



Introduction to EEG, MEG and analysis with the FieldTrip toolbox

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What is FieldTrip

a MATLAB toolbox for the analysis of MEG, EEG and animal electrophysiology data

can import data from many different file formats

contains algorithms for spectral analysis, source reconstruction, statistics, connectivity, ...

Talk outline

What kind of signals are generated in the brain

How do we record those signals

Analyzing those signals with FieldTrip

Background on the FieldTrip toolbox

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Background on the FieldTrip toolbox

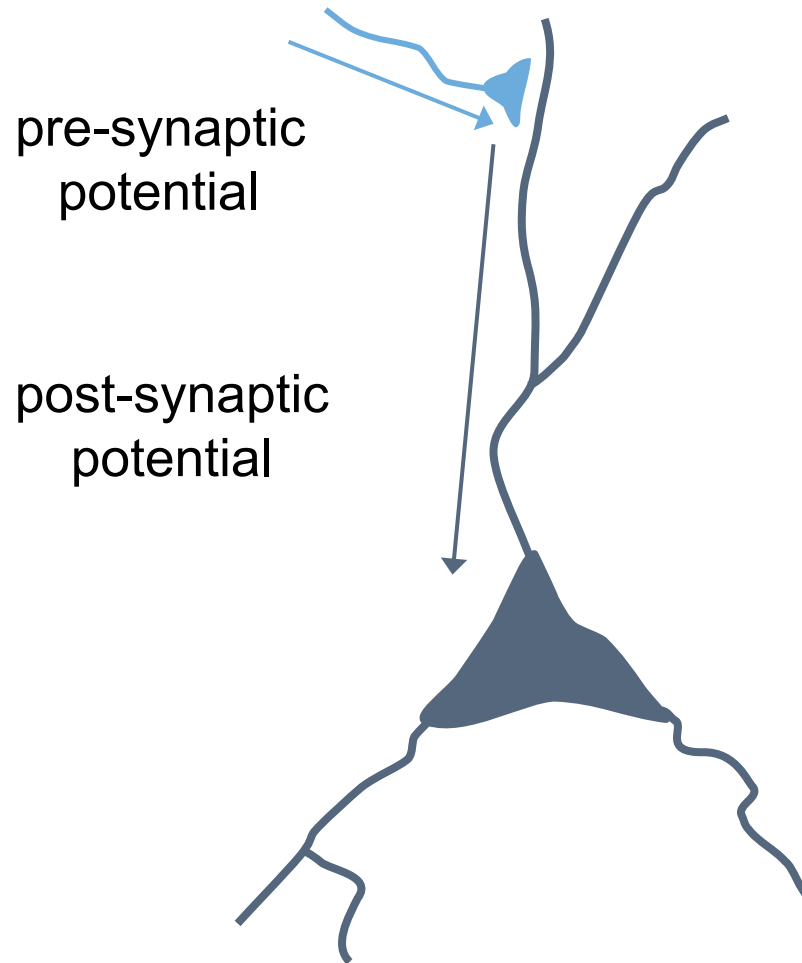
What kind of signals are generated in the brain

We measure the scalp potentials or field associated with post-synaptic potentials in pyramidal neurons

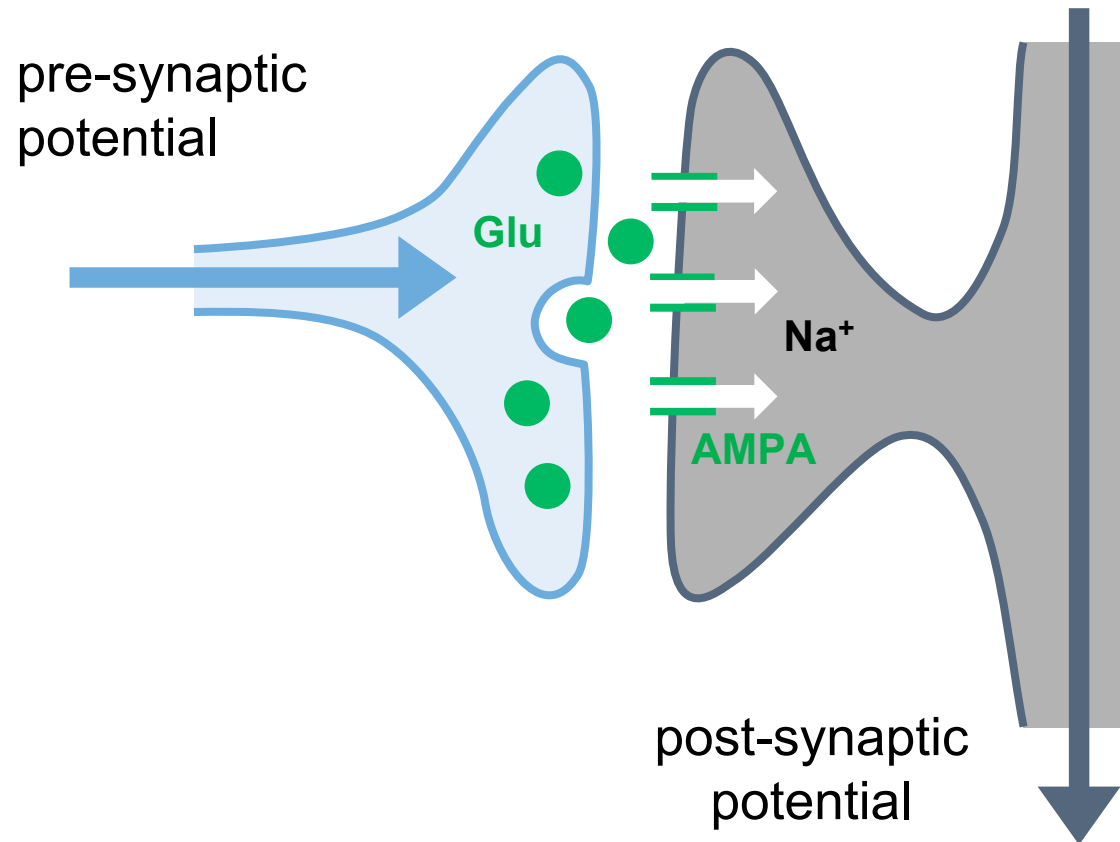
These PSPs represent the excitatory and inhibitory input that these neurons receive

Usually we study this neuronal input following the presentation of a stimulus or following a cognitive event

