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# Connectivity analysis – issues and how to's

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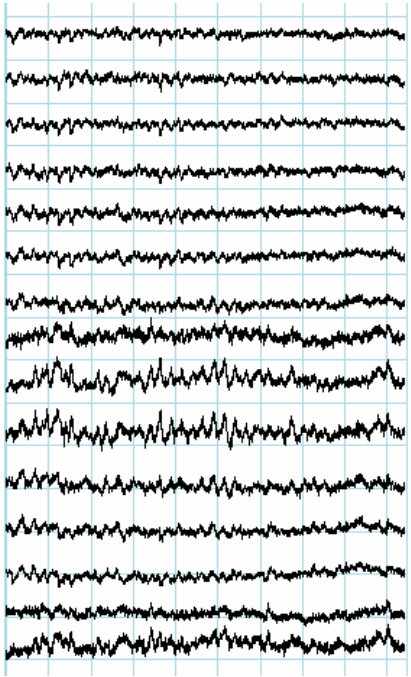
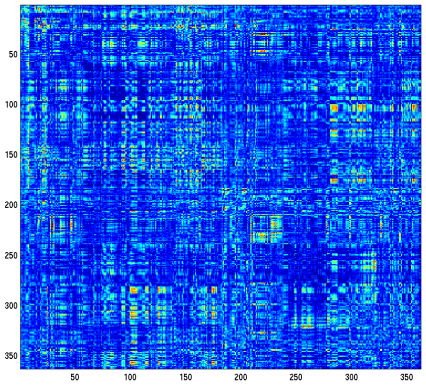
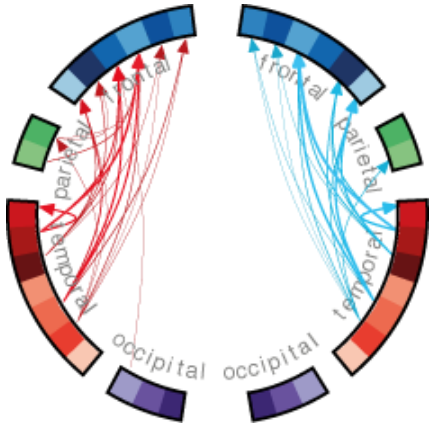
# From EEG/MEG data to results





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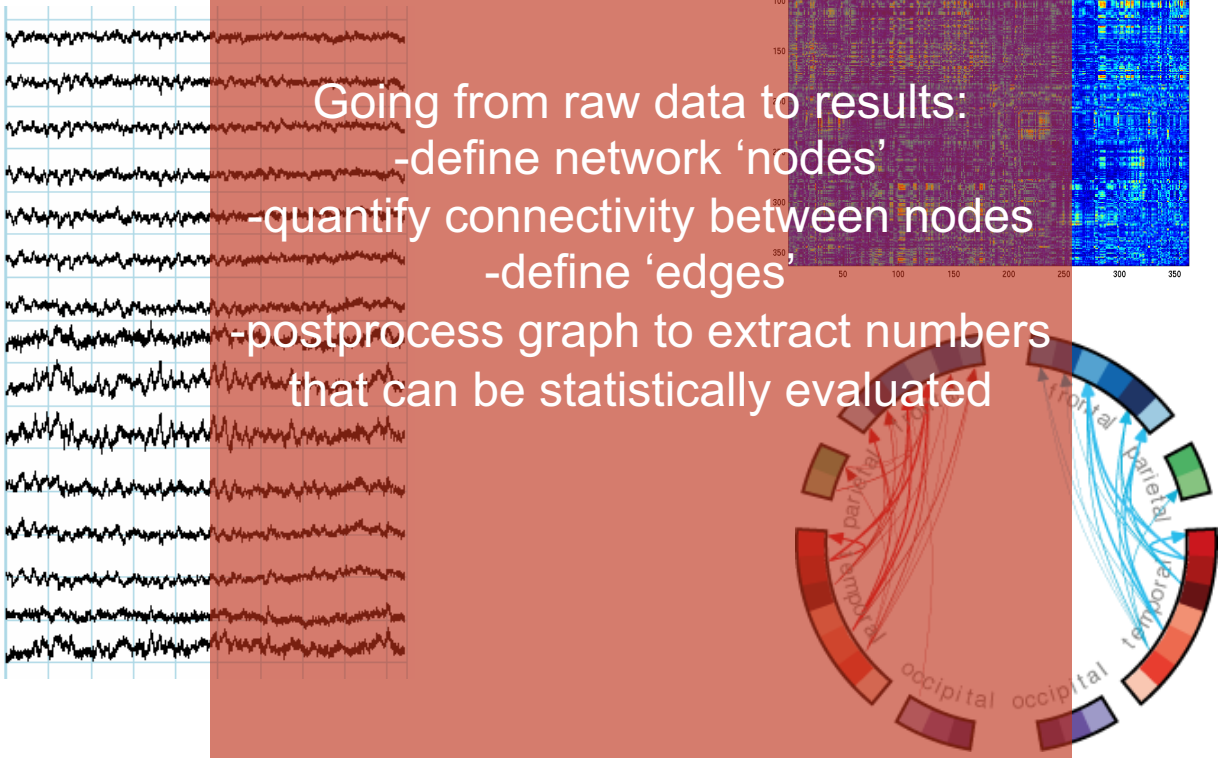
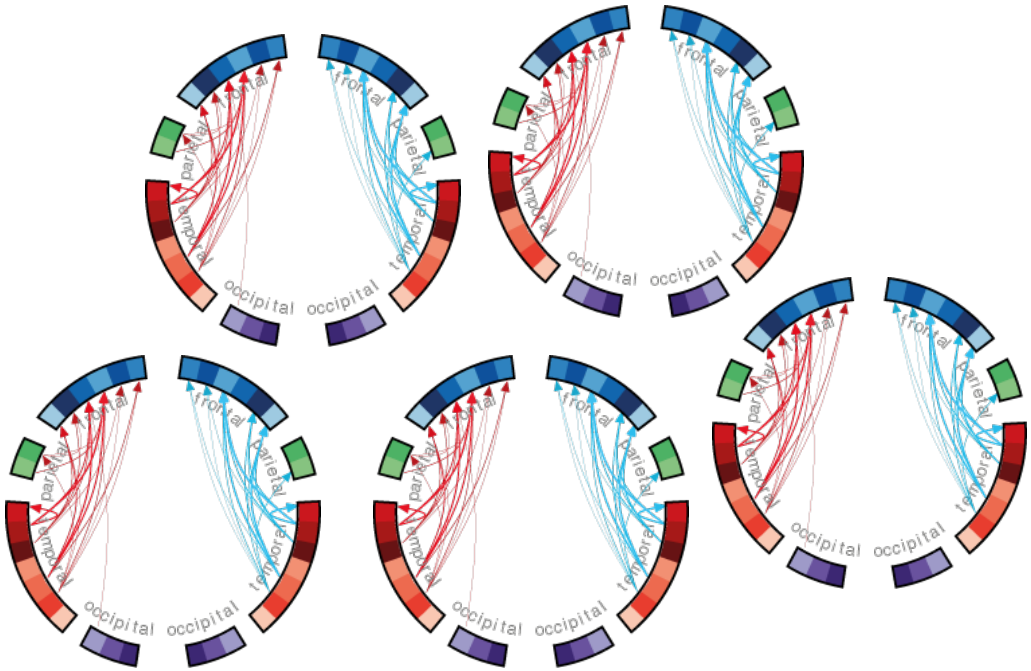


