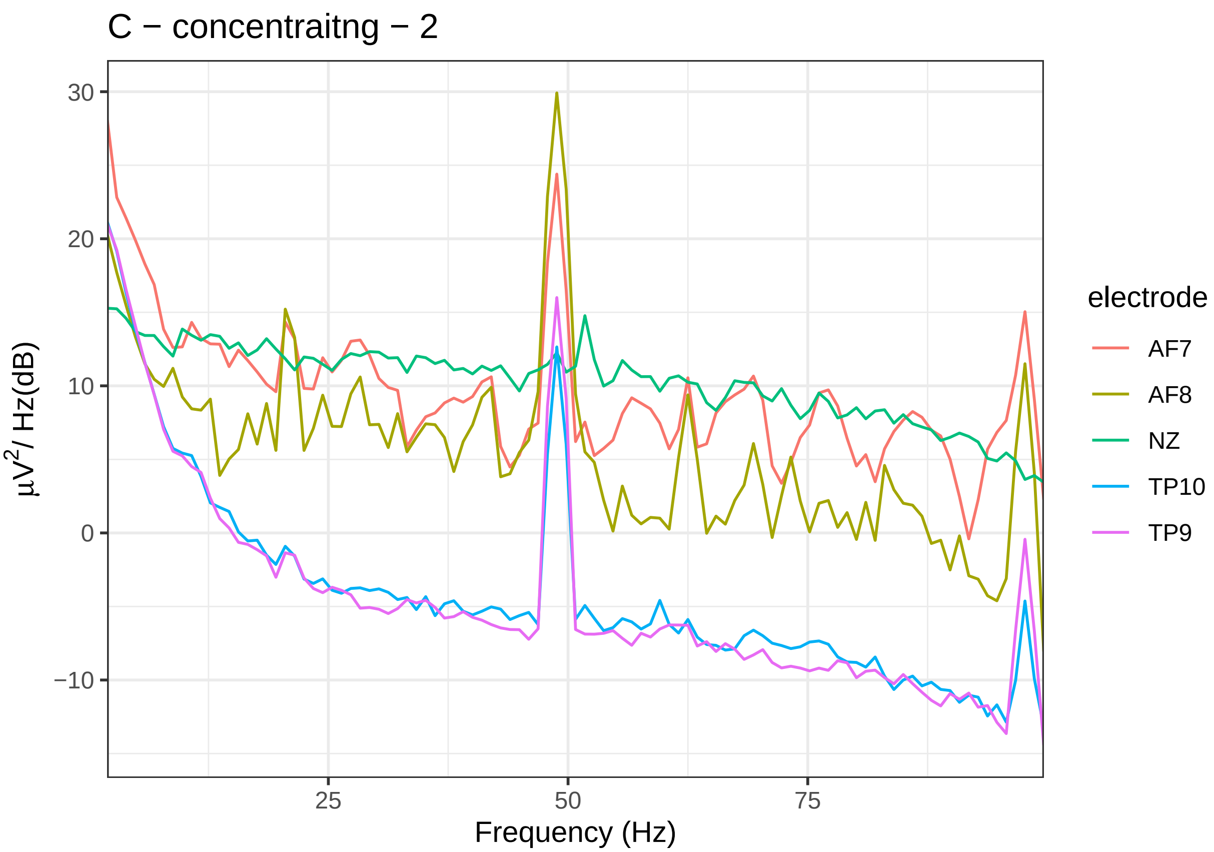
```
show_psd(b_concentrating_2_obj, "B - concentraitng - 2")
```



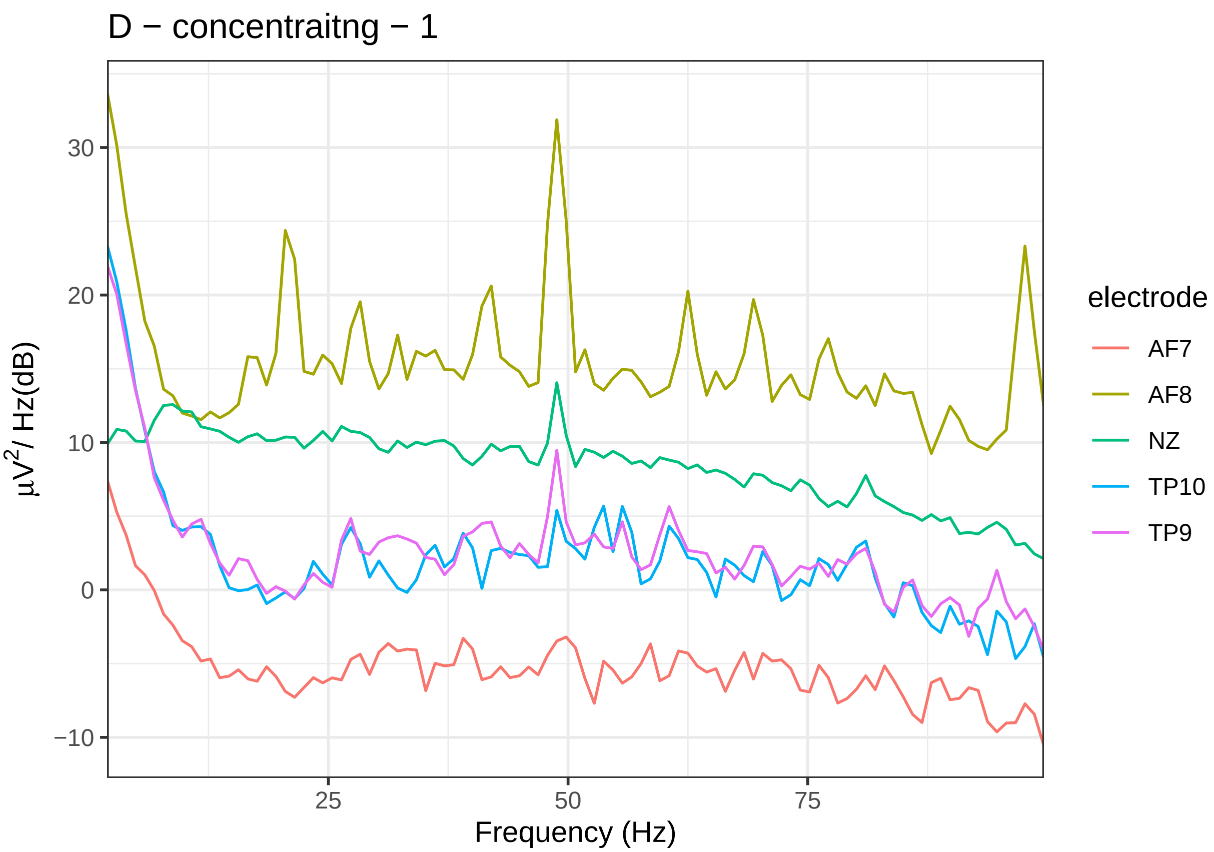
```
show_psd(c_concentrating_1_obj, "C - concentraitng - 1")
```



```