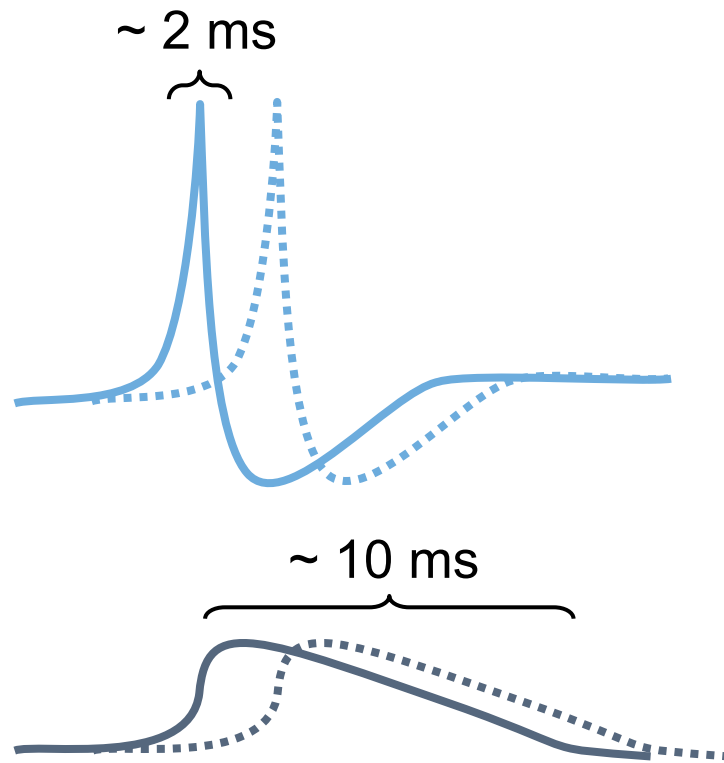
What generates the currents and fields



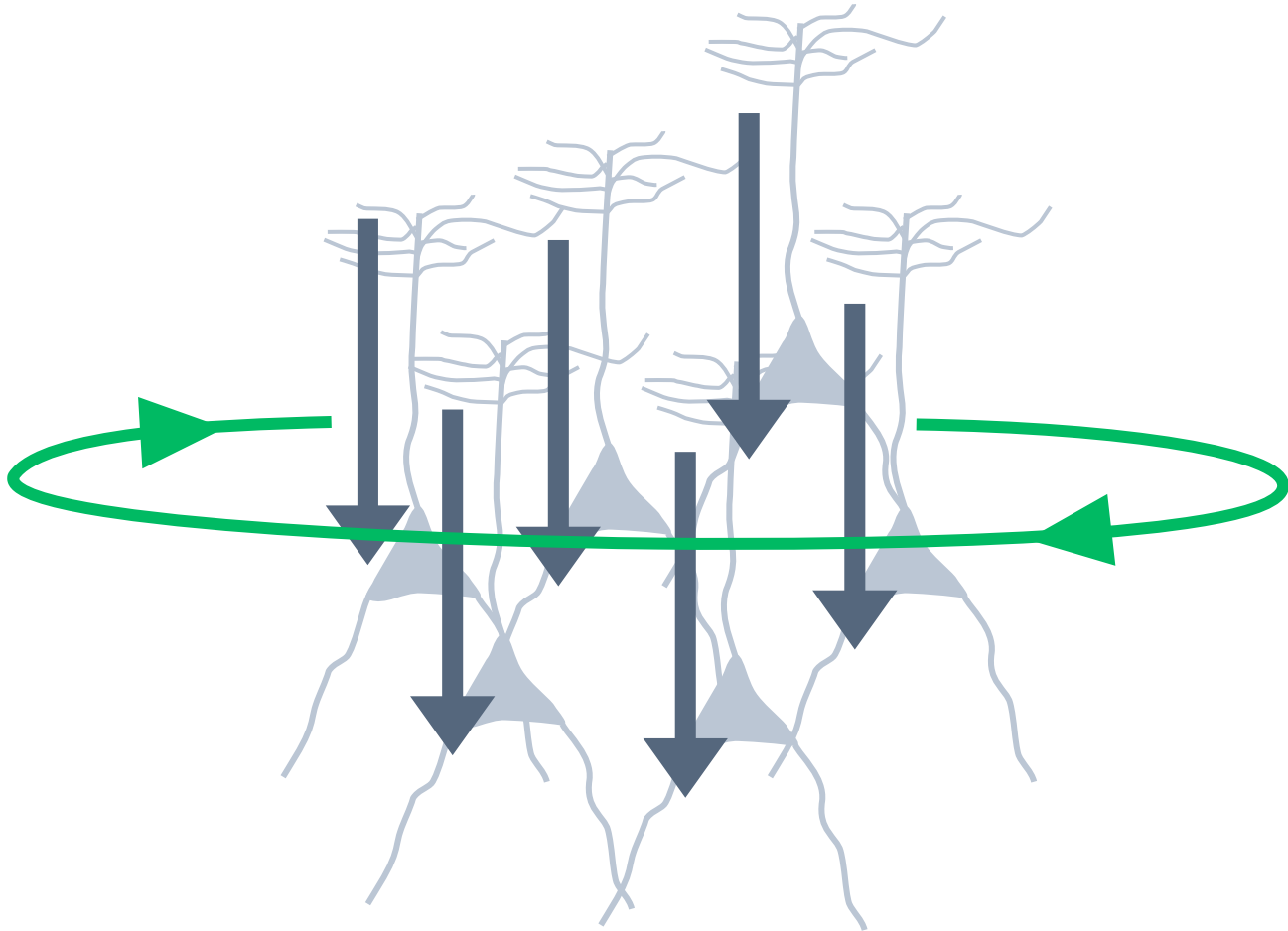
What generates the currents and fields



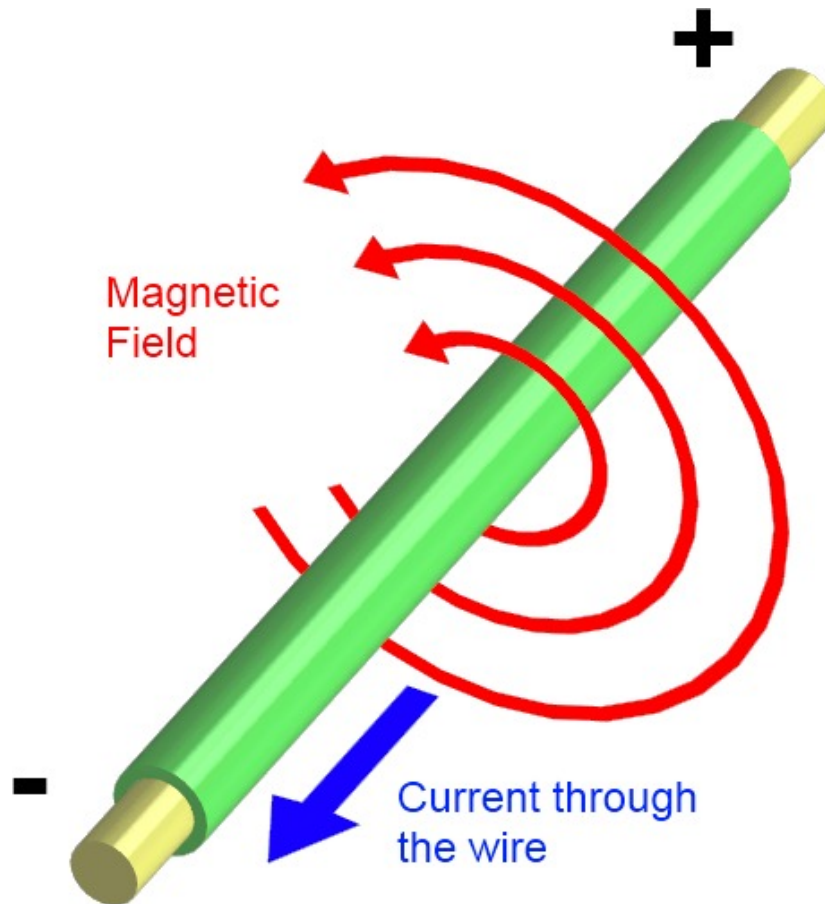
What generates the currents and fields



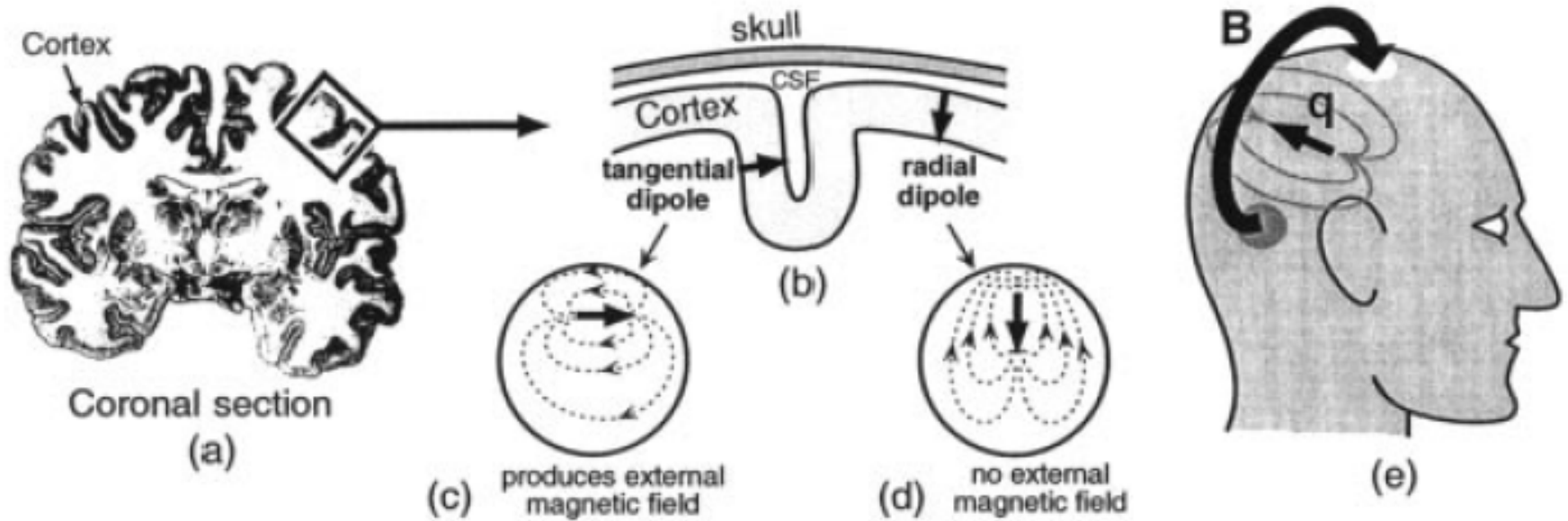
What generates the currents and fields



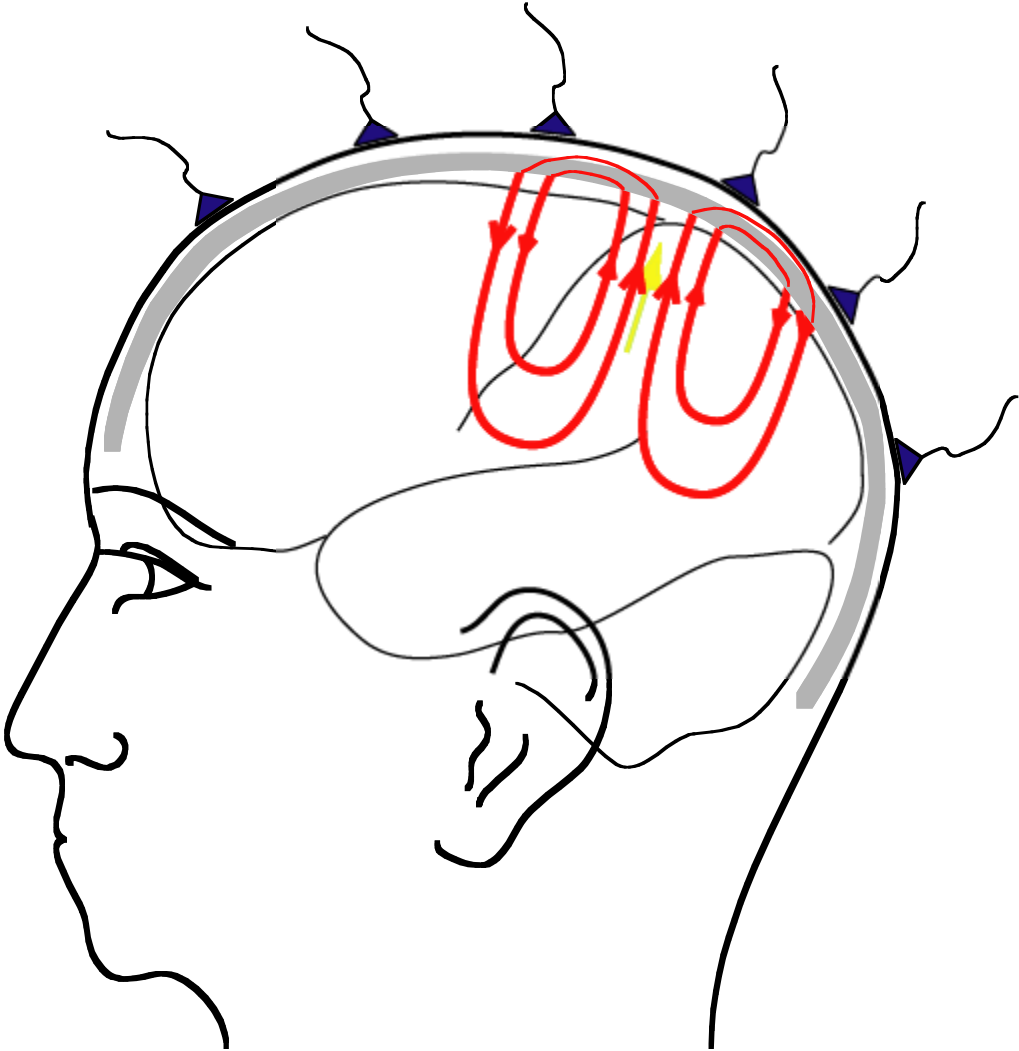
What generates the currents and fields



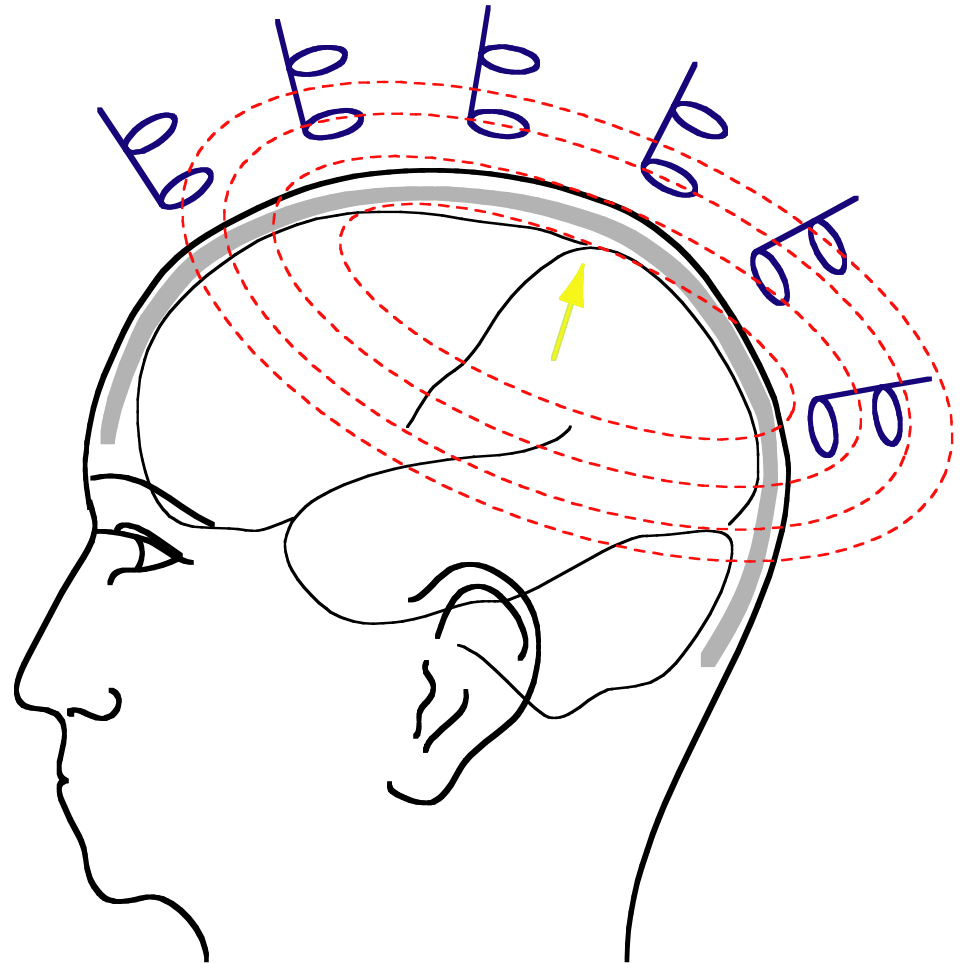
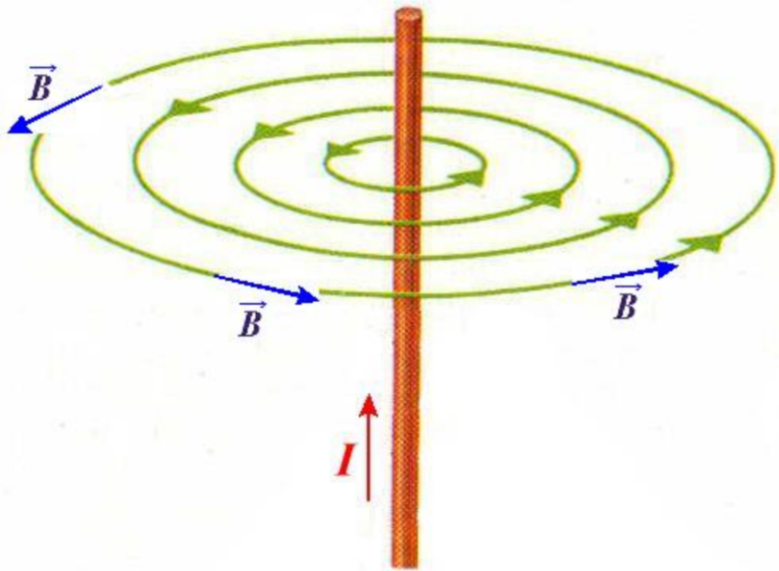
What generates the currents and fields



EEG volume conduction



Electric current \rightarrow magnetic field



Talk outline

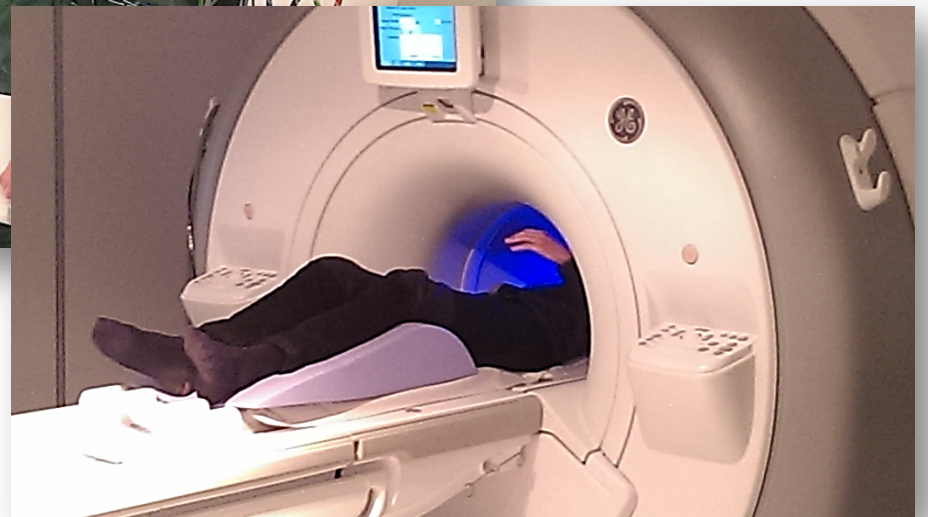
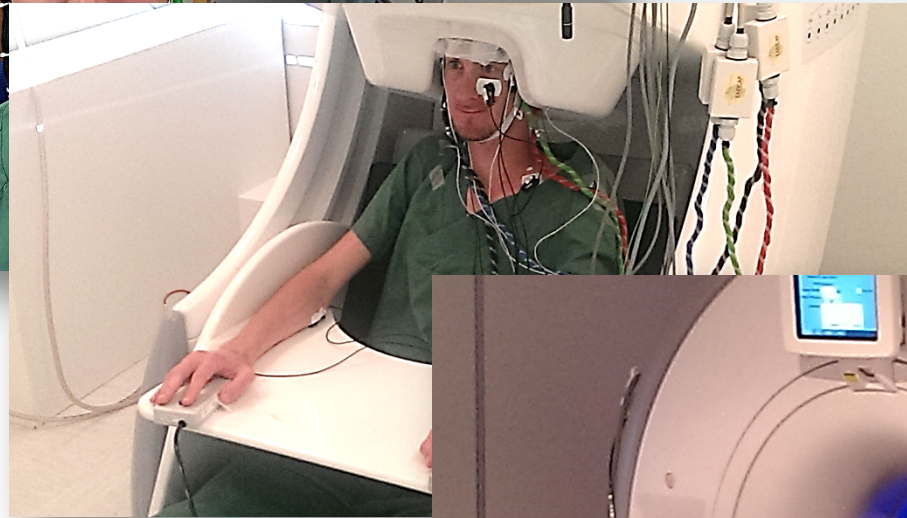
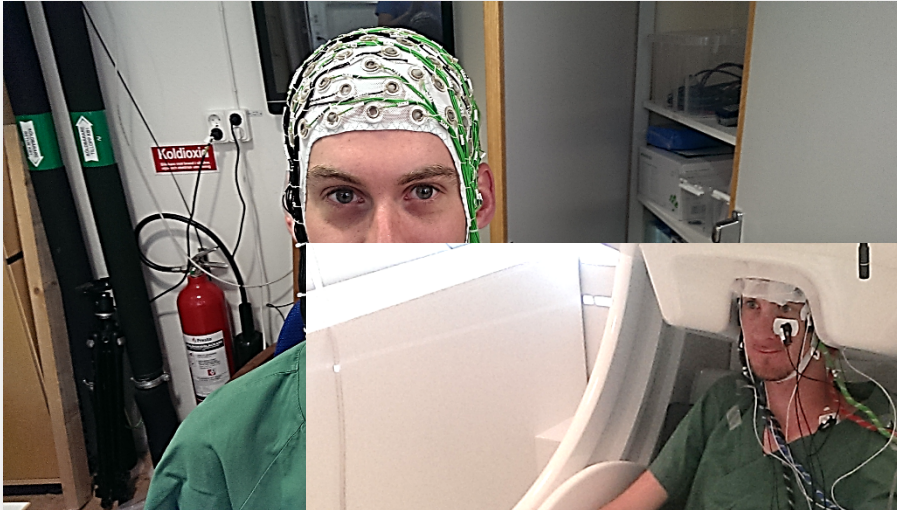
What kind of signals are generated in the brain