# From EEG/MEG data to results

1. Definition of network nodes: channels versus sources
2. Definition of connectivity
3. Definition of edges:
   - Few vs. many: seed-based
   - ROI vs. ROI
   - Many vs. many
4. Statistical evaluation (possibly after extraction of graph theoretic quantities)

# From results to interpretation



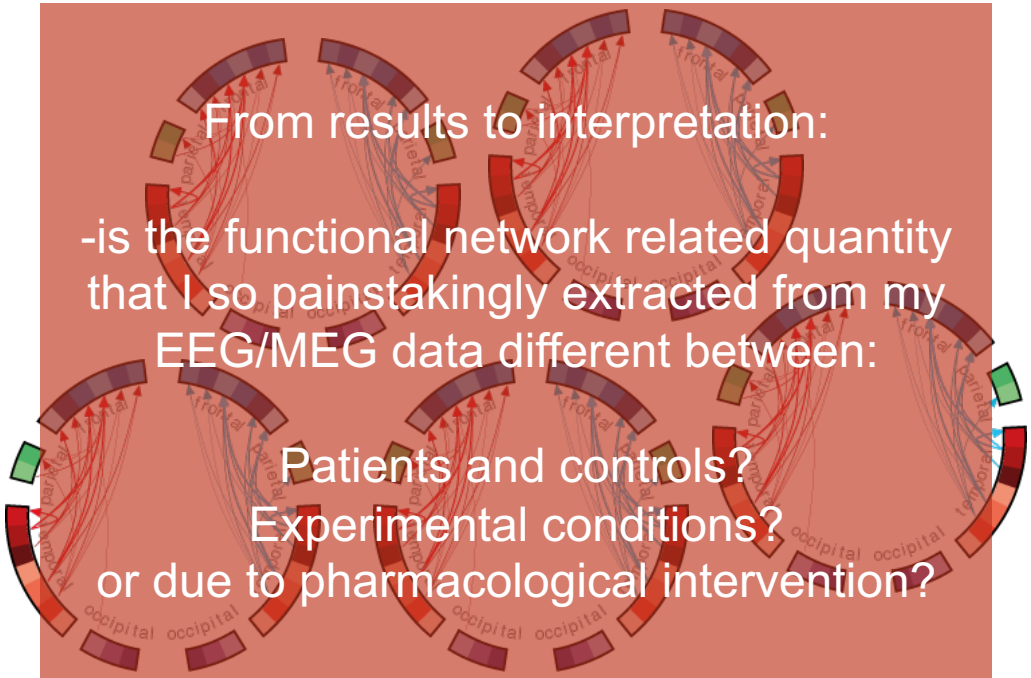
# From results to interpretation

From results to interpretation:

-is the functional network related quantity that I so painstakingly extracted from my EEG/MEG data different between:

Patients and controls?
Experimental conditions?
or due to pharmacological intervention?

-AND could such differences be explained by differences between groups that don't have anything to do with neuronal interactions?