show_psd(c_concentrating_2_obj, "C - concentraitng - 2")
```

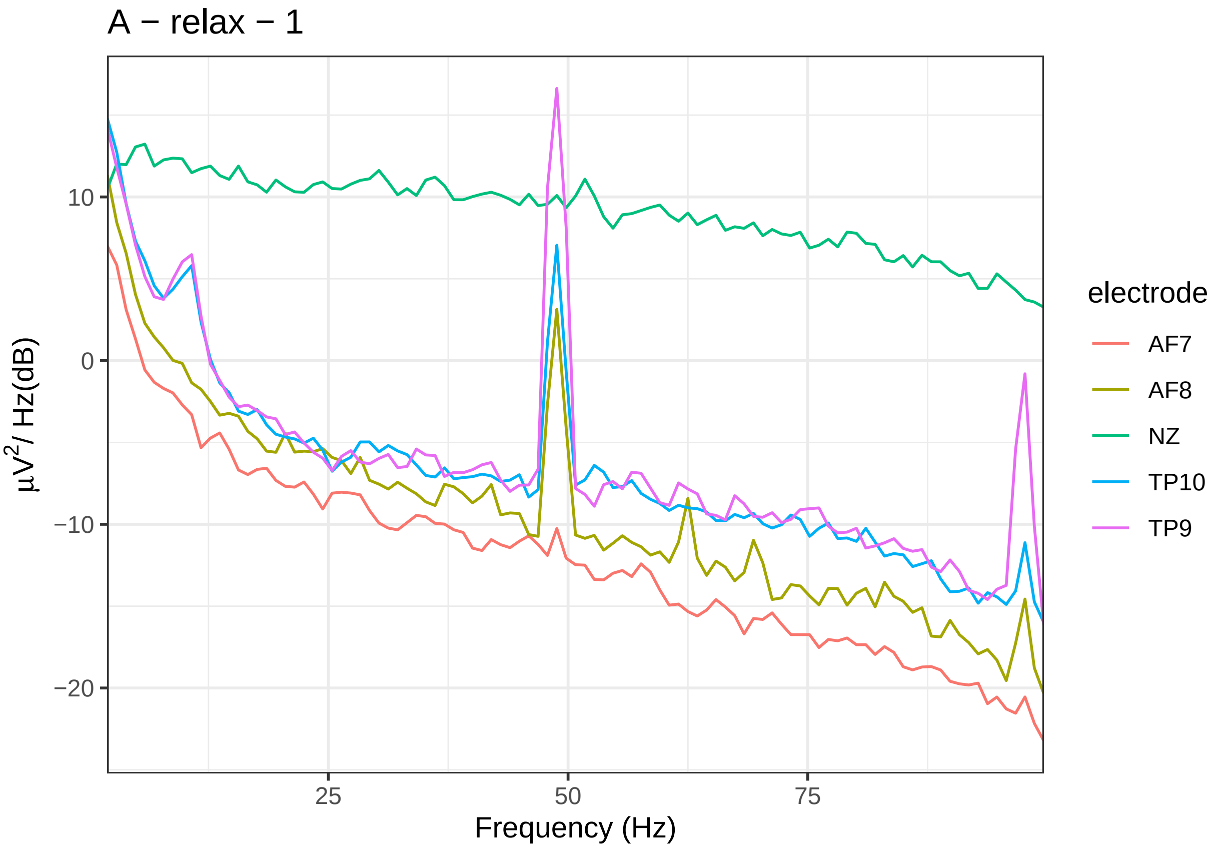


```r
show_psd(d_concentrating_1_obj, "D - concentraitng - 1")
```

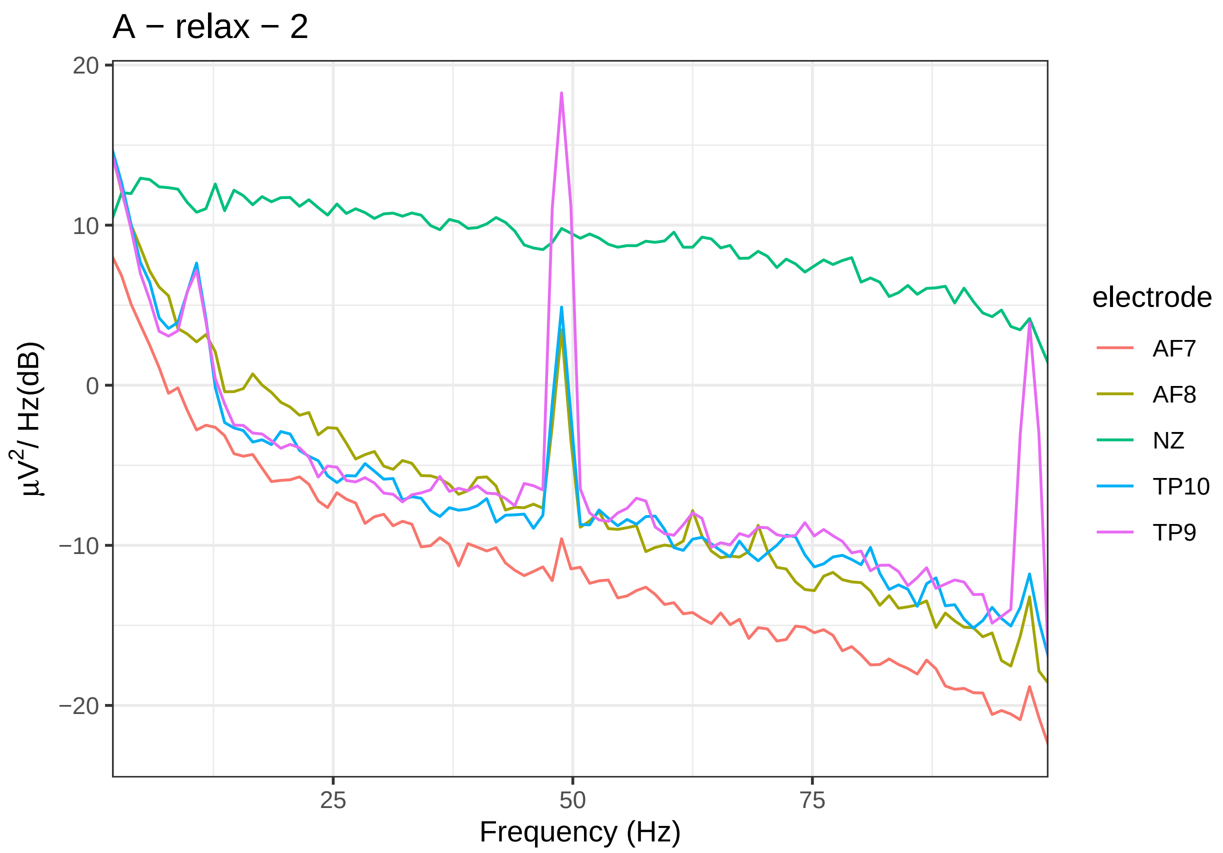


```