How do we record those signals

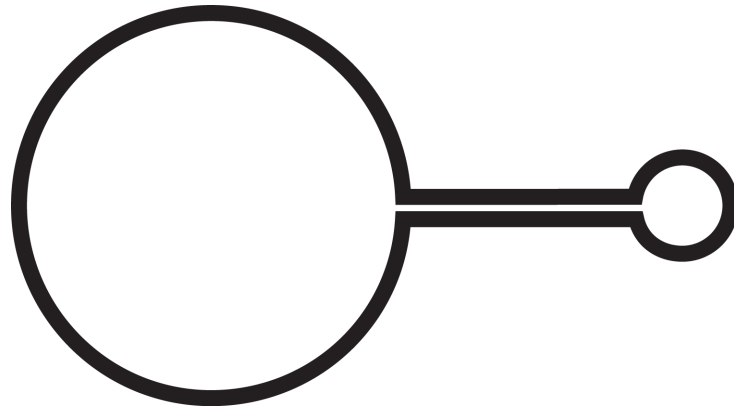
Analyzing those signals with FieldTrip

Background on the FieldTrip toolbox

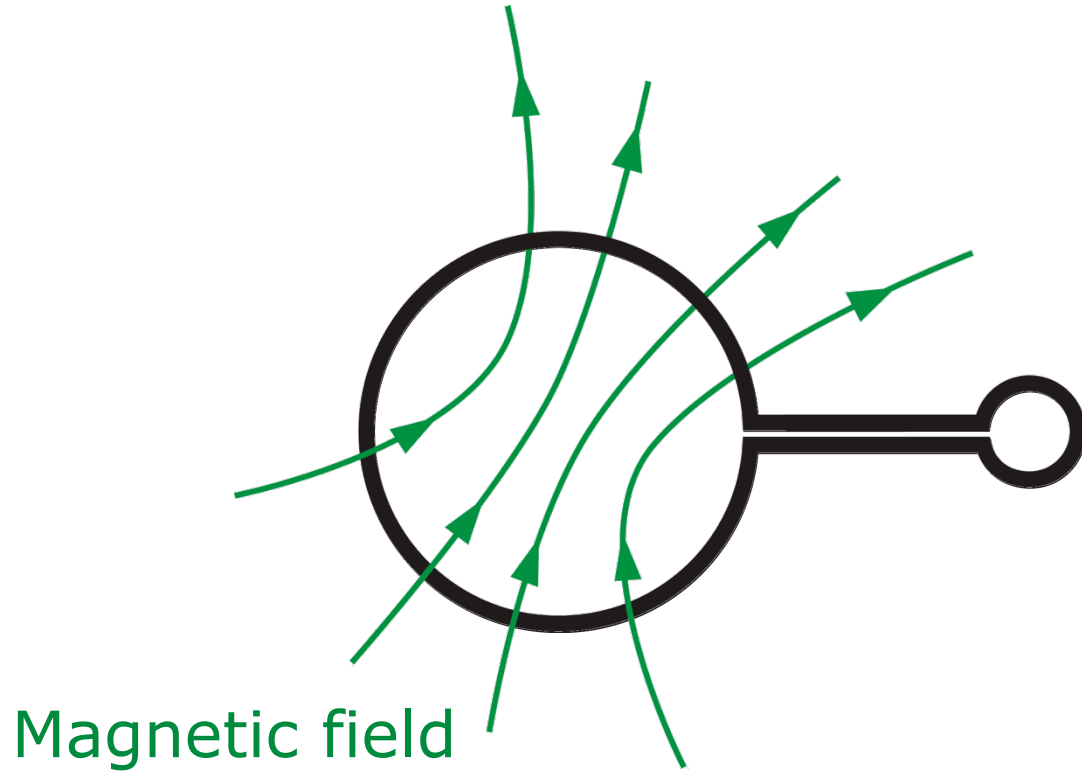
How do we record these signals from the brain



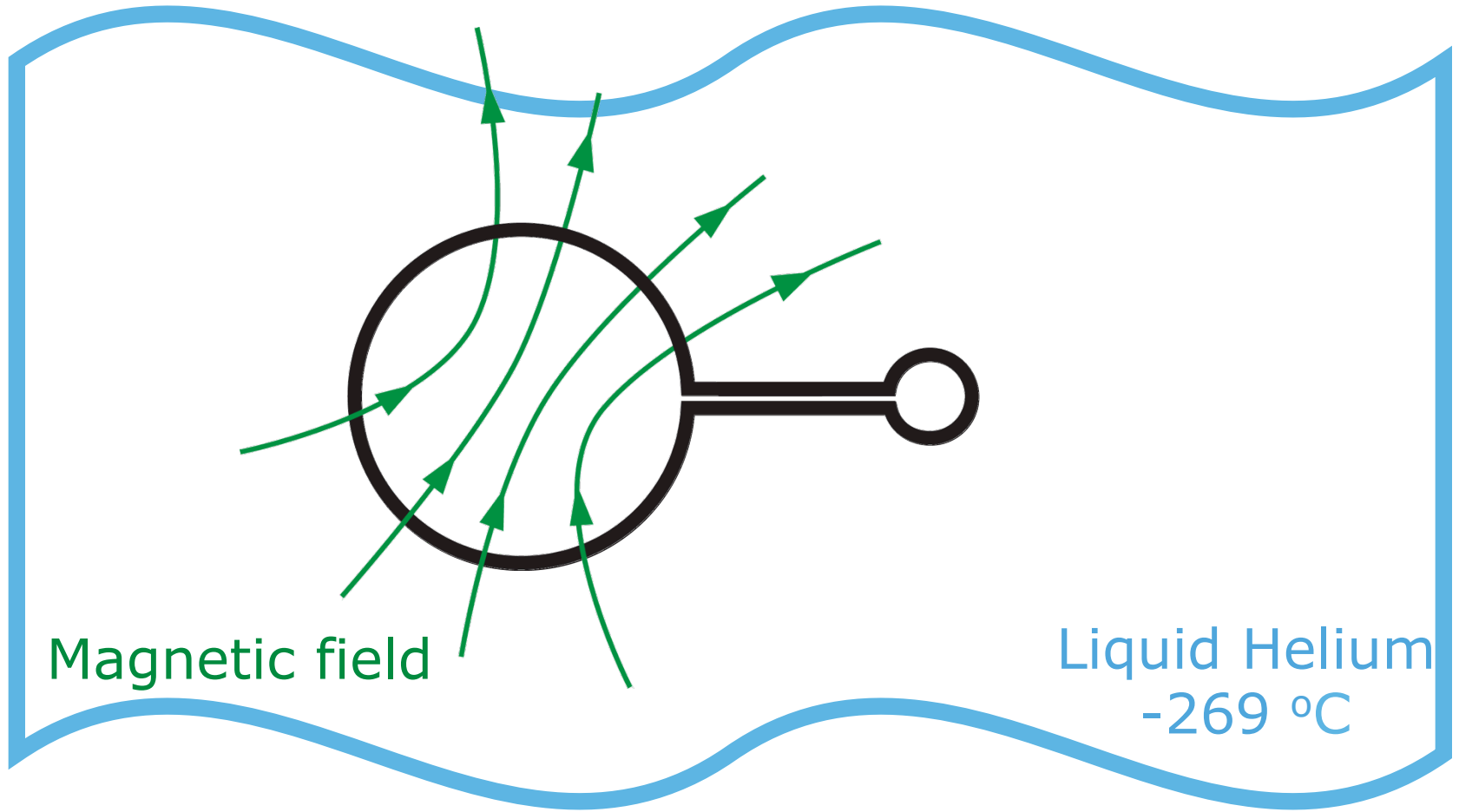
Recording small magnetic fields



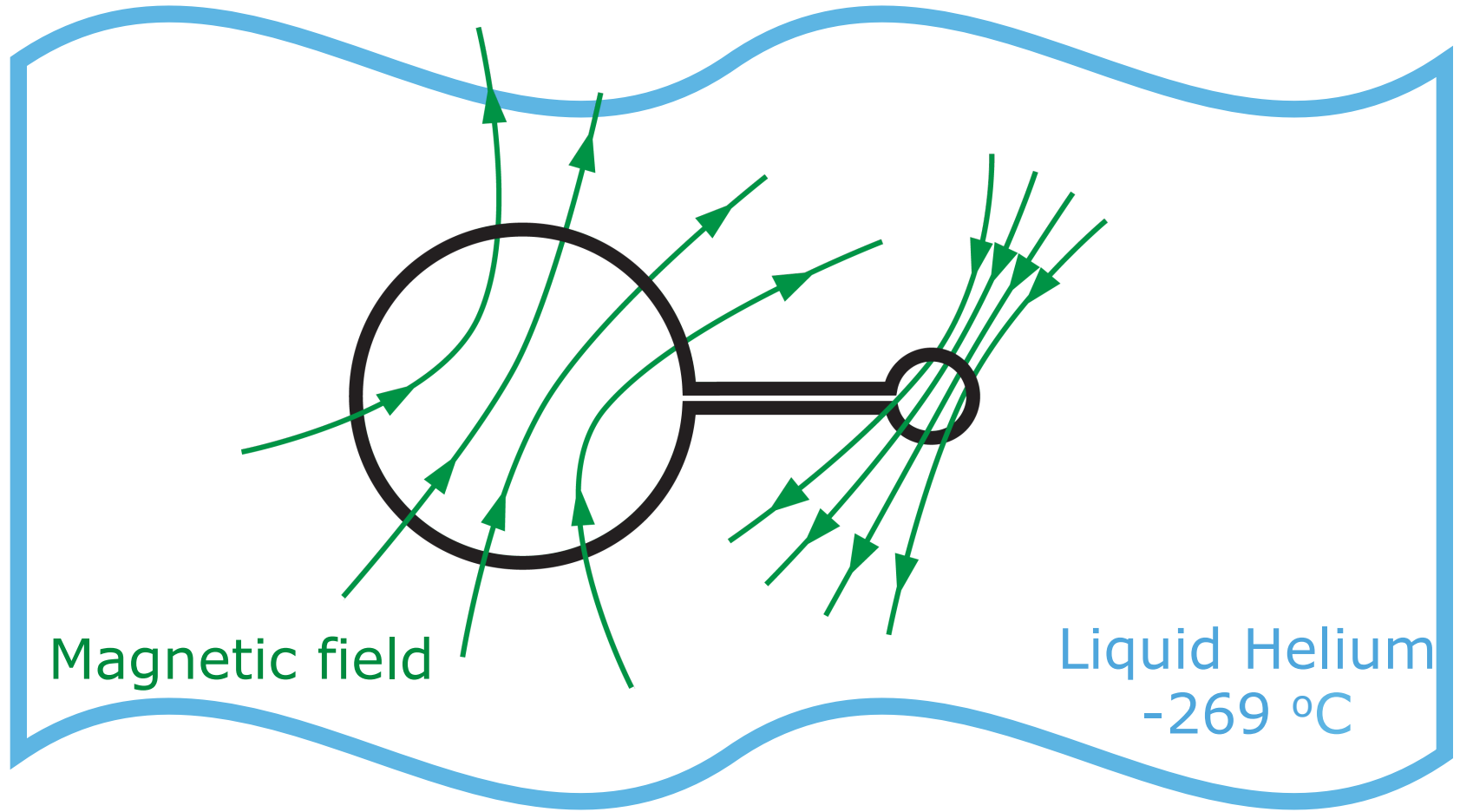
Recording small magnetic fields



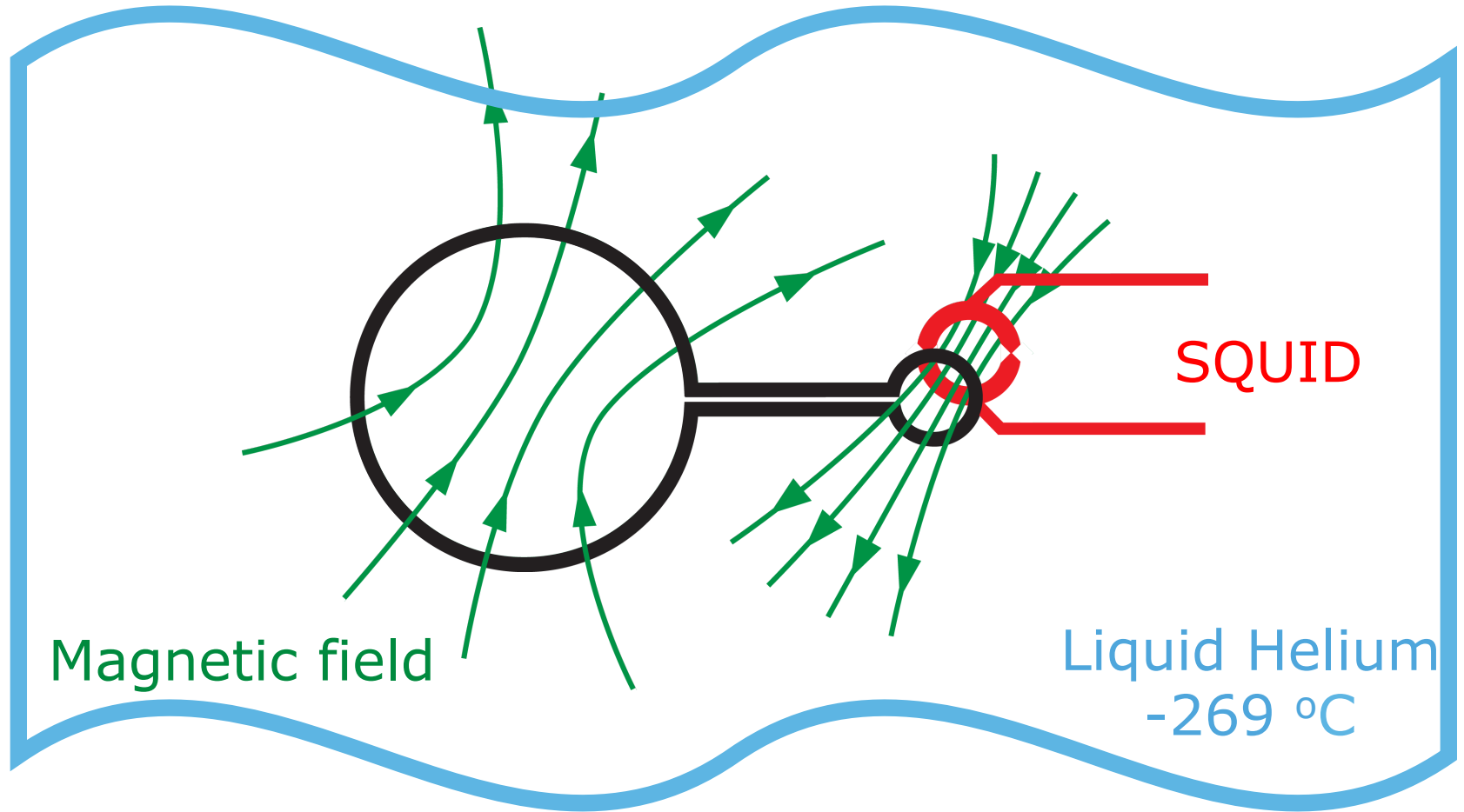
Recording small magnetic fields



Recording small magnetic fields

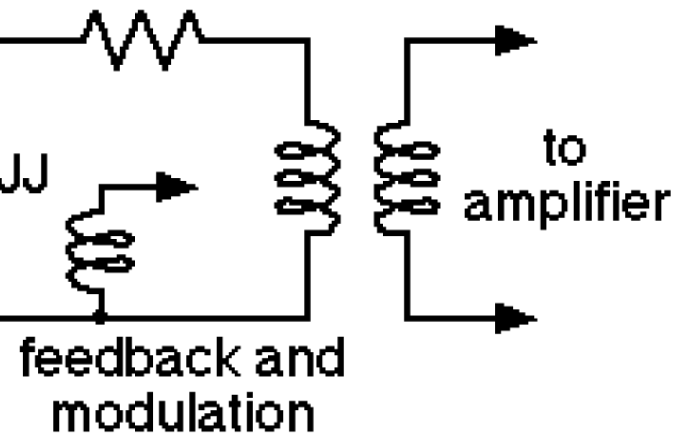
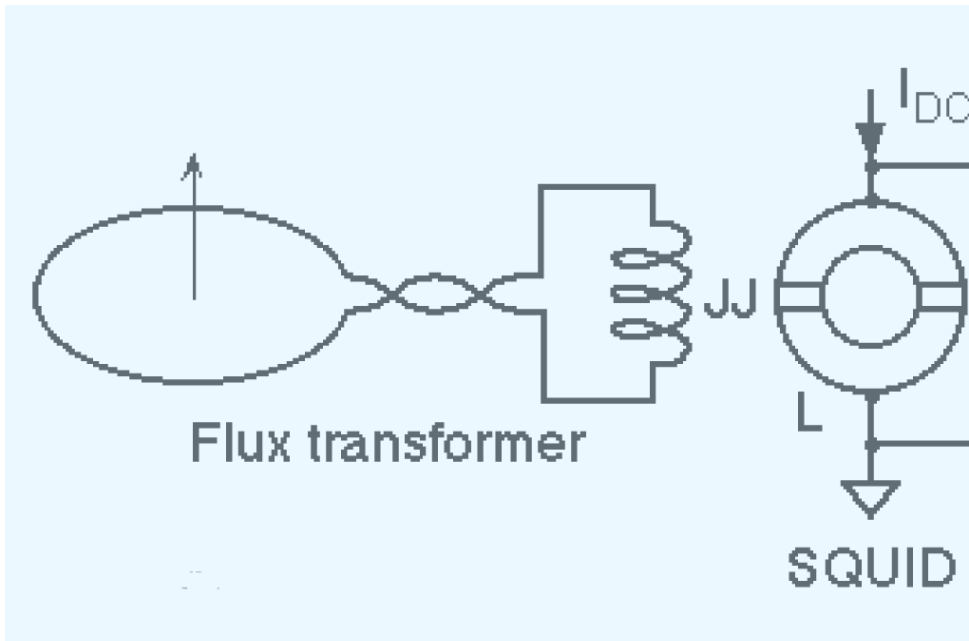
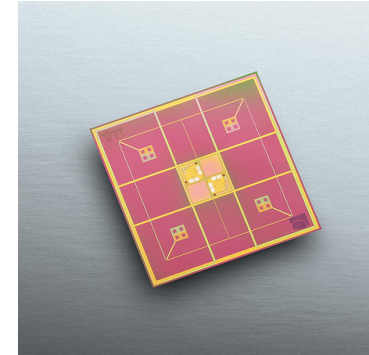


