Averaging and baseline correction

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Why perform baseline correction?

- the EEG signal slowly shifts over time, introducing differences in the zero levels between channels
- these can be due to brain activity or noise
- because of this, we need a time range where we can assume that the brain does not produce stimulus-related activity - the **baseline period**

Baseline correction

- baseline correction: for each channel, subtract the average of the baseline period from trials
- logic: the baseline period should be clean and thus similar in all conditions, so performing a baseline correction should bring the pre-stimulus interval closer to 0
- ensures that effect of interest is **not already present before the experimental event**

To correct or not to correct?

- sometimes, clean baselines are very difficult to define
- e.g. in language experiments, you often have parts of a sentence in the baseline (think of the N400 experiments)
- in these cases, baseline corrections are not a good option
- because baseline correction is used to get rid of slow drifts, it can be substituted by a highpass filter (Widmann, 2015)

Widmann, Schröger, Maess (2015) *J. Neurosci. Methods*

Baseline correction in FieldTrip

- use `ft_preprocessing` to perform baseline correction

"Averaging out" noise

- Only signal elicited by the experimental manipulation is assumed to be timelocked to the stimulus
- All other activity (noise and random activity) is assumed to be randomly distributed in time
- By averaging, randomly distributed positive and negative deflections cancel each other
- Thus, averaging increases the signal-to-noise ratio (SNR)

Averaging

- averaging is equivalent to summing up the EEG signal of all trials and dividing by the number of trials
- to prepare the data for statistical comparisons, we average within conditons:
  1. **single subject averages**: averaging across trials (one average per condition per subject)
  2. **grand averages**: averaging across subjects (one average per condition)

Averaging in FieldTrip

- in a new for loop: create single subject averages using `ft_timelockanalysis`
  - use `cfg.keeptrial = 'yes'`
  - save the single subject averages
  - plot your single subject averages using `ft_multiplotER`/ `ft_singleplotER`
- we only have one subject, so we won't be computing grand averages

Exercise

- now, instead of averaging your cleaned data, try averaging the raw data
- also try averaging only some of your cleaned trials (e.g. 5 trials, 10 trials, 50 trials, …)
- what do these averages look like, compared to your clean averages / those with more trials?