#show_psd(d_concentrating_2_obj, "D - concentraitng - 2")
```

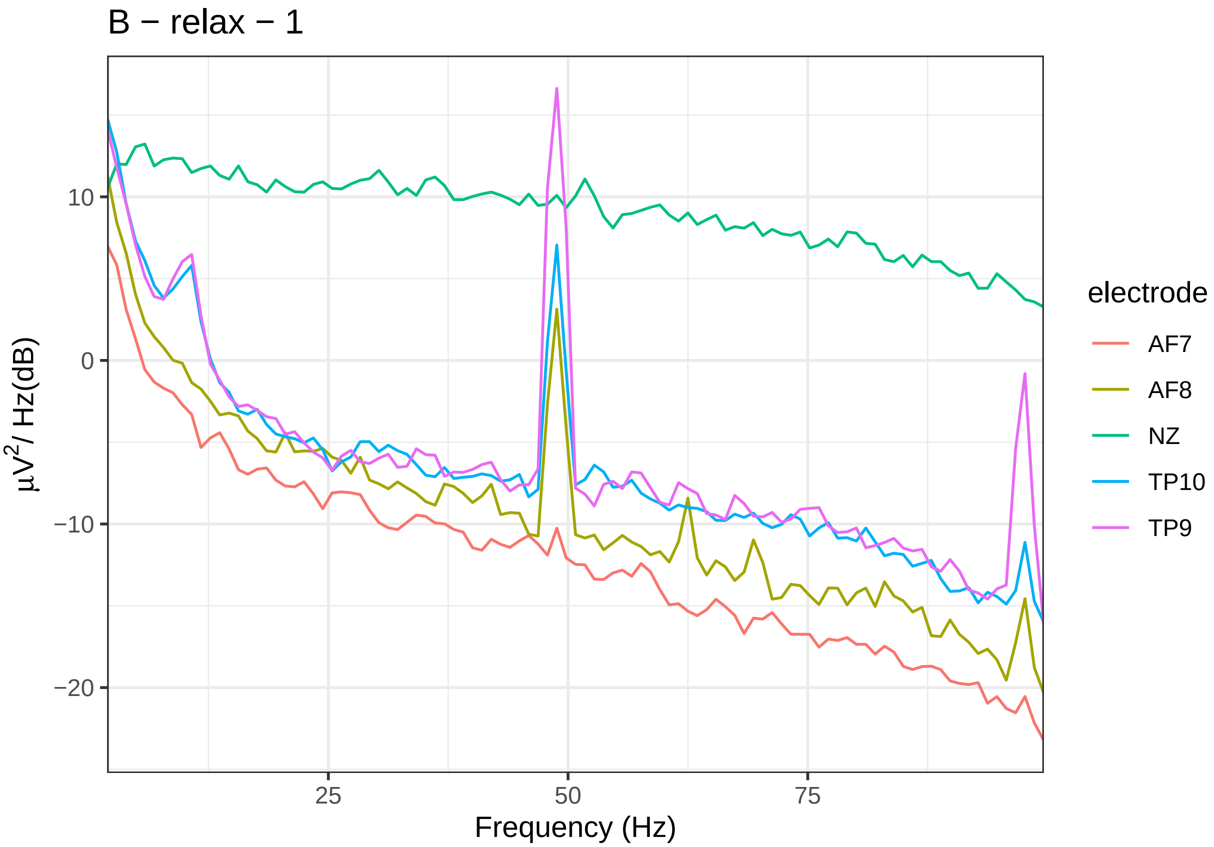
```
show_psd(a_relaxed_1_obj, "A - relax - 1")
```



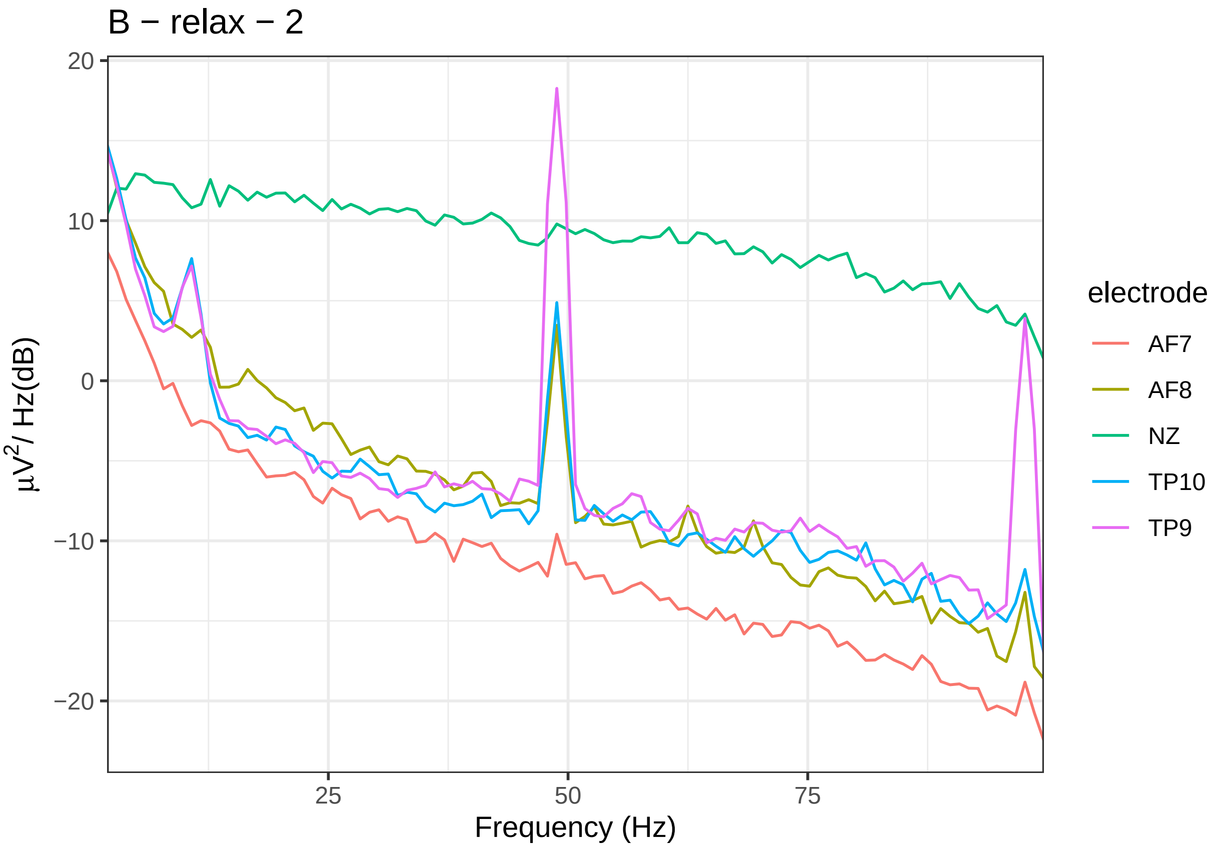
```
show_psd(a_relaxed_2_obj, "A - relax - 2")