Recording small magnetic fields



Magnetic field detectors

Superconducting **QU**antum **I**nterference **D**evice



Magnetic field strength - compared

10^{-12}	0.1 - 1.0 picoTesla	human brain
10^{-9}	0.1 -10 nanoTesla	heliosphere
10^{-6}	24 microTesla	magnetic tape near tape head
10^{-5}	300-600 μ T microTesla	earth's magnetic field
10^{-3}	5 milliTesla	typical refrigerator magnet
10^0	1.5 - 7 Tesla	MRI systems

Technical challenges of MEG

Requires sensitive magnetic detectors

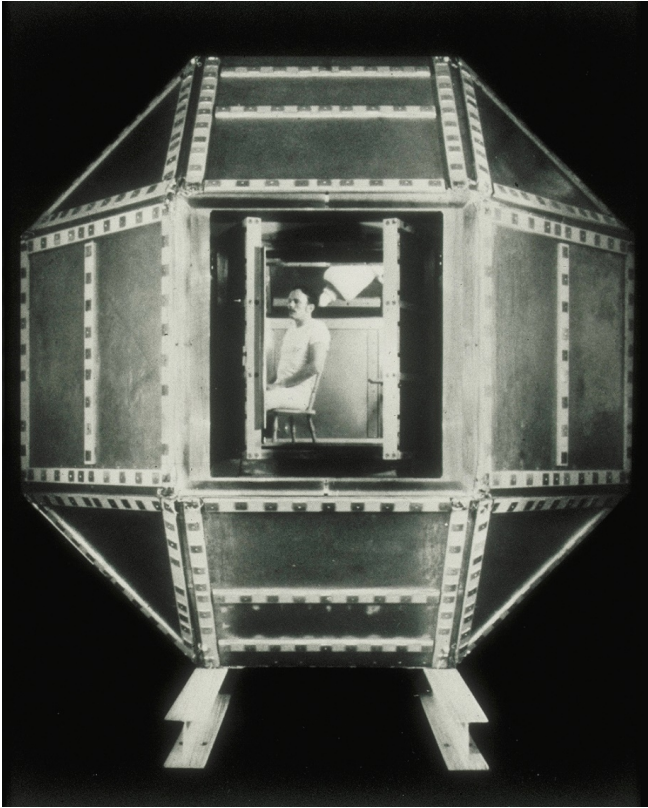
Deal with environmental noise

- shielding

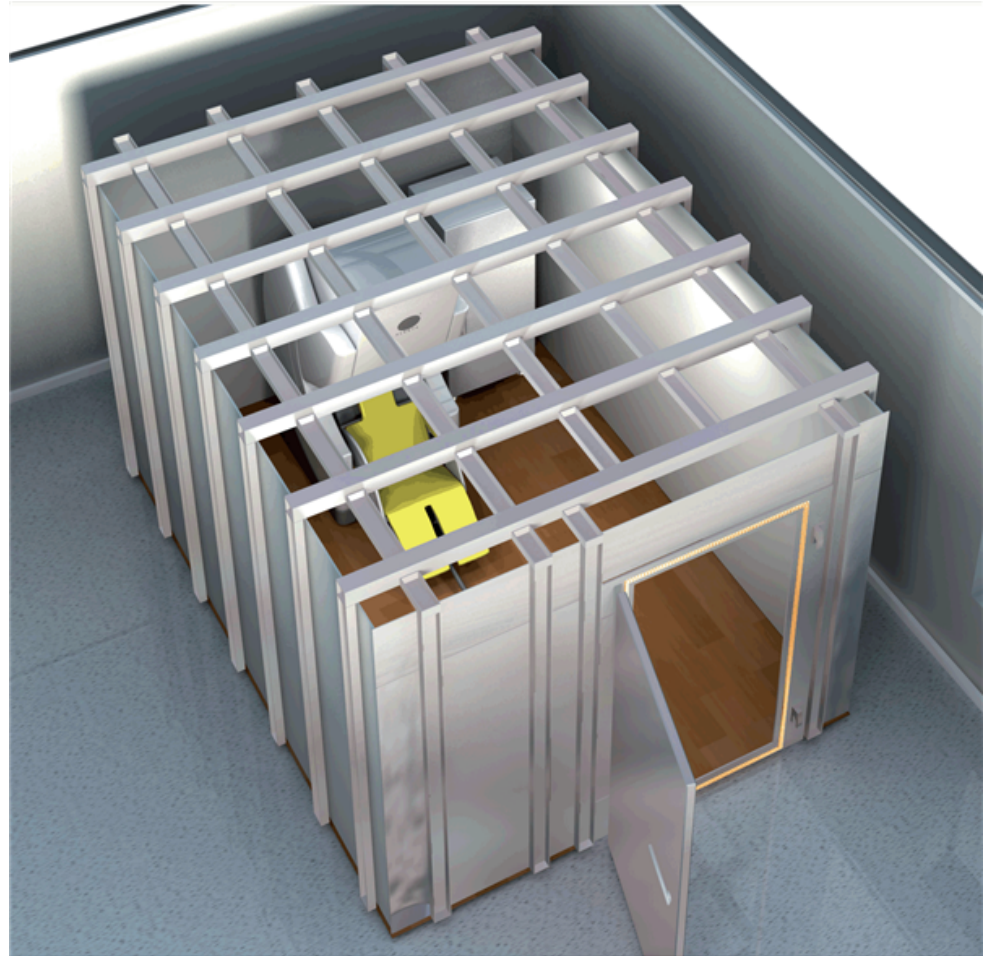
- sensor design

- reference sensors for noise subtraction

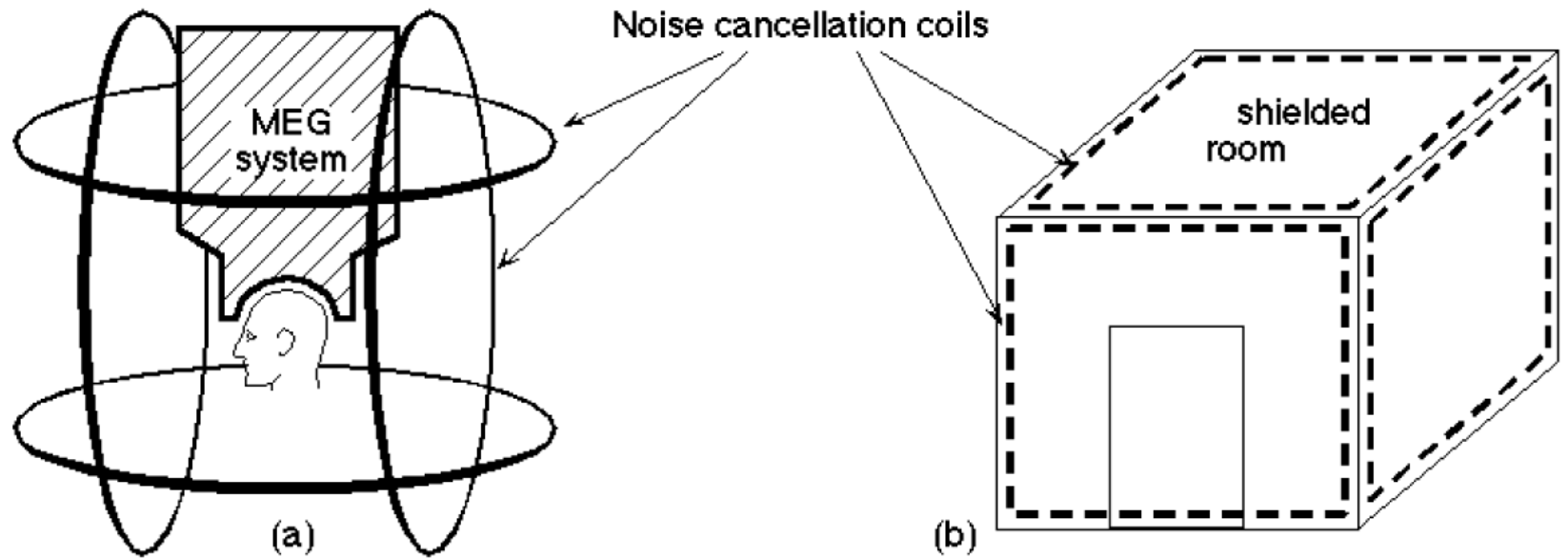
Shielding - passive



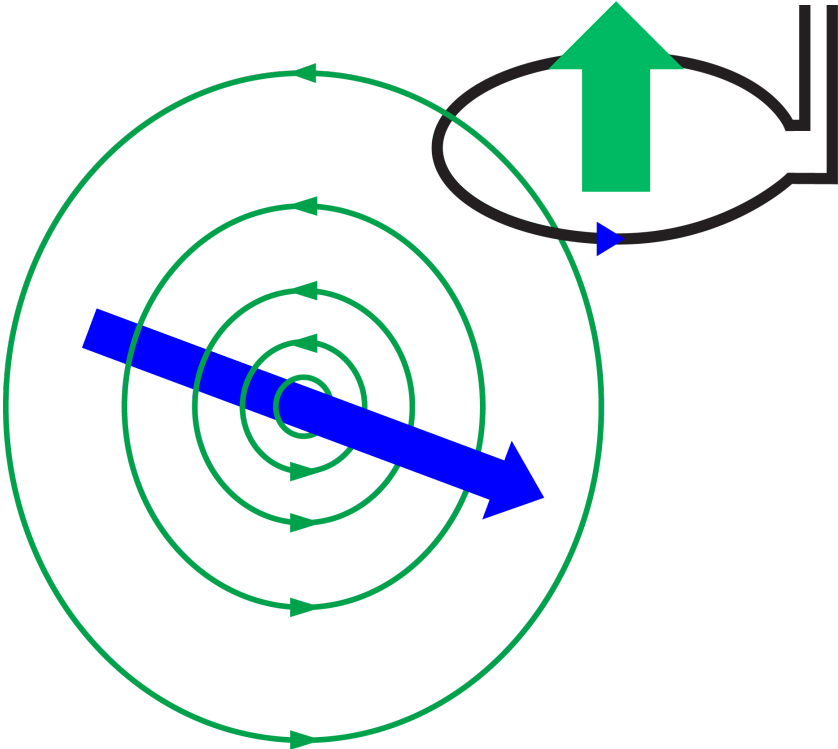
The magnetically shielded room built by David Cohen at MIT's Francis Bitter National Magnet Laboratory in 1969.