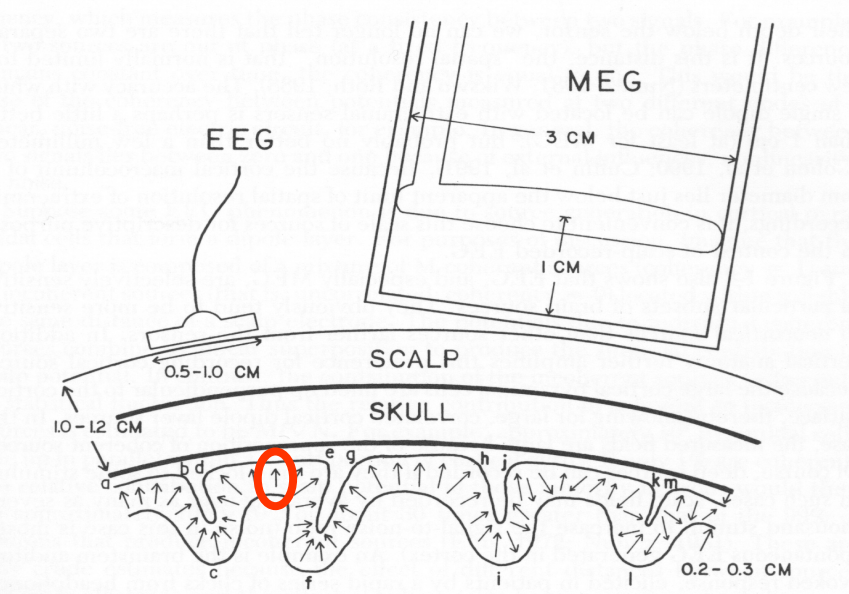


# Take home messages

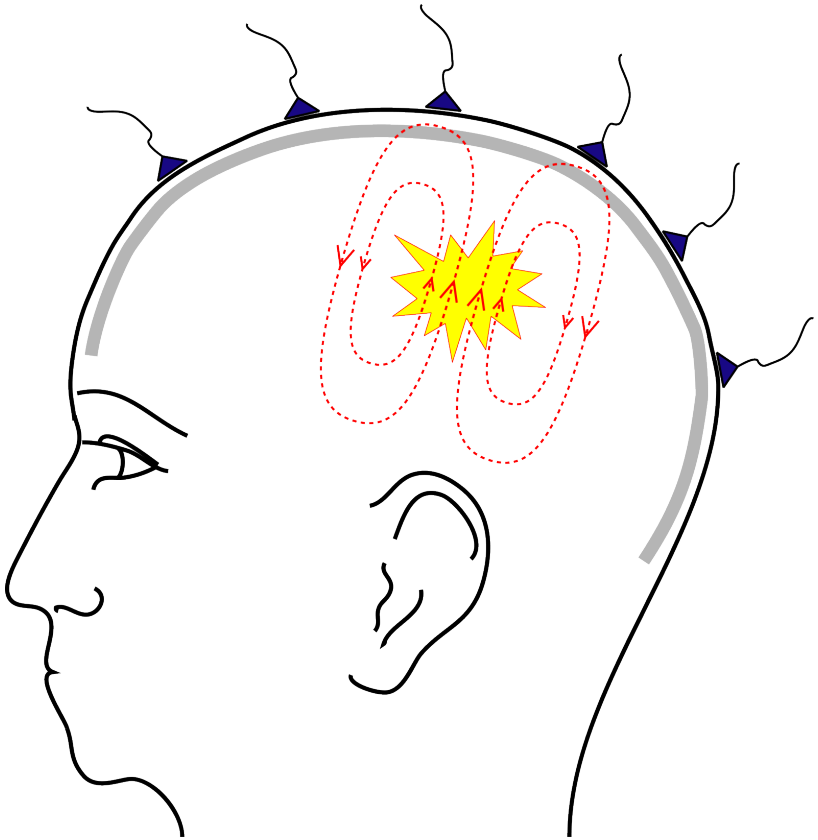
- Always keep in mind what is measured with M/EEG
- Interpret your results with care

- Don't forget what is measured with M/EEG
  - Don't over-interpret your results

# Generation of M/EEG signals: synchronized post-synaptic potentials

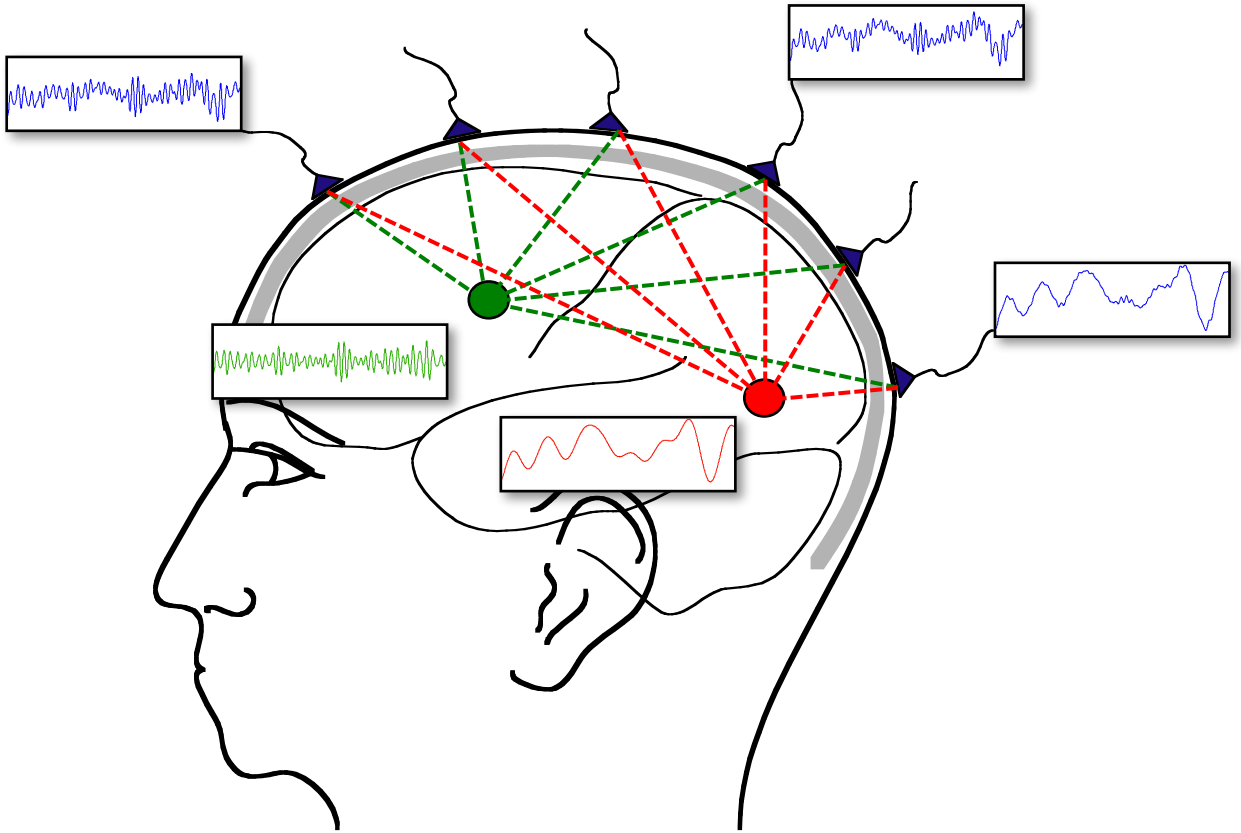


# Generation of M/EEG signals: primary currents lead to volume currents



# Generation of M/EEG signals:

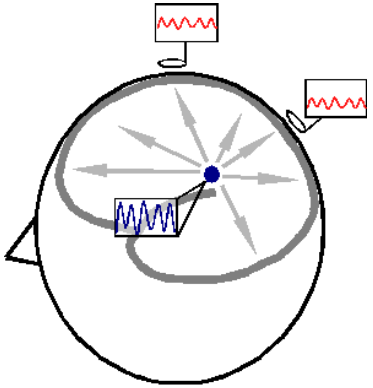
## signals represent an instantaneous unknown mixture of underlying neuronal sources

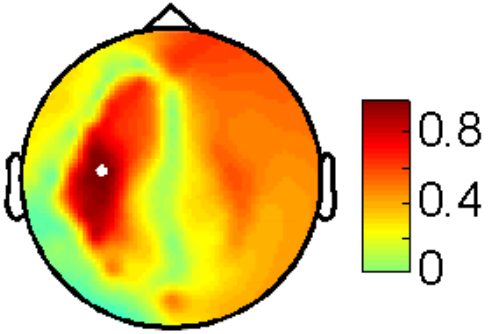


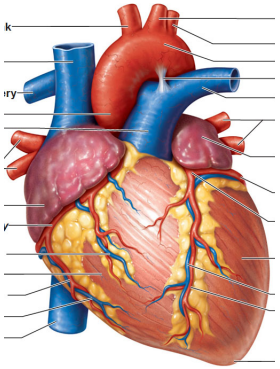
## Quantification and interpretation of networks at channel level does not really make sense.