```



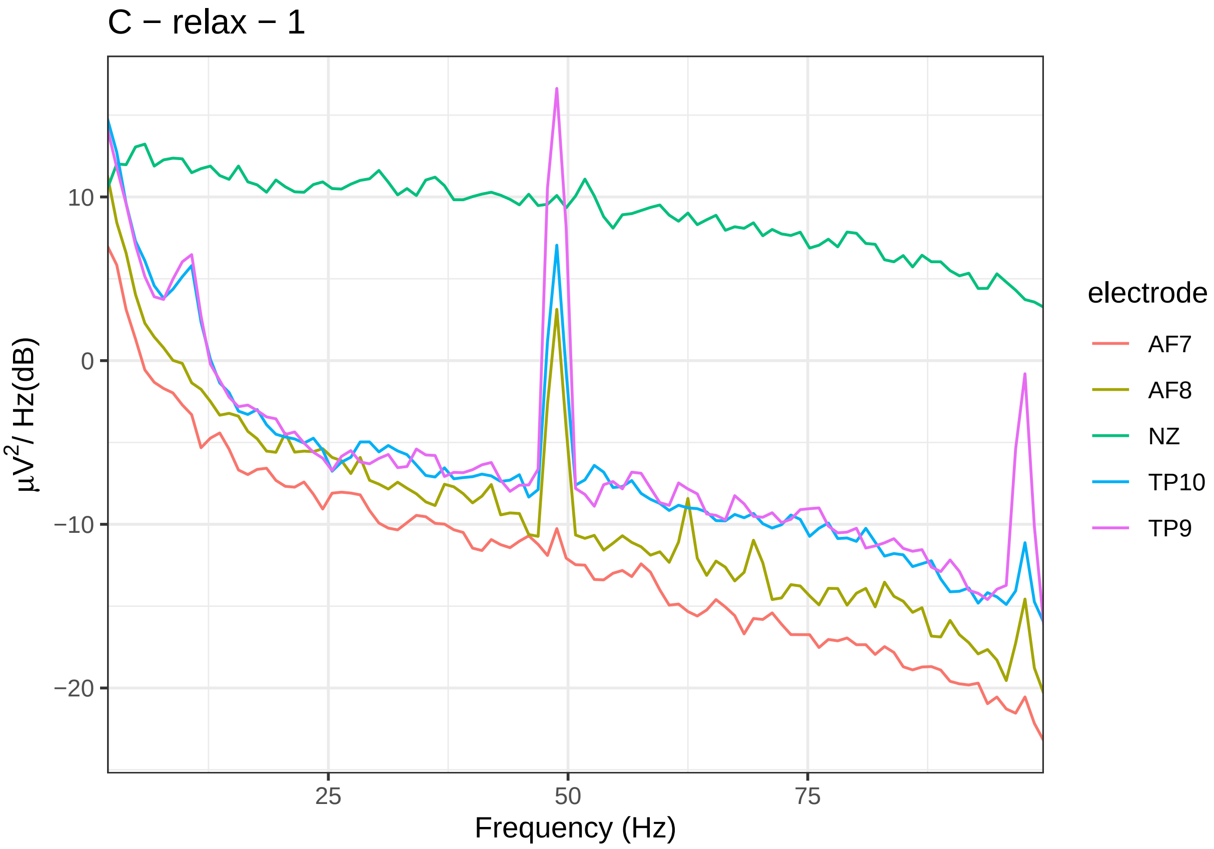
```
show_psd(a_relaxed_1_obj, "B - relax - 1")
```



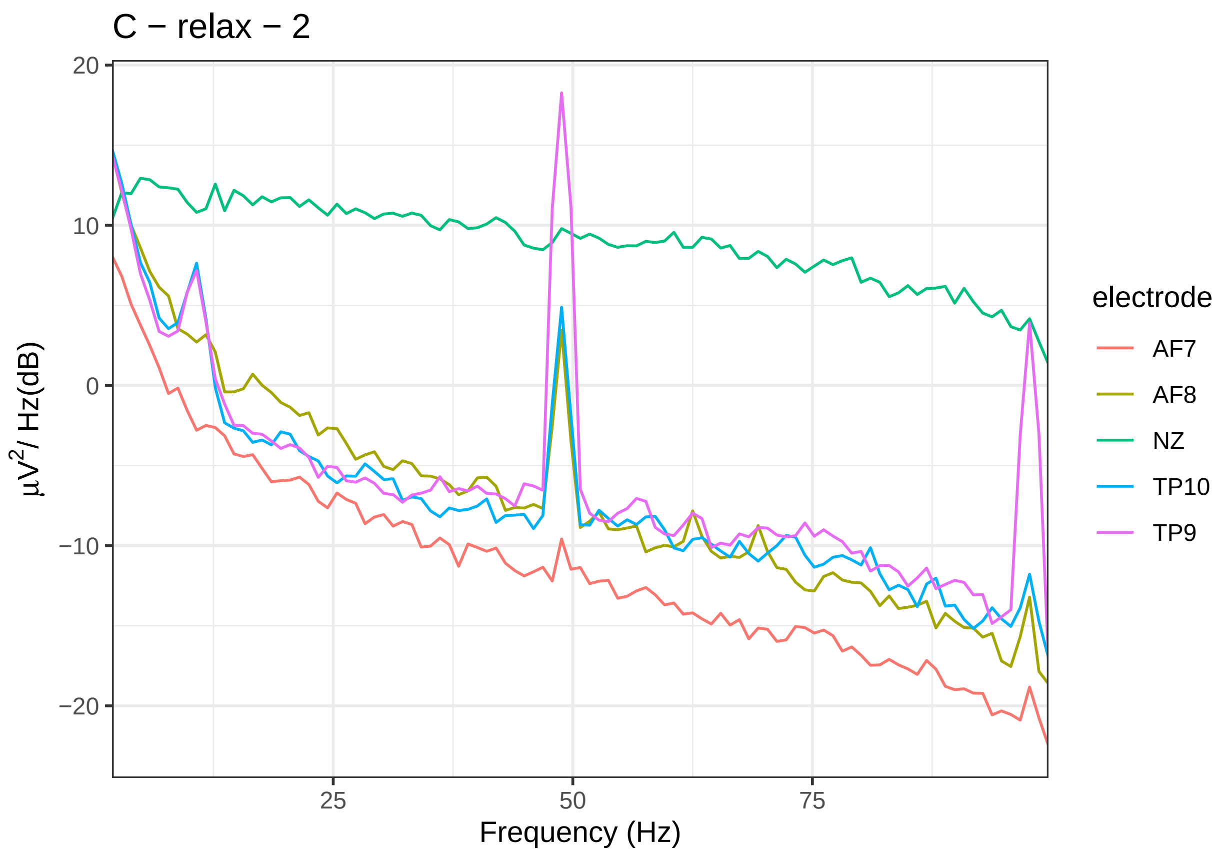
```
show_psd(a_relaxed_2_obj, "B - relax - 2")
```



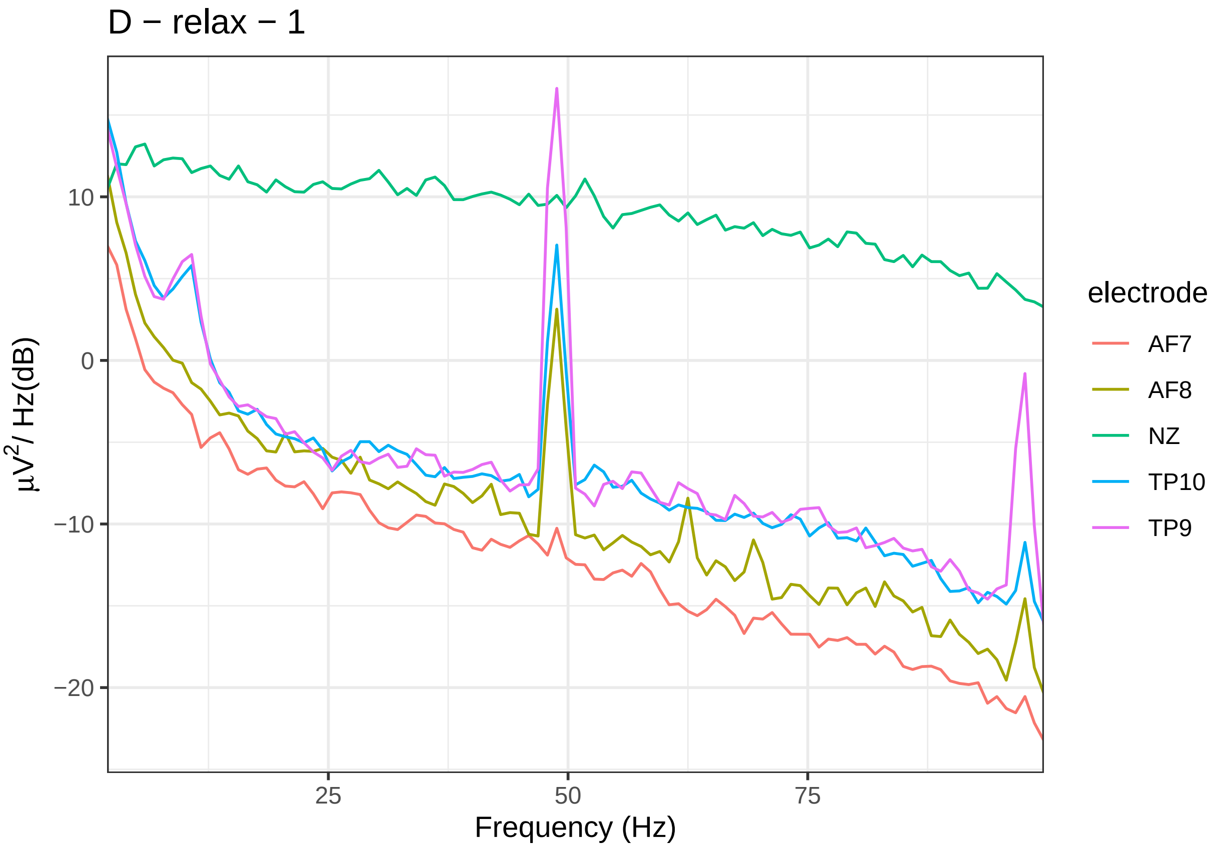