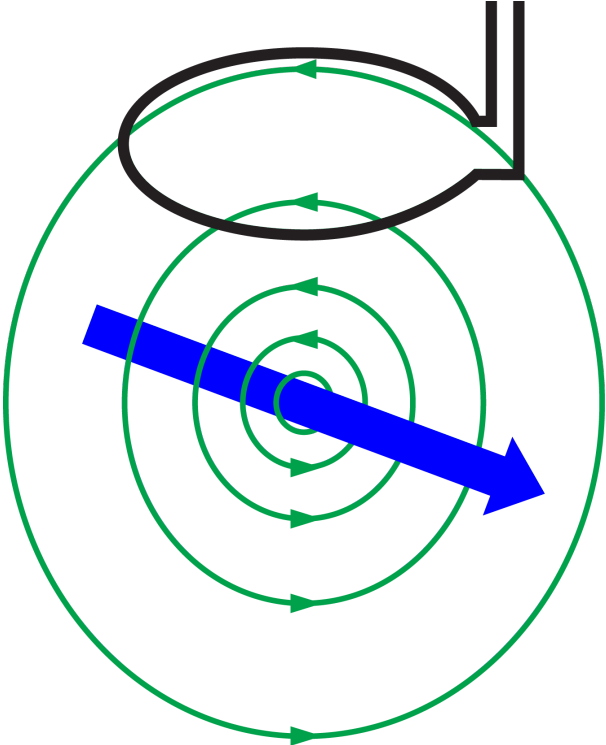
Shielding - active



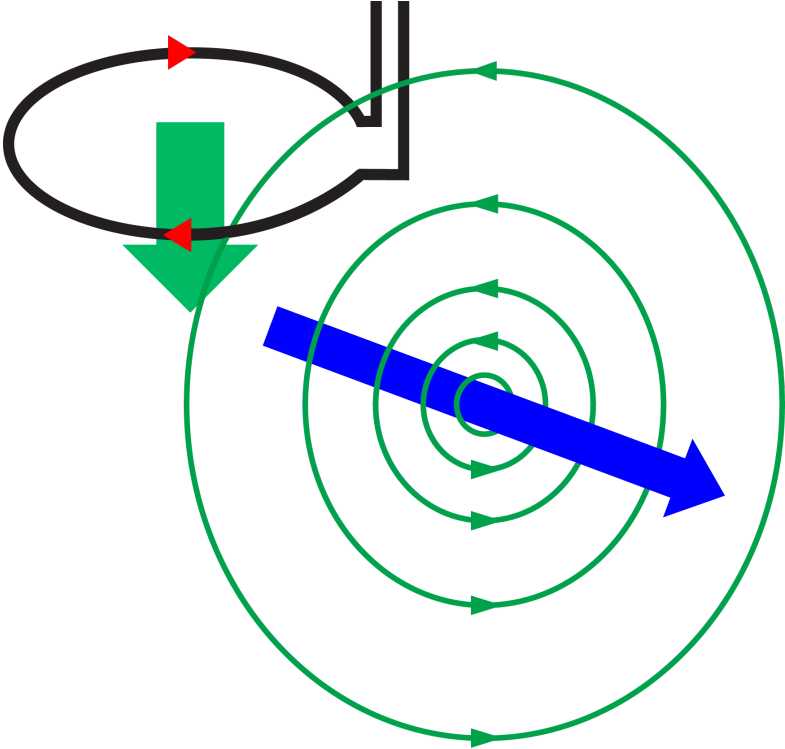
Magnetometer



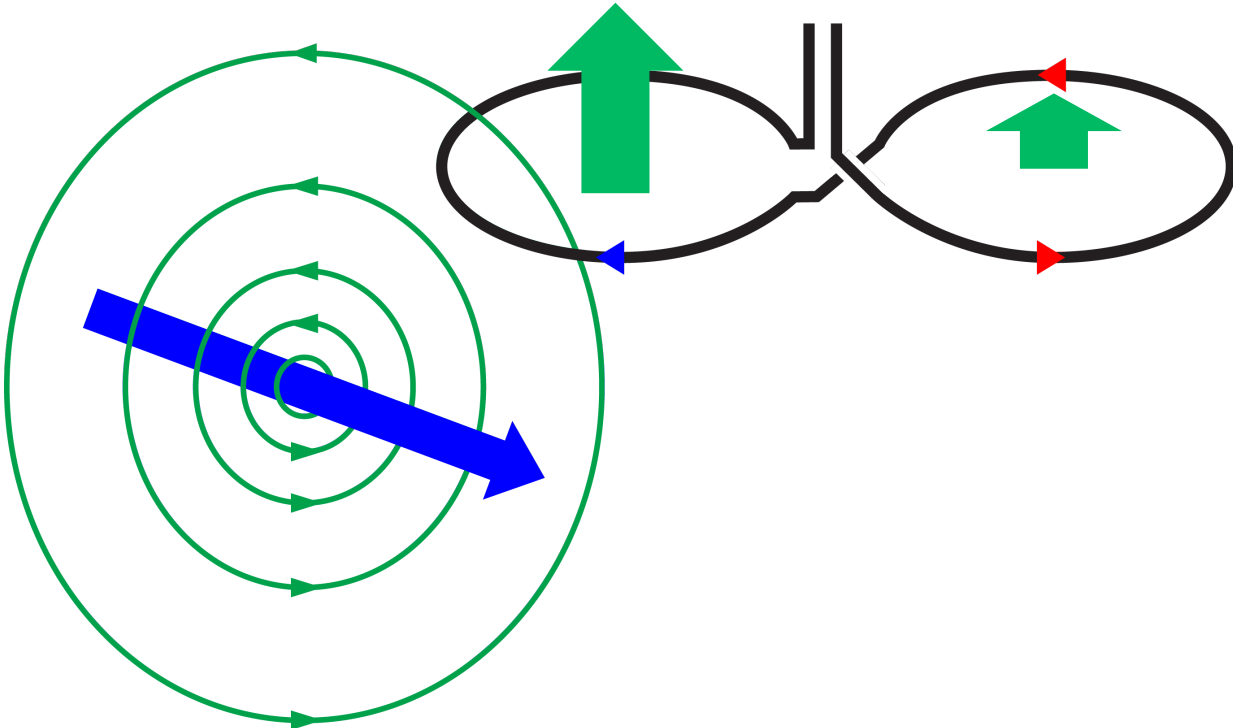
Magnetometer



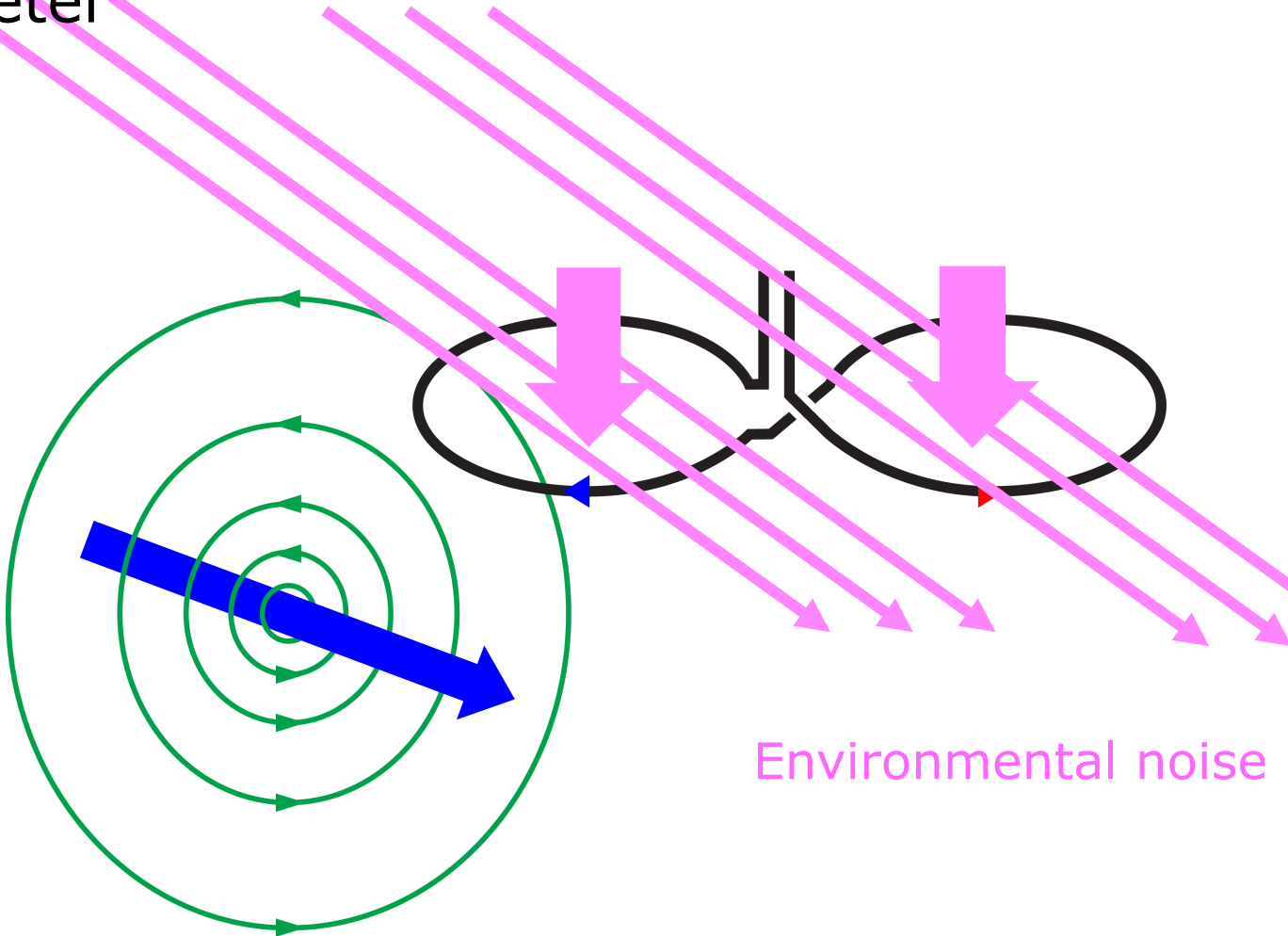
Magnetometer



Planar gradiometer

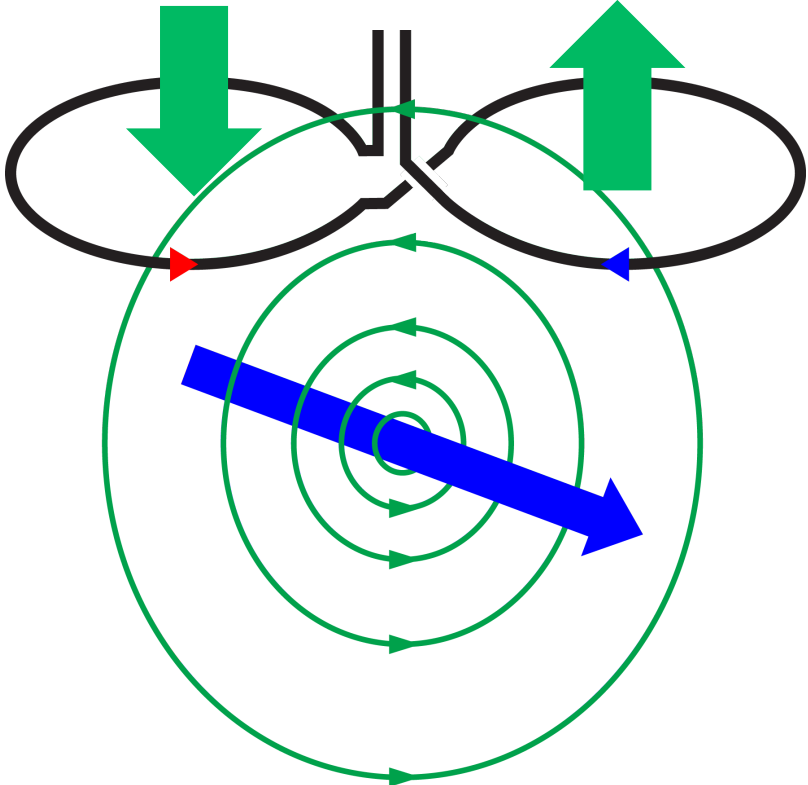


Planar gradiometer

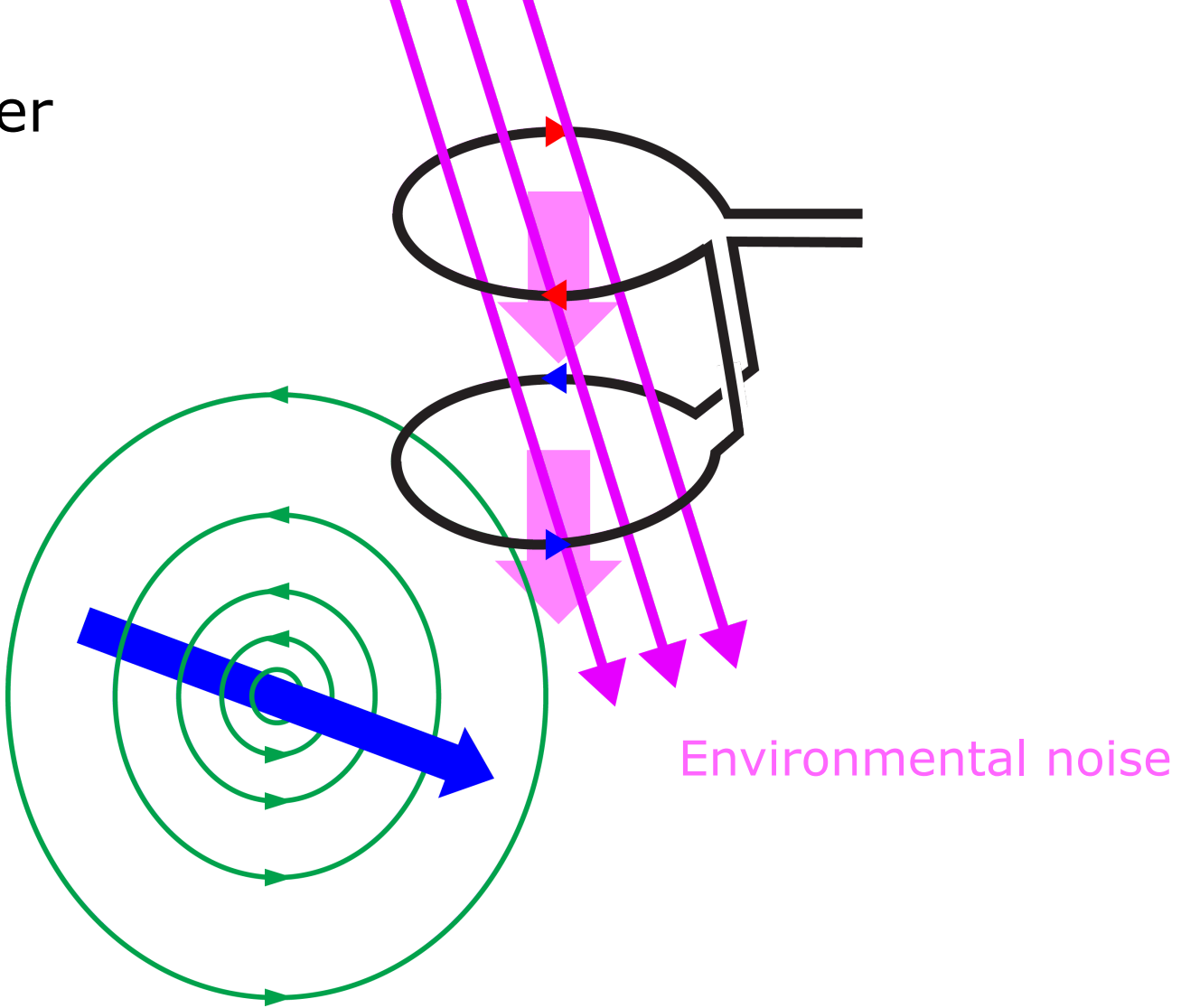


Environmental noise

Planar gradiometer

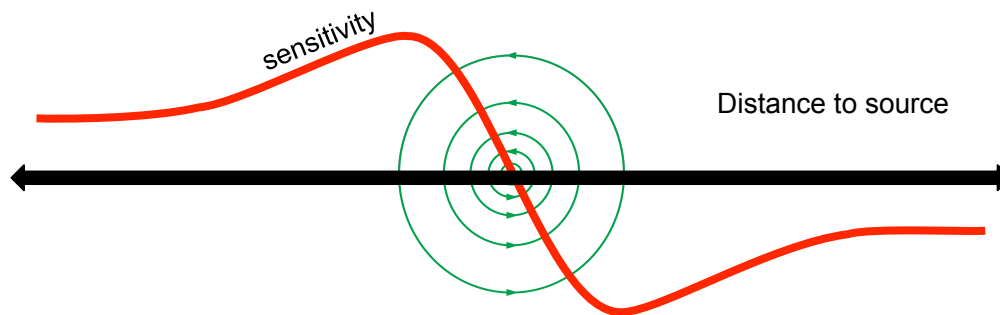
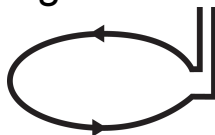


Axial gradometer

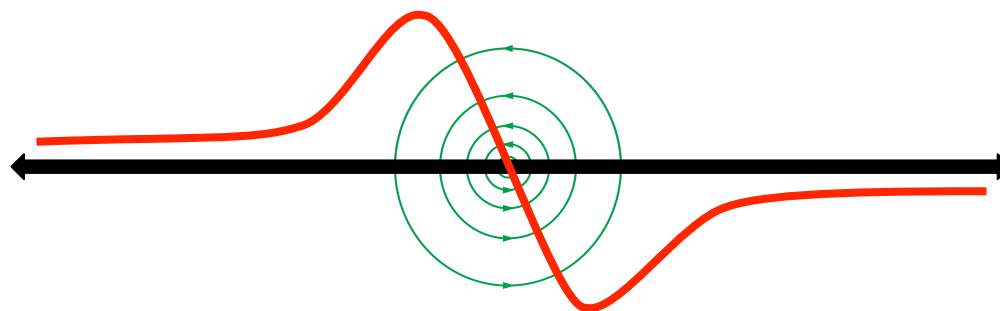
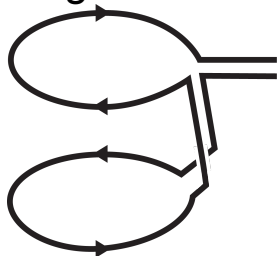