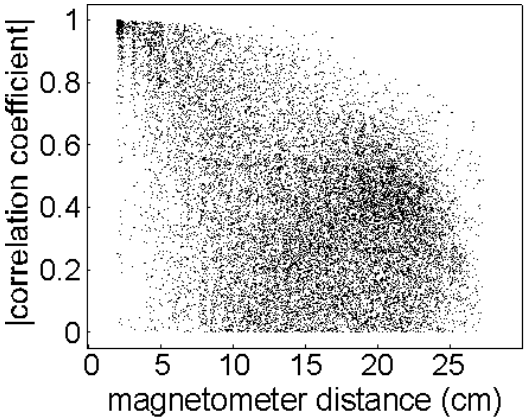
- No unambiguous relationship between network nodes and anatomical regions.
- Instantaneous mixing leads to mis-estimation (typically spurious) of connectivity

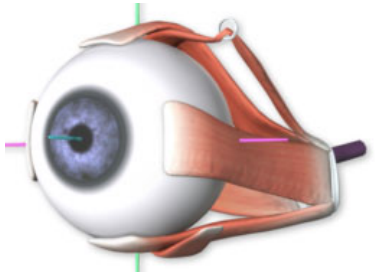
Quantification and interpretation of networks at channel level does not really make sense.







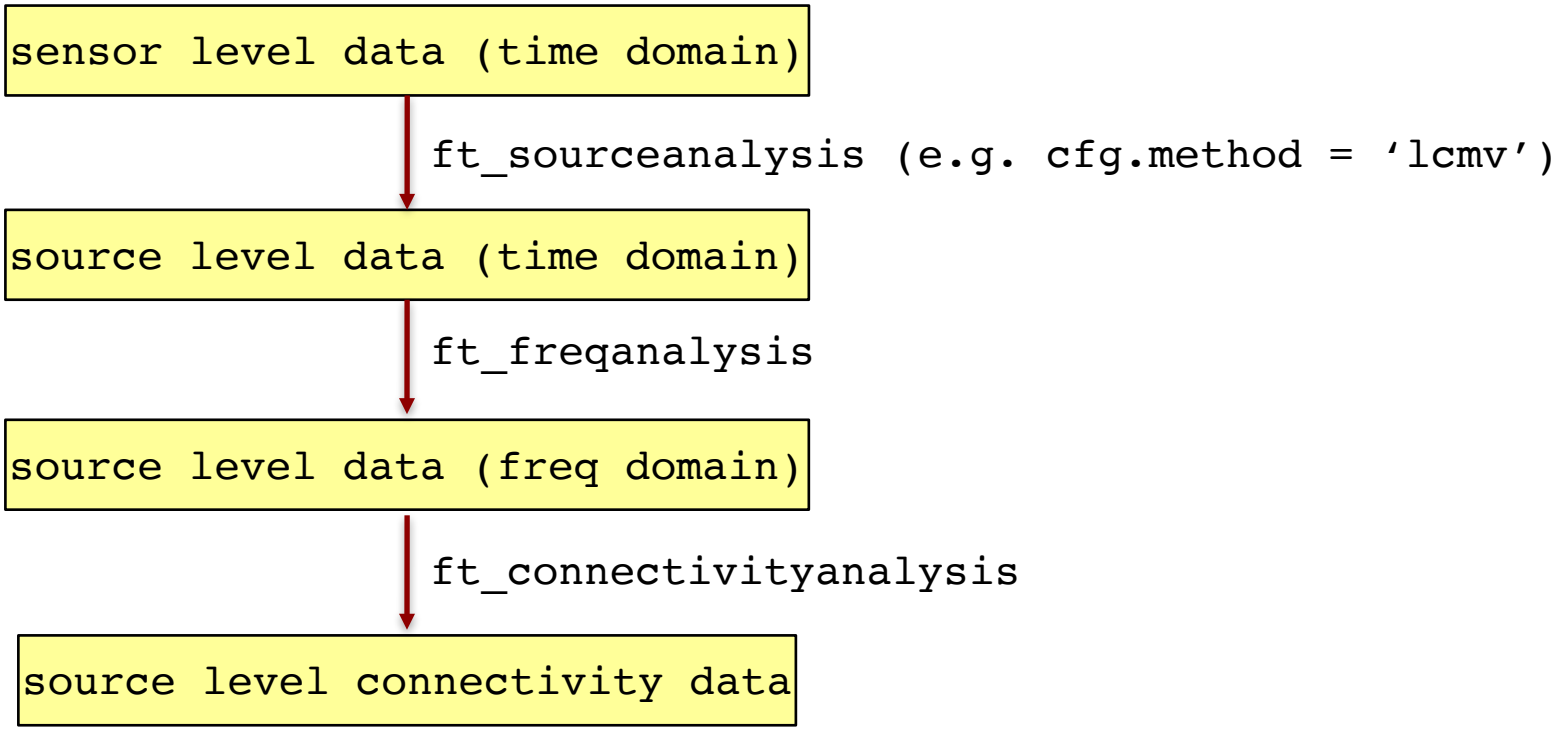
## Address the issue of spurious estimates due to instantaneous mixing

- Use a connectivity measure that 'discards' the instantaneous contribution to the interaction estimate (e.g.: imaginary part of coherency, (weighted) phase
- lag index,  orthogonalized amplitude envelope correlations).
- Do the network analysis at the level of the reconstructed sources