```r
show_psd(a_relaxed_1_obj, "C - relax - 1")
```



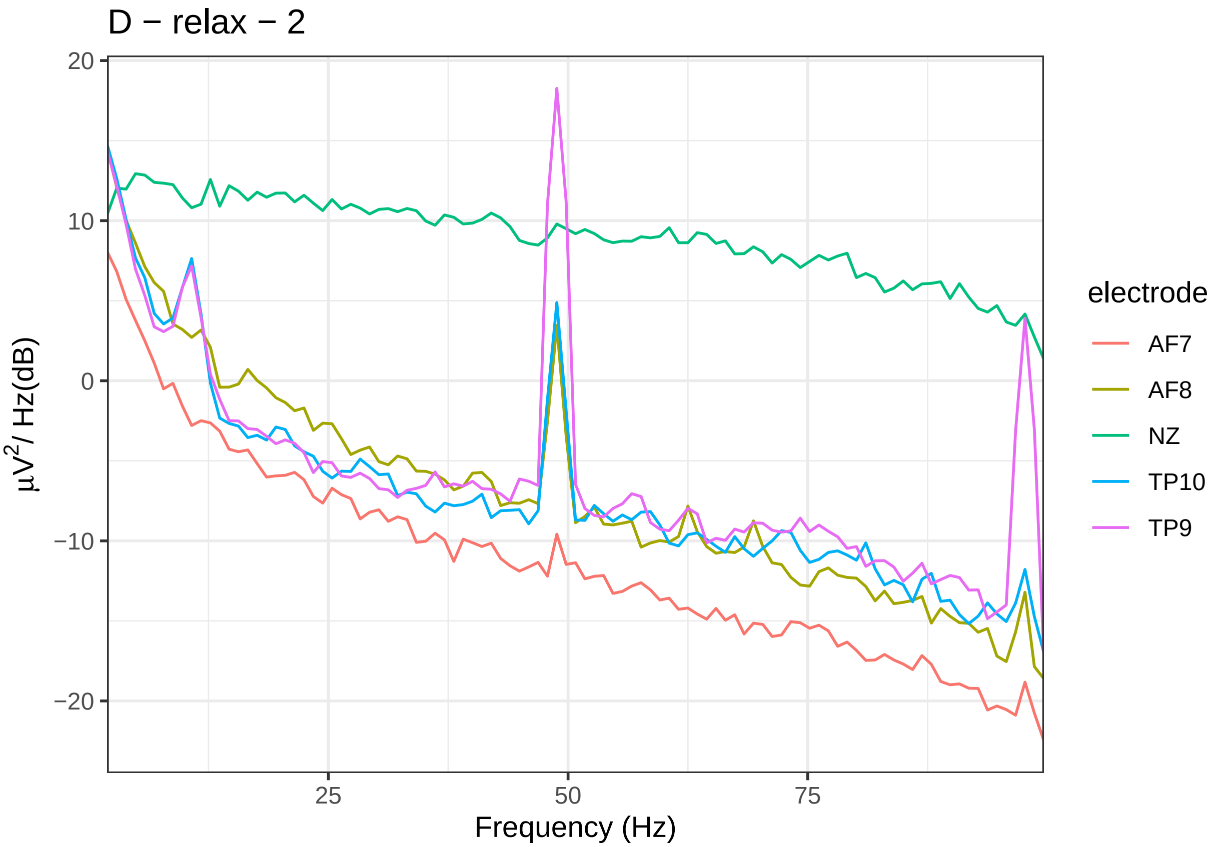
```
show_psd(a_relaxed_2_obj, "C - relax - 2")
```



```
show_psd(a_relaxed_1_obj, "D - relax - 1")
```



```
show_psd(a_relaxed_2_obj, "D - relax - 2")
```



Implications

Brain waves analysis enables effective interactions with a subject via BCI. In the article we showcase methods for removing artifacts from a signal (bandpass- and notch-filter). PSD was helpful during feature selection and the baseline is an example how to extract useful information from the signal. Leveraging this knowledge can lead to the creation of BCI systems that enable seamless and intuitive interactions between humans and software or computers, opening up new possibilities for communication, control, and interaction for various applications, including assistive technology, gaming, virtual reality, healthcare and education.