MEG sensor – sensitivity profile

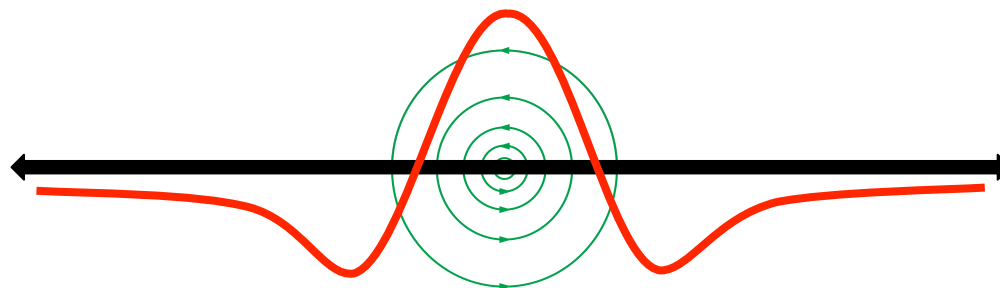
Magnetometer



Axial gradiometer



Planar gradiometer



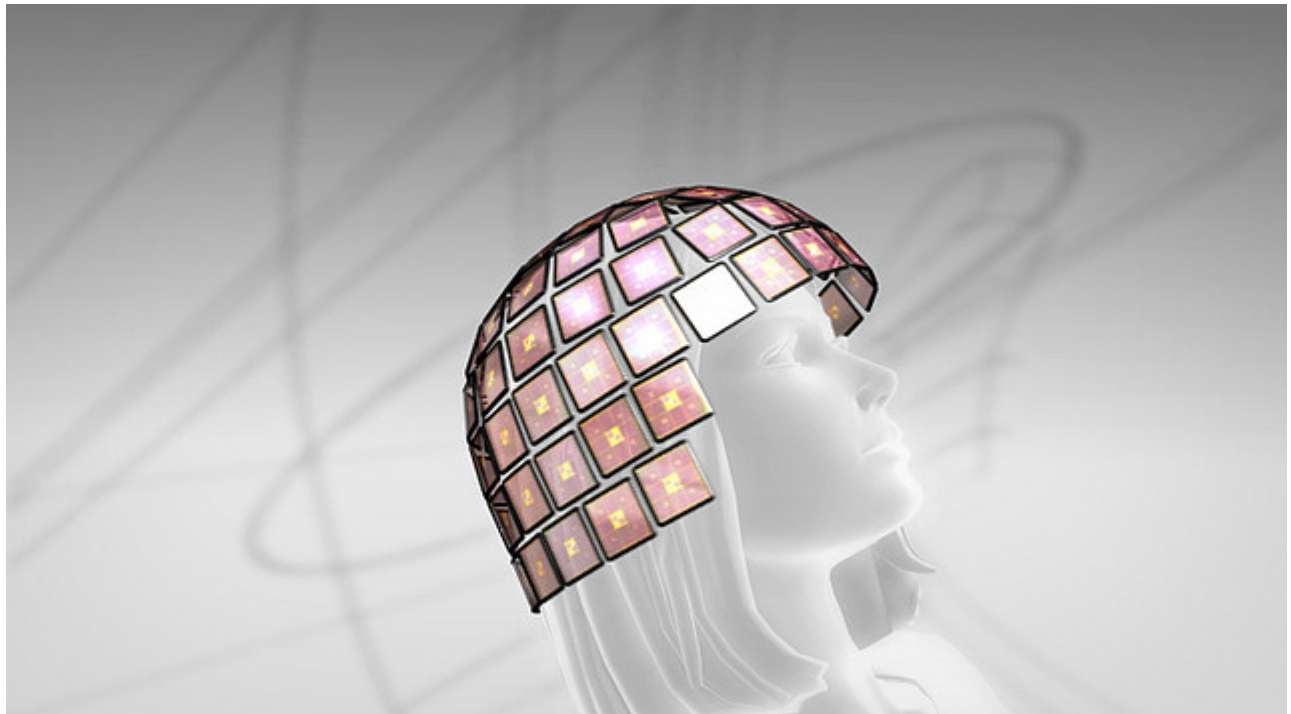
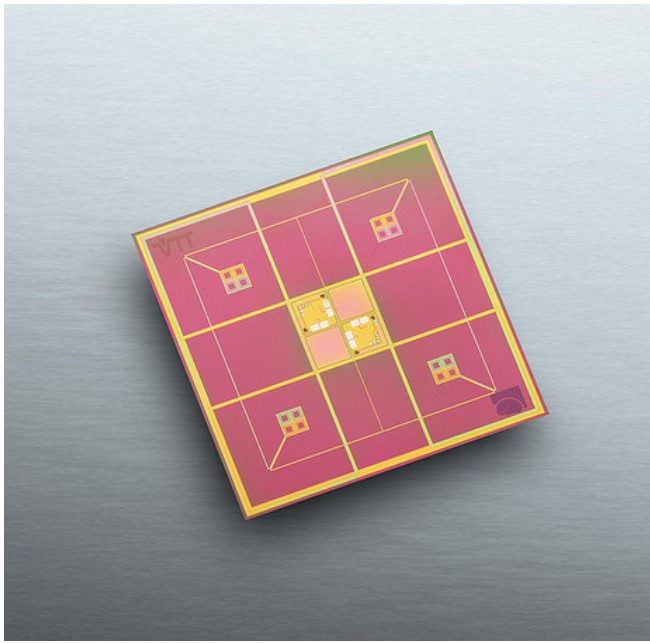
MEG systems

about 100-150 installations worldwide
two in the Netherlands

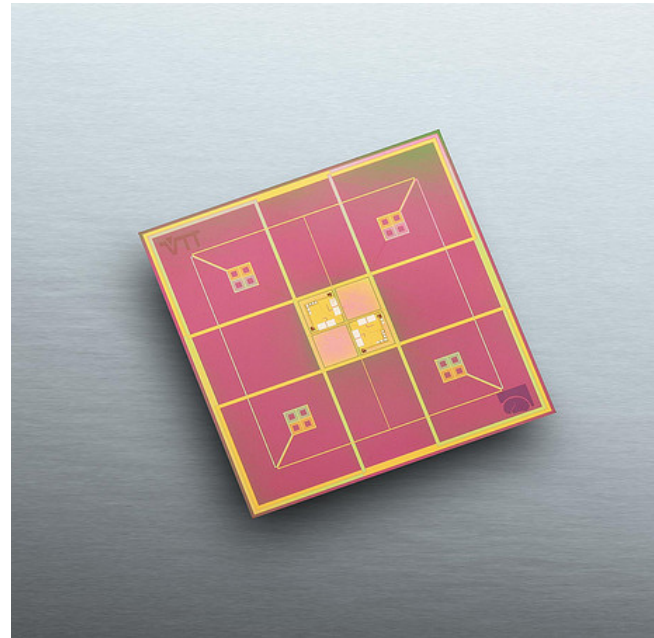
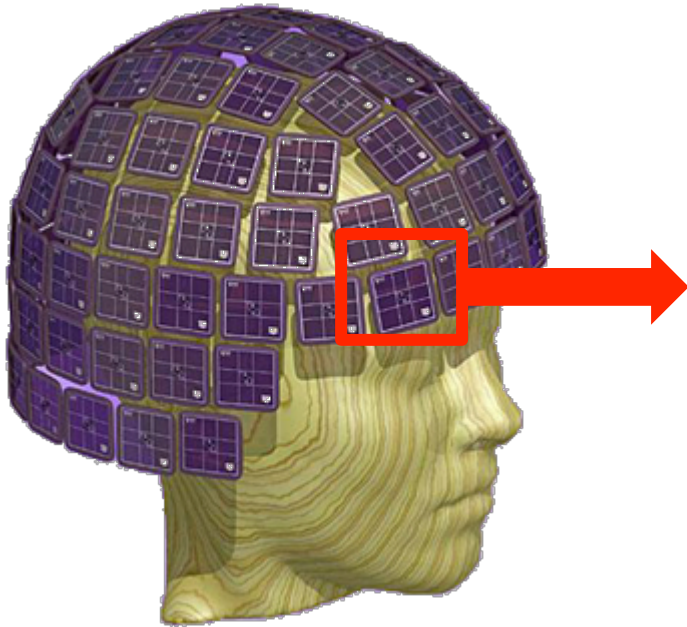


Elekta Neuromag

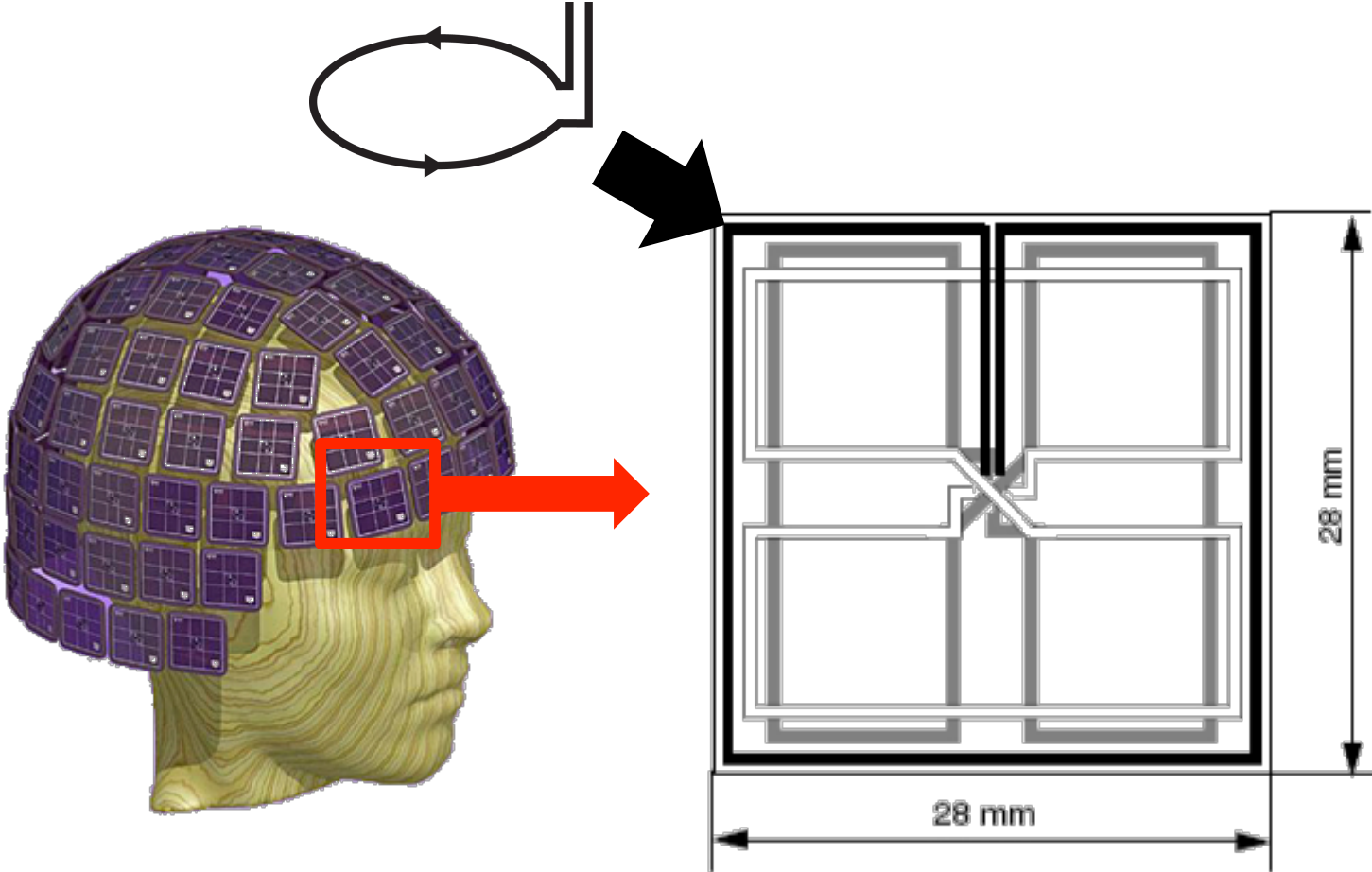
102 magnetometers
204 planar gradiometers
306 channels total