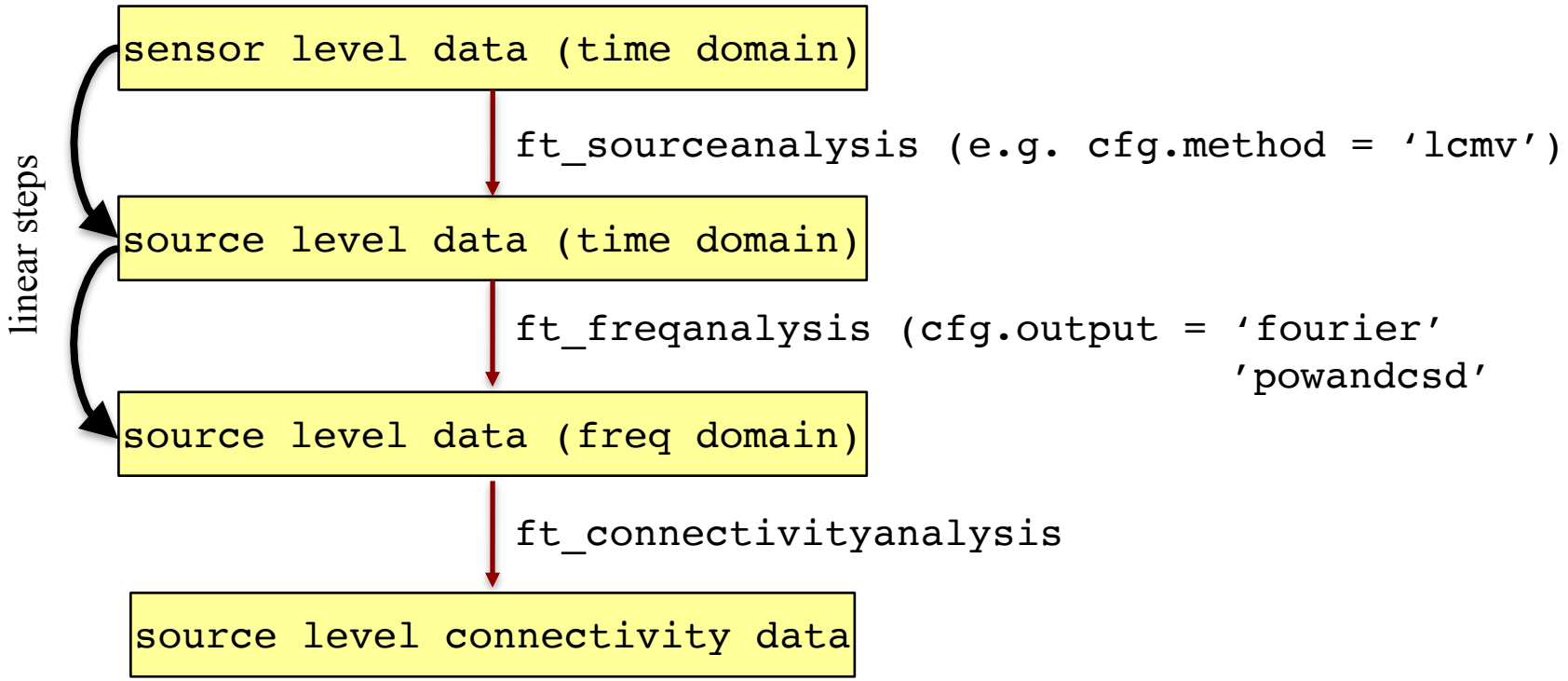
## Source reconstruction prior to connectivity estimation

- 'Unmix' the instantaneous mixing.
- Adds a level of complexity to the analysis
- Limits meaningful interpretable connectivity studies to recordings with large number of electrodes
- Unmixing is never perfect: spatial leakage of activity
- Define spatial 'granularity' in source space

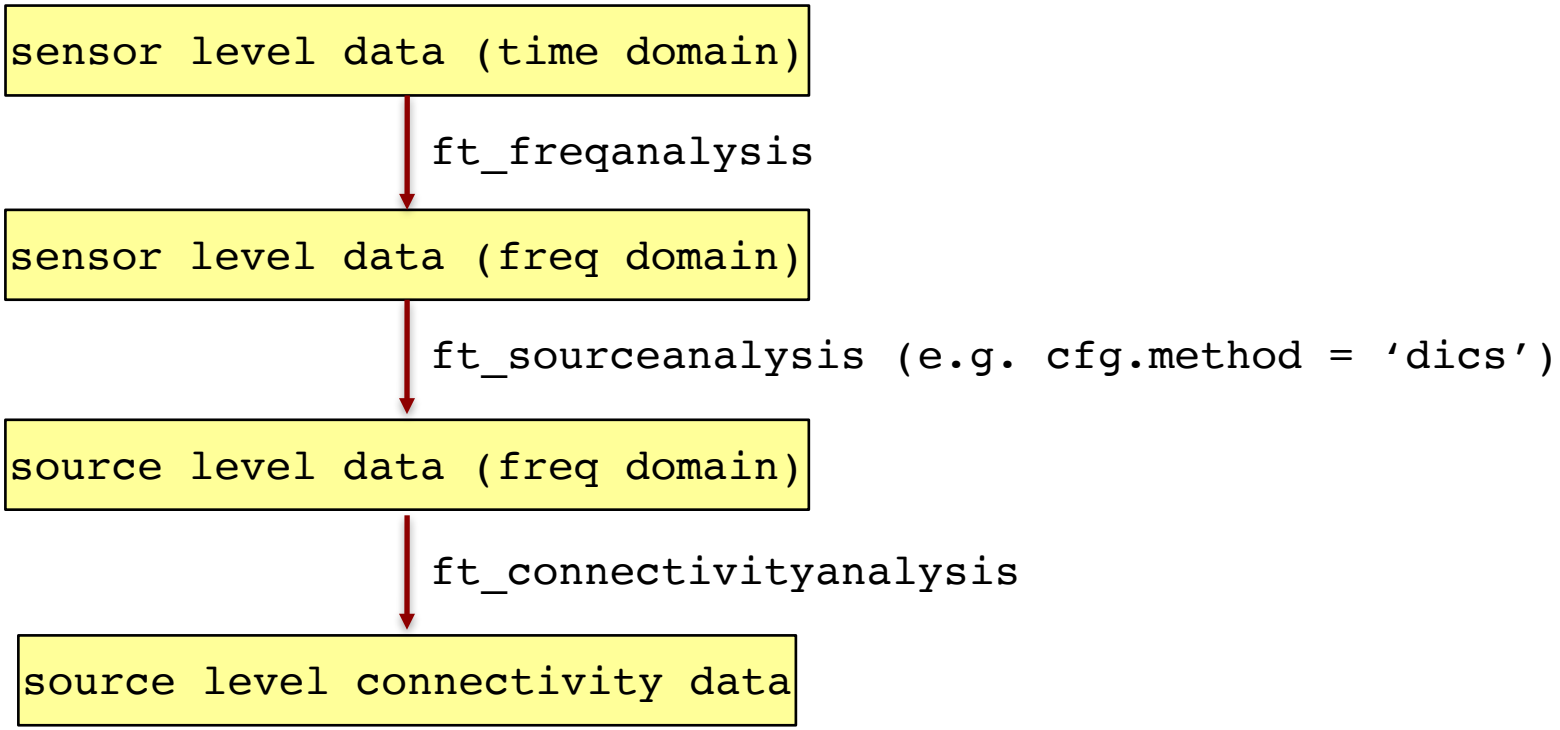
# Analysis recipe



# Analysis recipe



# Analysis recipe (revised)



## Ft_sourceanalysis how to's

```
% get spatial filter, common across conditions
% (assuming there's more than one condition
cfg                  = [];
cfg.method           = 'dics';
cfg.headmodel        = headmodel;
cfg.grid             = sourcemodel;
cfg.dics.keepfilter = 'yes';
source = ft_sourceanalysis(cfg, freqall);

% use computed spatial filter to get single
% condition data
cfg                  = [];
cfg.method           = 'dics';
cfg.headmodel        = headmodel;
cfg.grid.filter      = source.avg.filter;
cfg.dics.keepfilter = 'no';
source1 = ft_sourceanalysis(cfg, freq1);
source2 = ft_sourceanalysis(cfg, freq2);
```

## If there is only a single condition, e.g. resting state, or when single trial data are needed

```
% get spatial filter
cfg                  = [];
cfg.method           = 'dics';
cfg.headmodel        = headmodel;
cfg.grid             = sourcemodel;
cfg.dics.keepfilter  = 'yes';
source = ft_sourceanalysis(cfg, freqall);

% use computed spatial filter to get single
% trial data
cfg                  = [];
cfg.method           = 'dics';
cfg.headmodel        = headmodel;
cfg.grid.filter      = source.avg.filter;
cfg.dics.keepfilter  = 'no';
cfg.rawtrial         = 'yes';
source1 = ft_sourceanalysis(cfg, freq1);
source2 = ft_sourceanalysis(cfg, freq2);
```

## More efficient: use 'pcc' as method

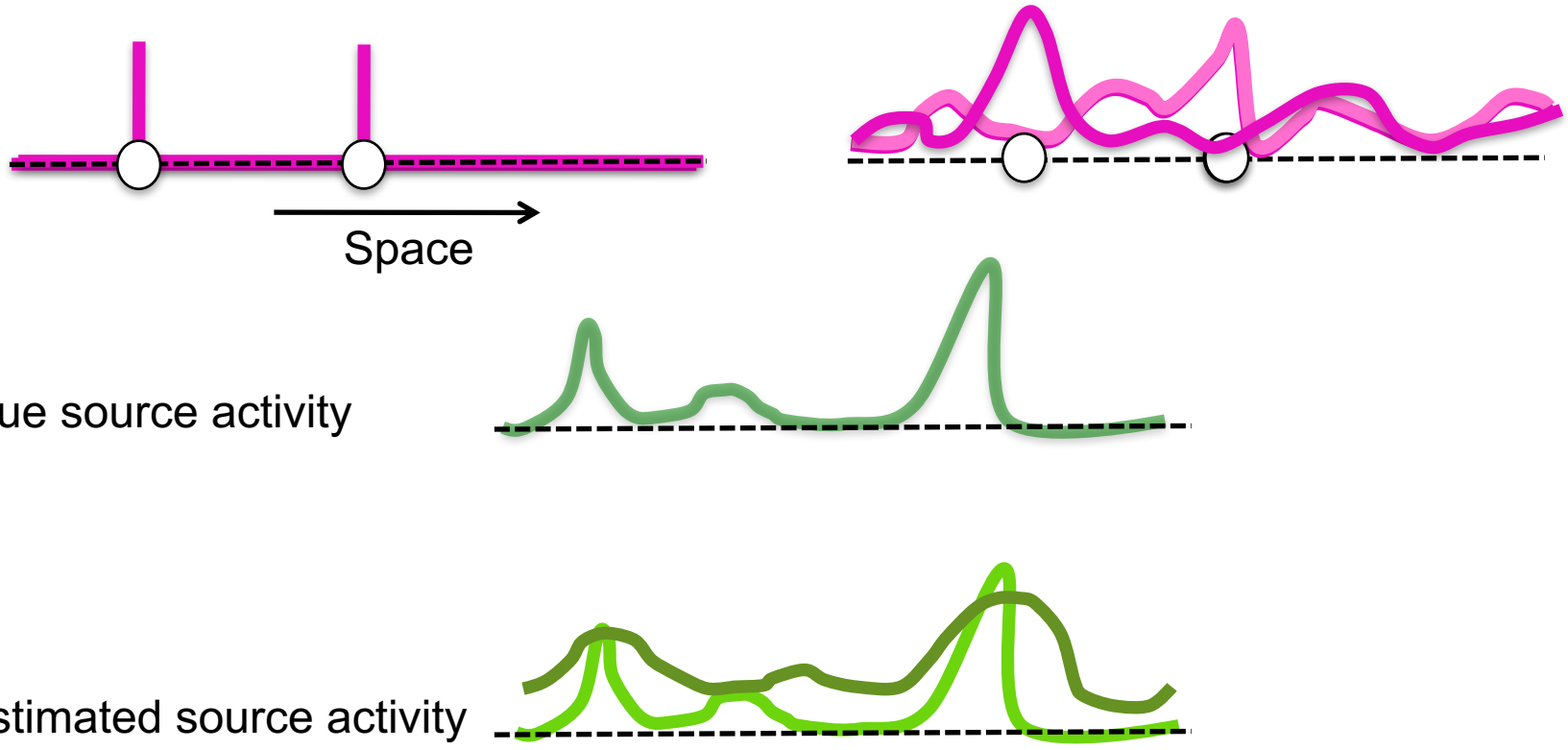
```
% get spatial filter + source-level fourier data in a single fast
% fast call to ft_sourceanalysis
cfg                  = [];
cfg.method           = 'pcc';
cfg.headmodel        = headmodel;
cfg.grid             = sourcemodel;
cfg.pcc.keepfilter   = 'yes';
source = ft_sourceanalysis(cfg, freqall);

% note, optimal benefit only when freq-domain channel data is
% computed as follows
freqall = ft_freqanalysis(cfg, data); % with cfg.output = 'fourier';

% then, the single trial (taper) data is in the following data field
>> source.avg

ans =
        csd: {Nx1 cell}
        mom: {Nx1 cell} % per dipole location fourier coefficients
   csdlabel: {Nx1 cell}
```