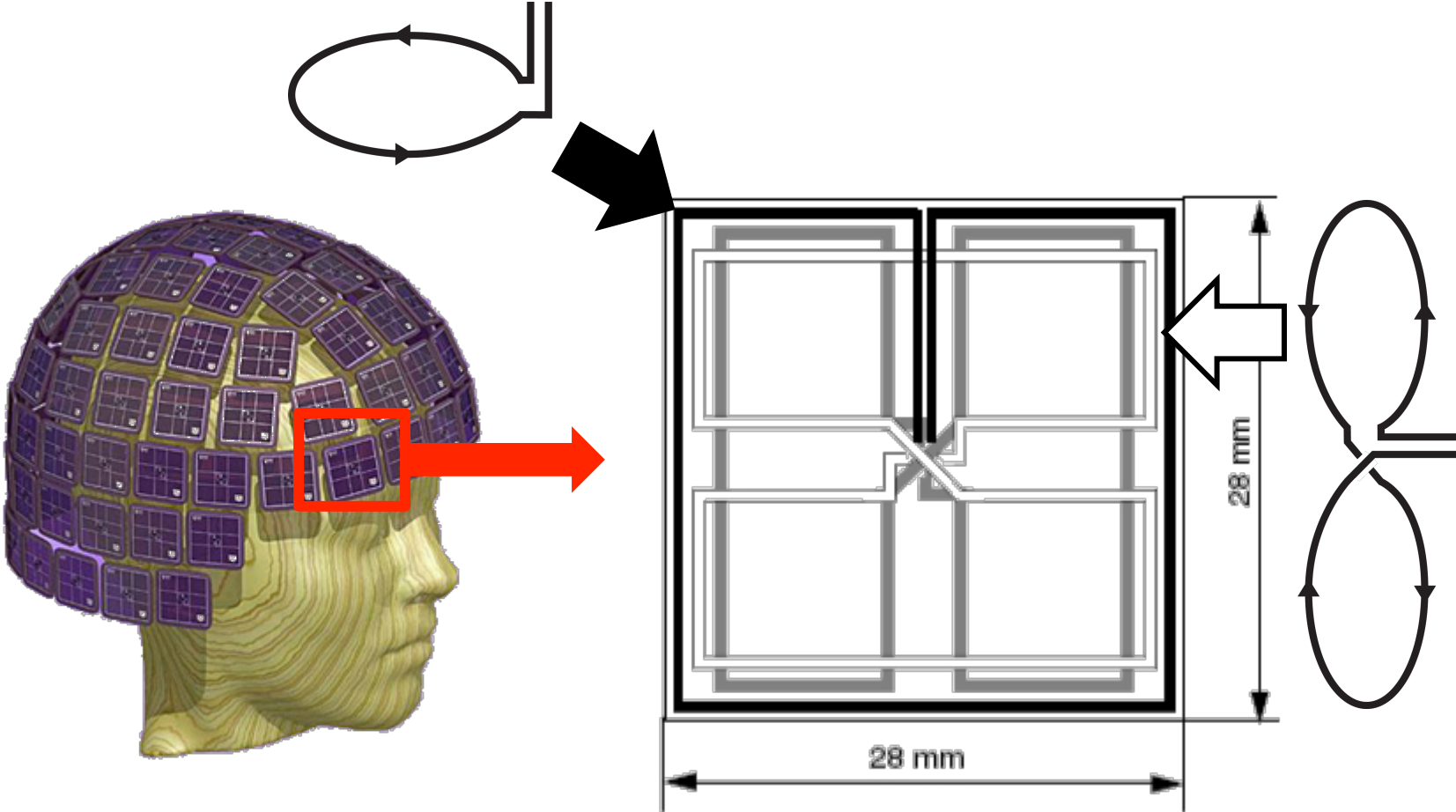
Elekta Neuromag



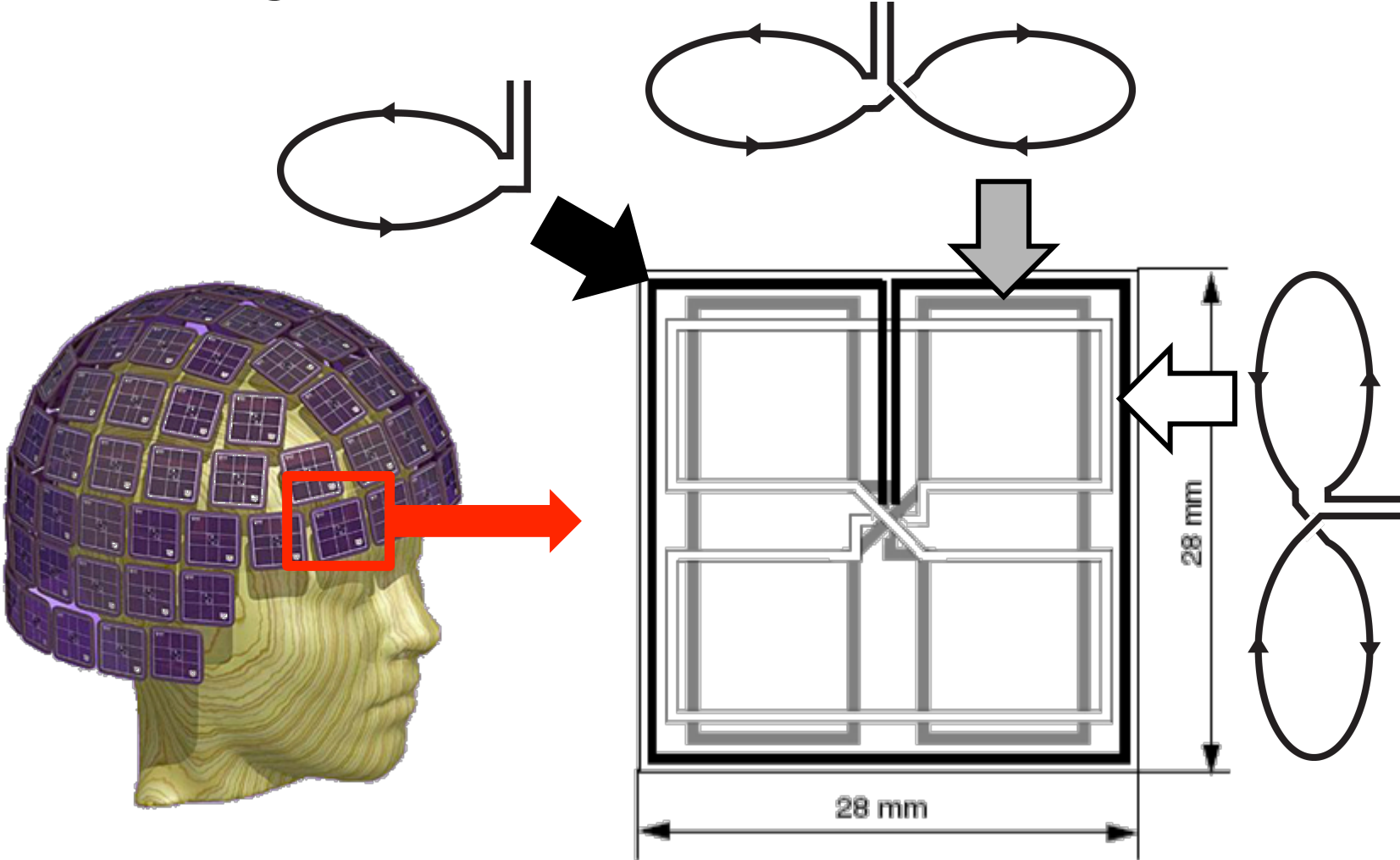
Elekta Neuromag



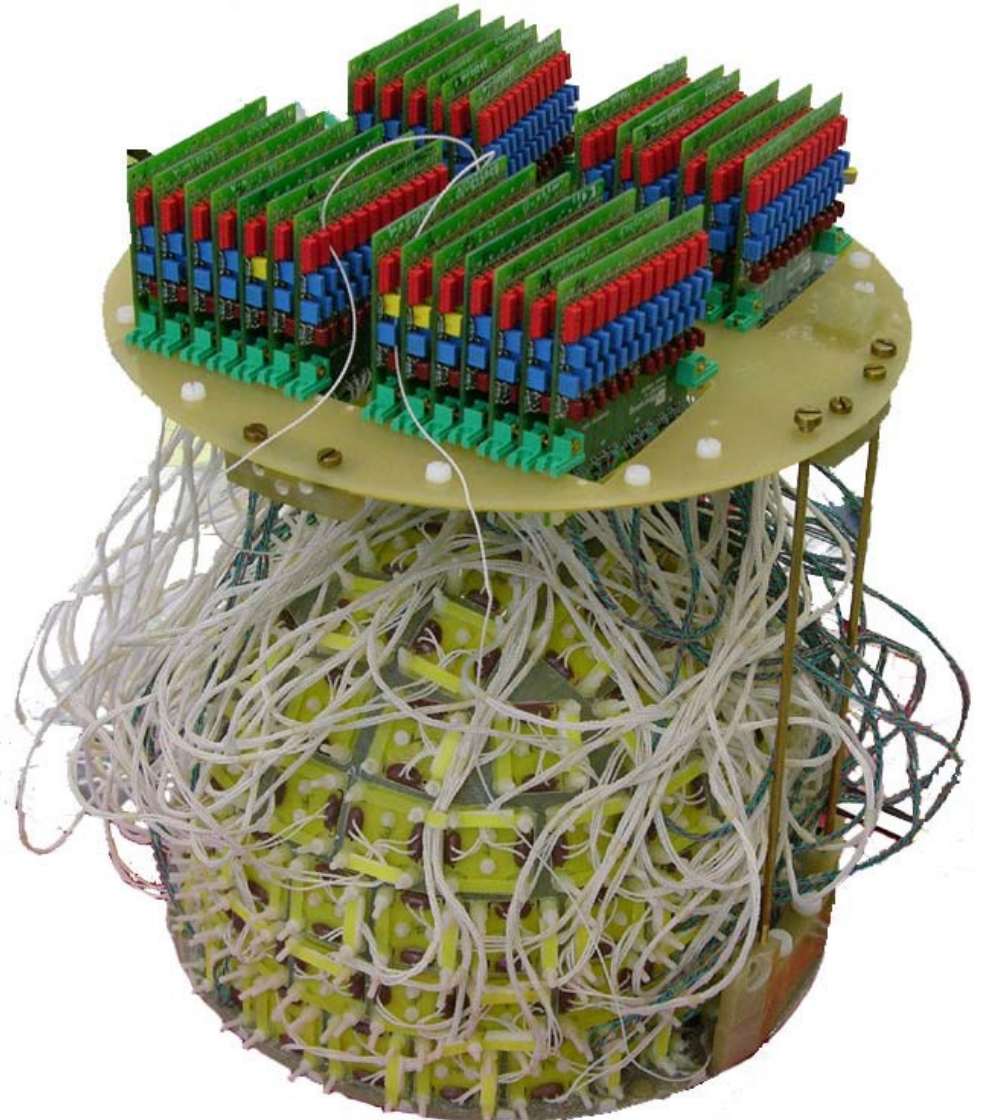
Elekta Neuromag



Elekta Neuromag

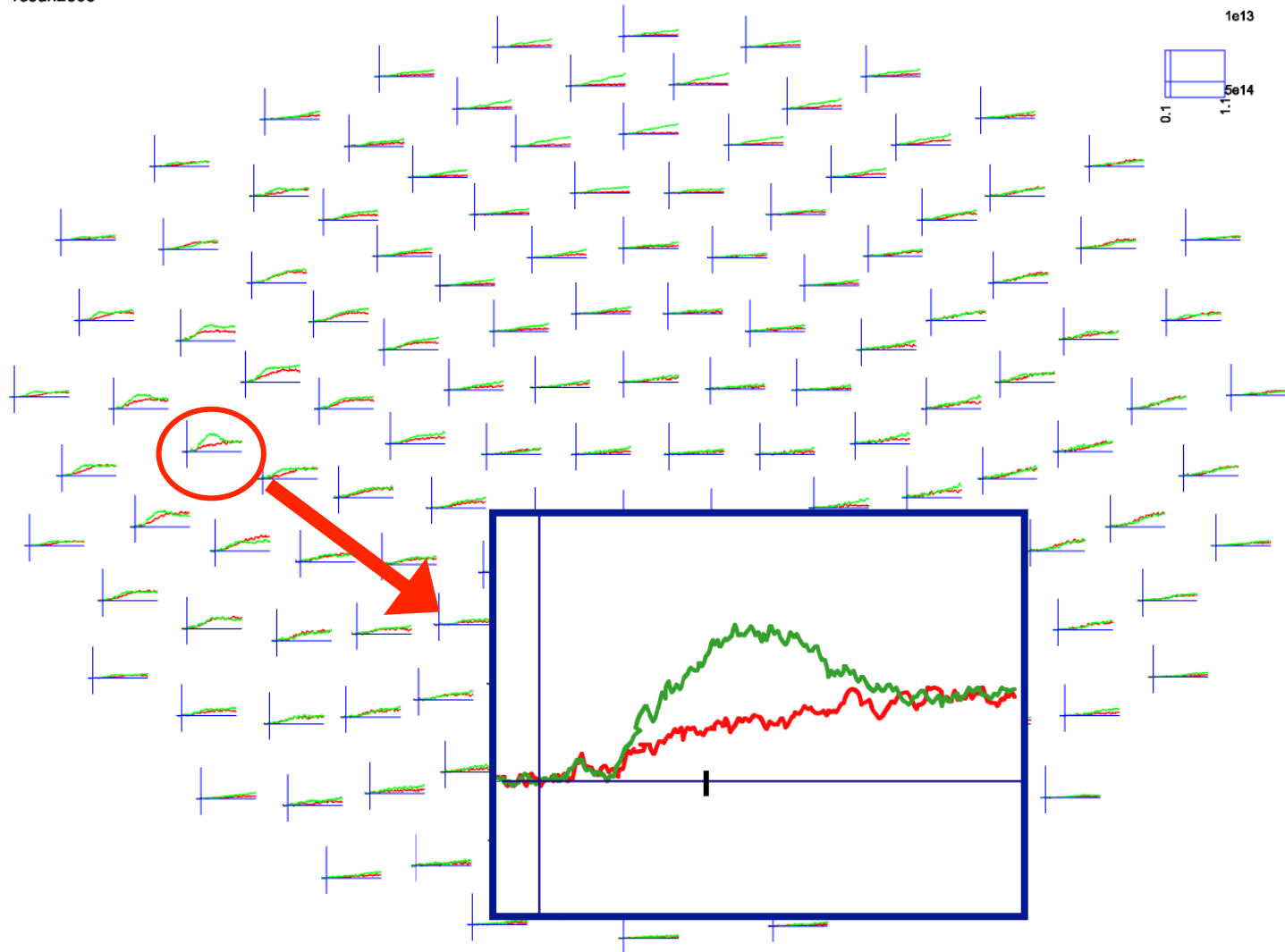


Elekta Neuromag

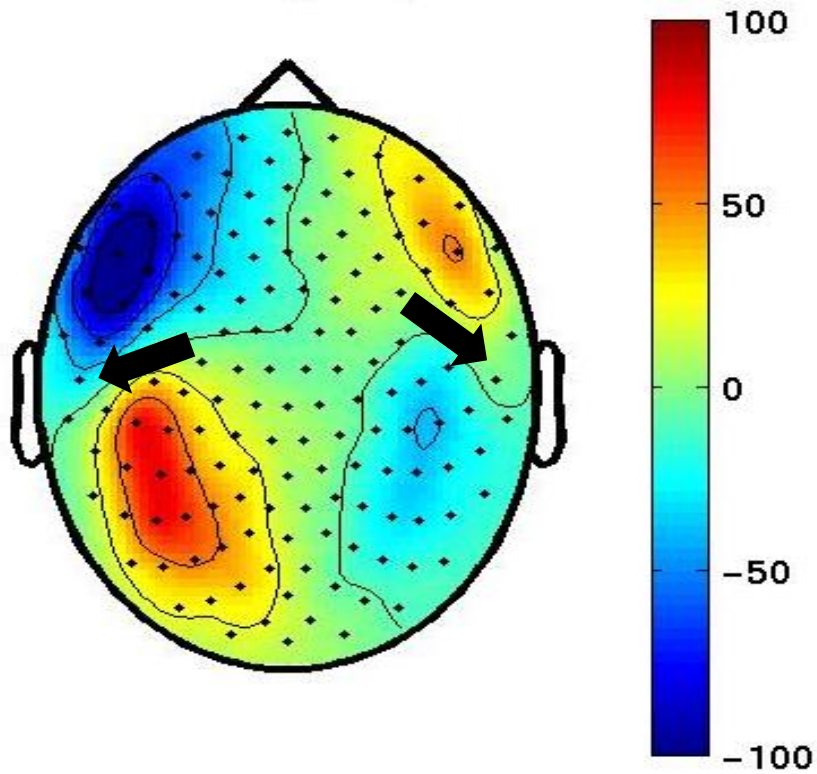


N400 response in MEG

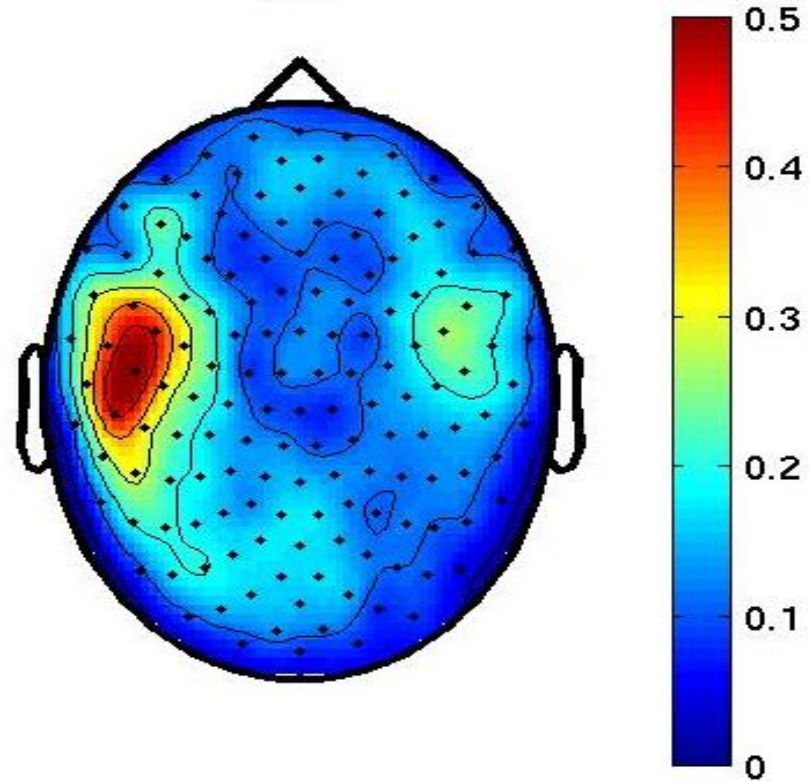
18Jun2003



N400 response - compared between MEG systems

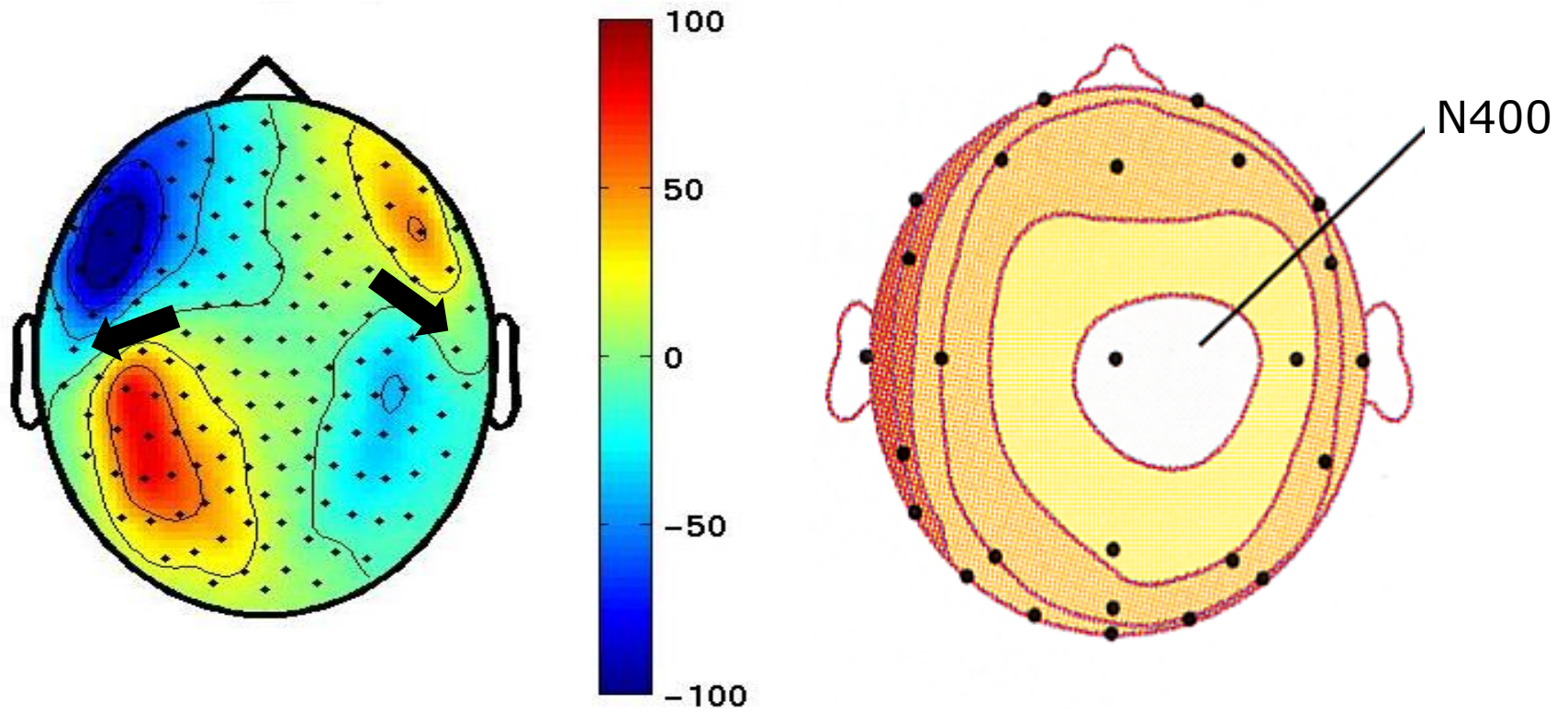


axial magnetic field



planar gradient

N400 response - compared between MEG and EEG



axial magnetic field

potential distribution

Talk outline

What kind of signals are generated in the brain

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Analyzing those signals with FieldTrip