# Spatial leakage at the source level warrants careful interpretation



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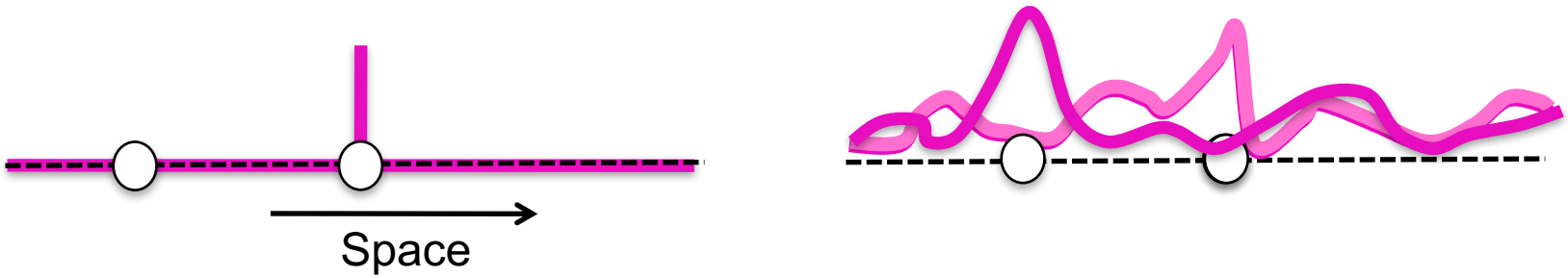
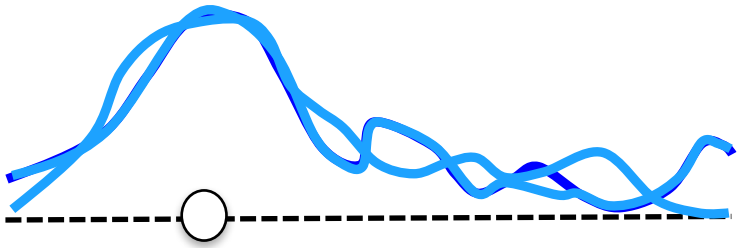



True source connectivity

Estimated source conn



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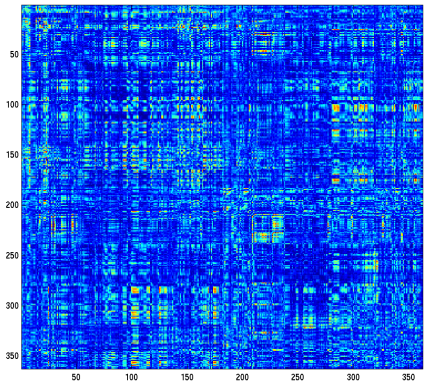
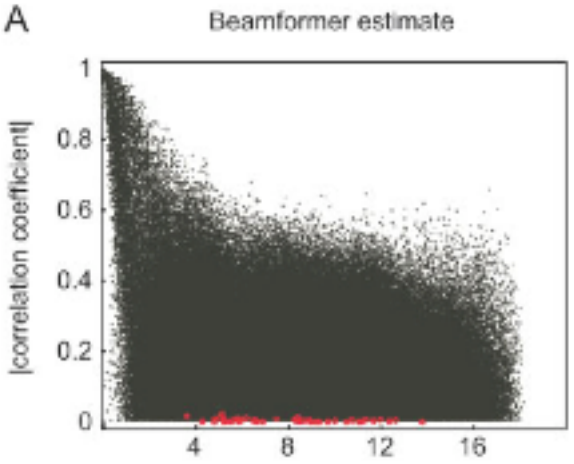
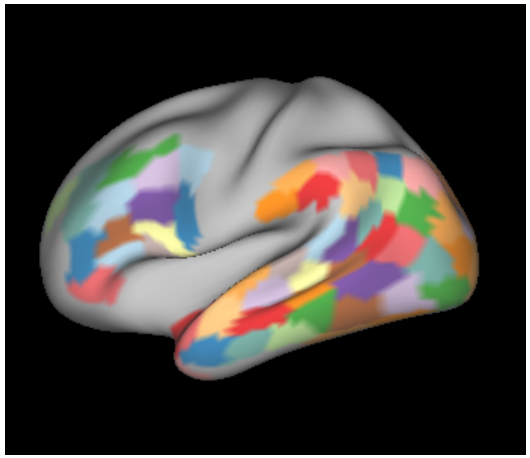


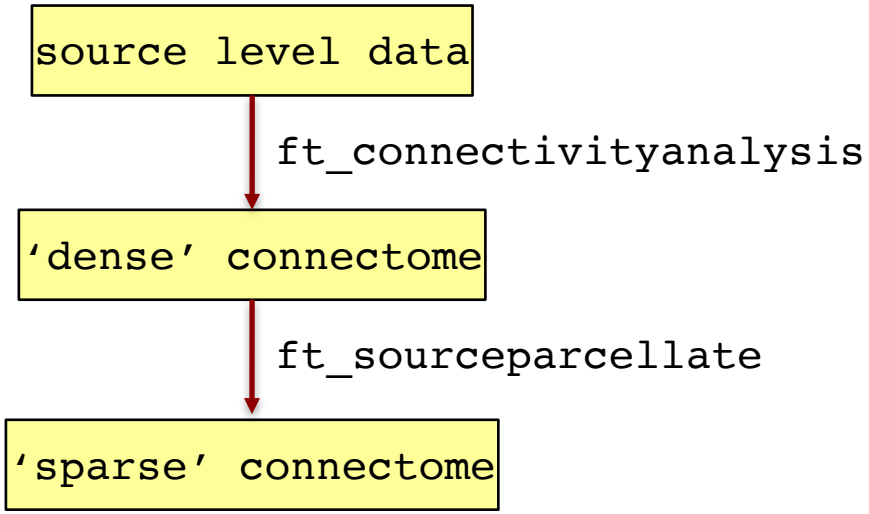



## Spatial granularity

- Acknowledge spatial noise in the connectivity maps
- Pool across dipole locations to increase SNR
  - Spatial resolution is relatively low
  - From a generative model point of view: regional sources rather than dipoles
- Strategy: use 'parcellation' scheme to go from 5000x5000 to 250x250 edges
- Parcellation also relevant when adding time / frequency dimensions to connectivity maps (data reduction)



# Analysis recipe parcellation



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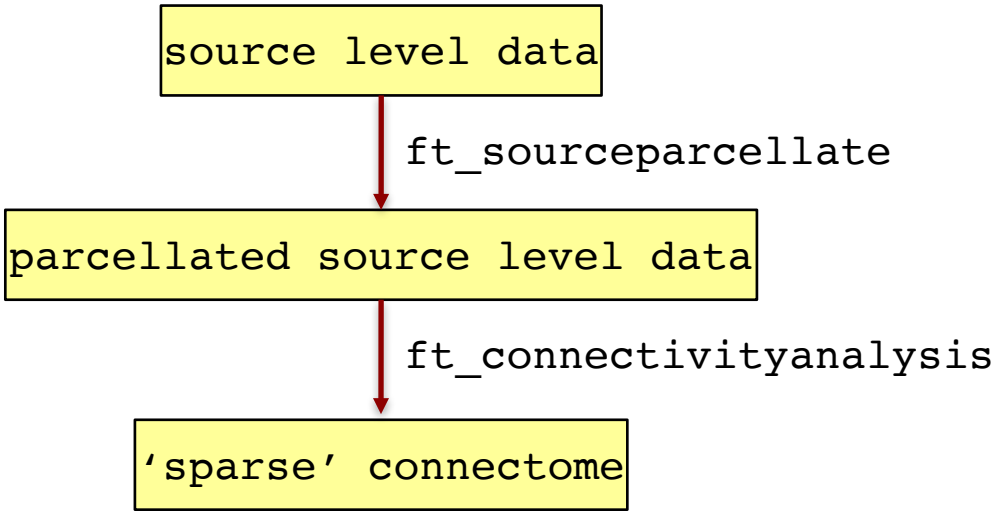


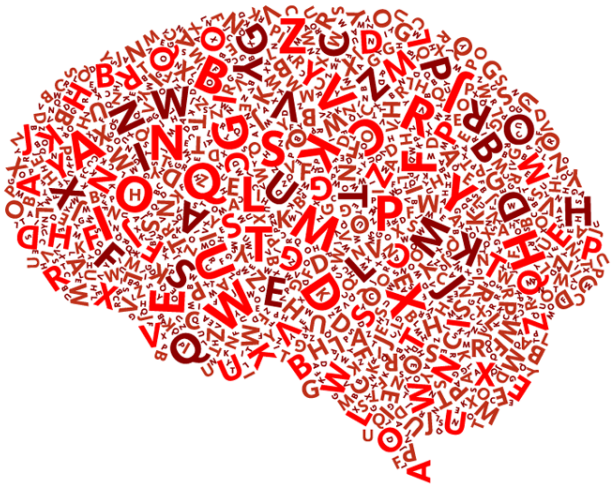

```
source_parc =

              label: {Mx1 cell}
          cohspctrm: [MxM double]
     cohspctrmdimord: 'chan_chan'
                cfg: [1x1 struct]
```

## Statistical evaluation (group level)

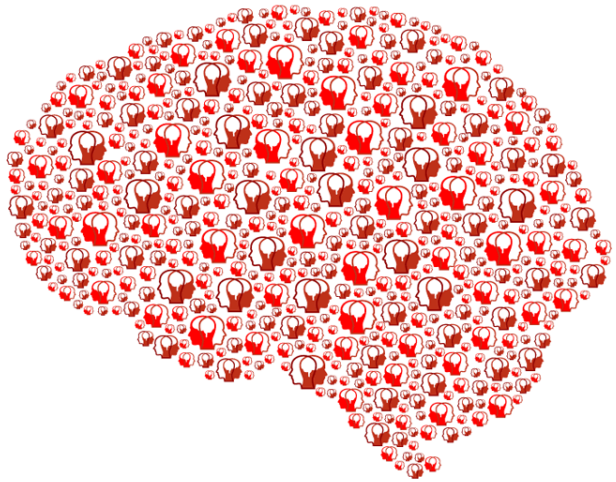
- Unlike ft_freqstatistics/ft_timelockstatistics, FT does not have a 'ft_connectivitystatistics'.
- Yet, working with parcellated data, in which each parcel is represented as a channel, allows for the use of ft_freqstatistics

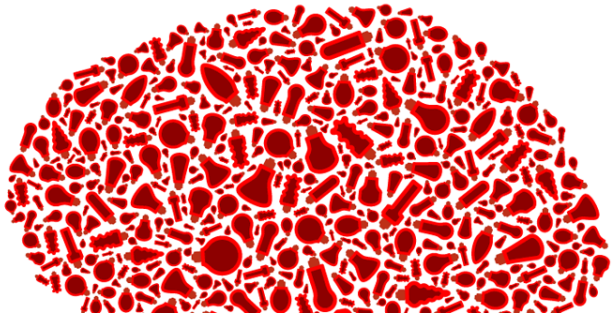
- Interpretation: report on condition/group differences in power
- If possible: account for condition/group differences in power



www.ru.nl/donders

www.fieldtriptoolbox.org





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