Background on the FieldTrip toolbox

M/EEG signal characteristics considered during analysis

timecourse of activity

-> ERP

spectral characteristics

-> power spectrum

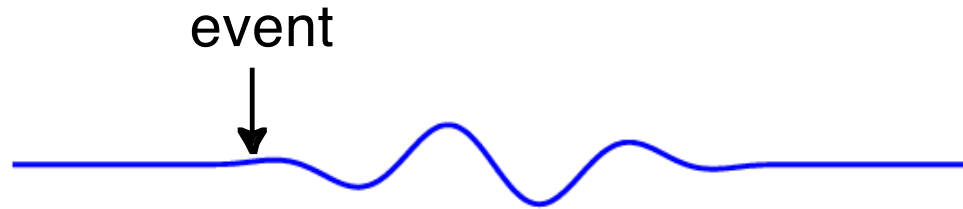
temporal changes in power

-> time-frequency response (TFR)

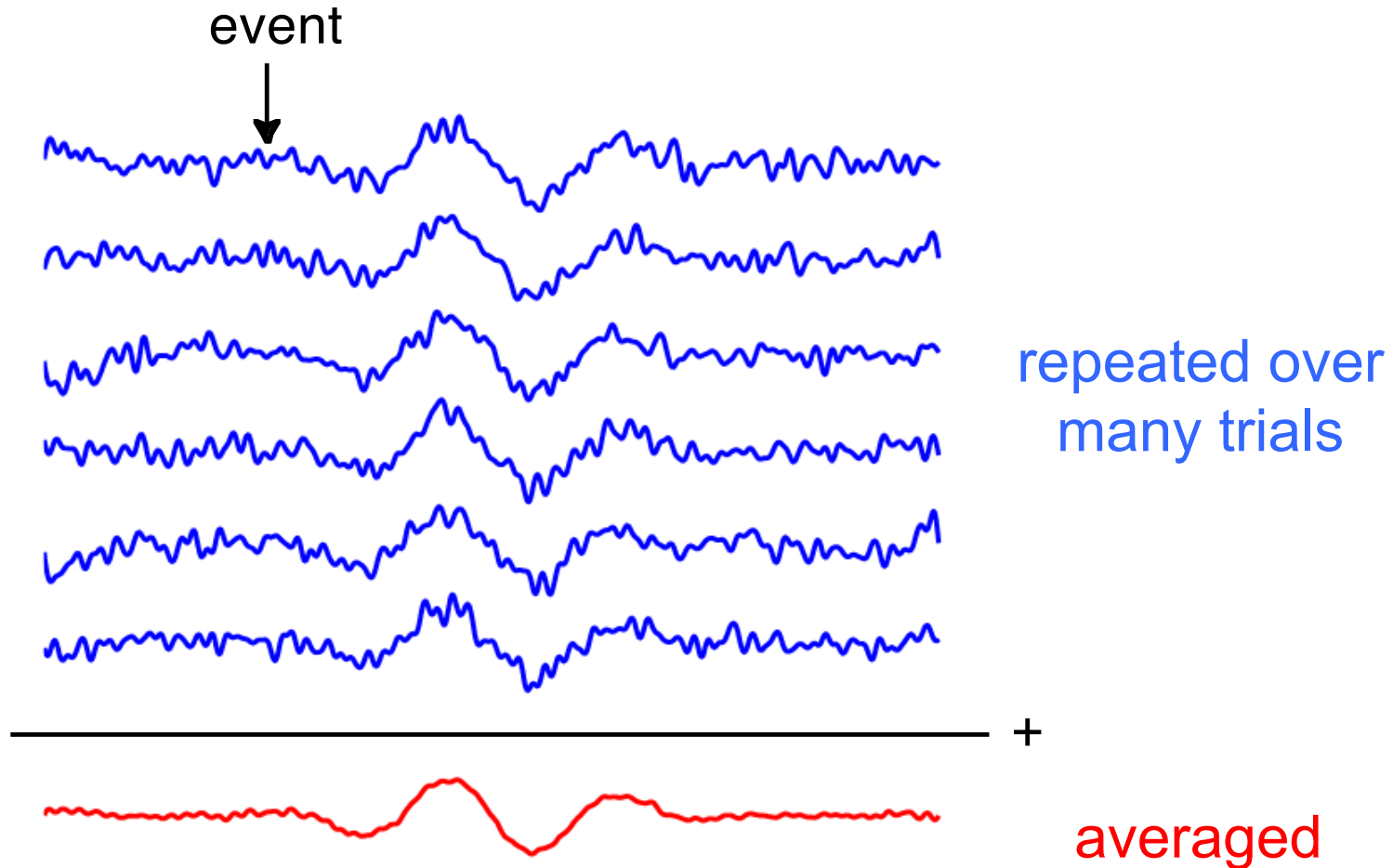
spatial distribution of activity over the head

-> source reconstruction

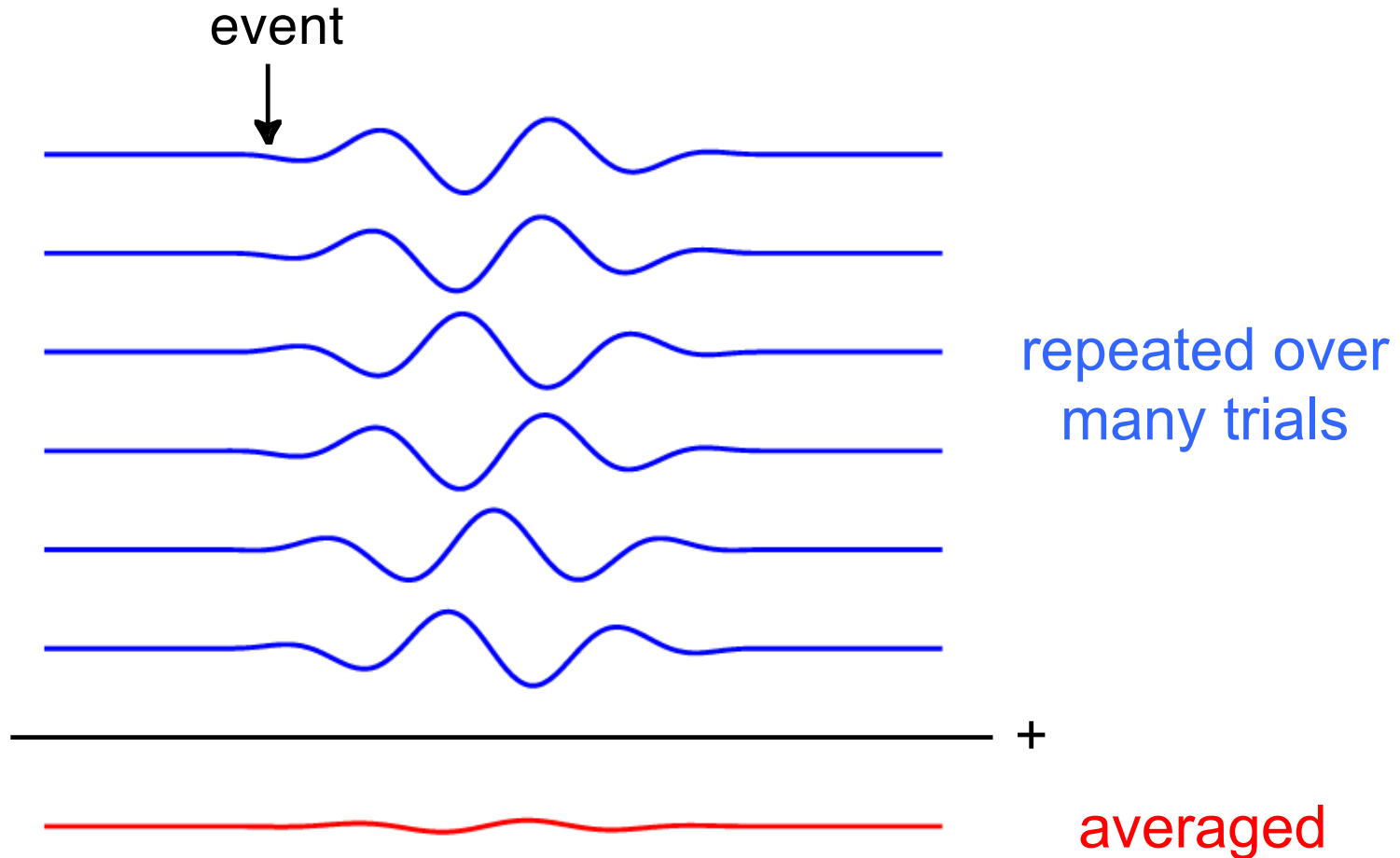
Evoked activity



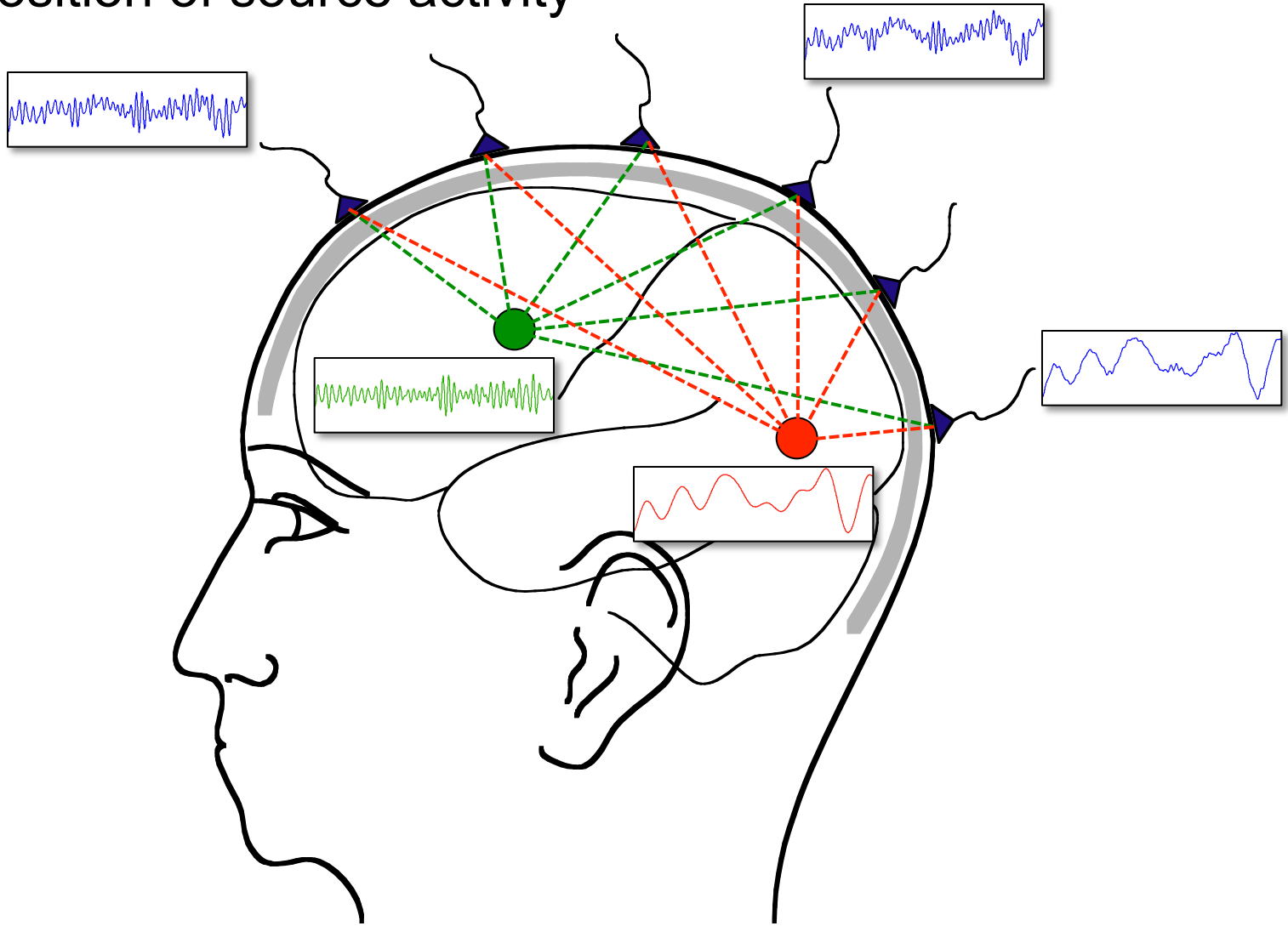
Evoked activity



Induced activity



Superposition of source activity



Separating activity of sources

Use the temporal aspects of the data
at the channel level

- ERF latencies

- ERF difference waves

- Filtering the time-series

- Spectral decomposition

Use the spatial aspects of the data

- Volume conduction model of head

- Estimate source model parameters

Talk outline

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Some FieldTrip basics

```
dataout = functionname(cfg, datain, ...)
```

```
functionname(  
dataout = func
```



the “cfg” argument is a configuration structure, e.g.

```
cfg.channel = {'C3', 'C4', 'F3', 'F4'}
```

```
cfg.foilim = [1 70]
```

FieldTrip v.s. default Matlab

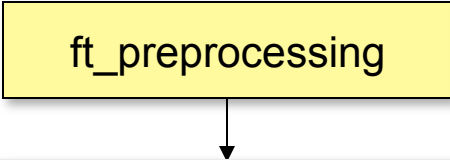
```
dataout = functionname(cfg, datain, ...)
```

```
    cfg.key1 = value1  
    cfg.key2 = value2
```

```
dataout = functionname(datain, 'key1', 'value1', ...)
```

Using functions in an analysis protocol

ft_preprocessing



FT_PREPROCESSING reads MEG and/or EEG data according to user-specified trials and applies several user-specified preprocessing steps to the signals.

Use as

```
[data] = ft_preprocessing(cfg)
```

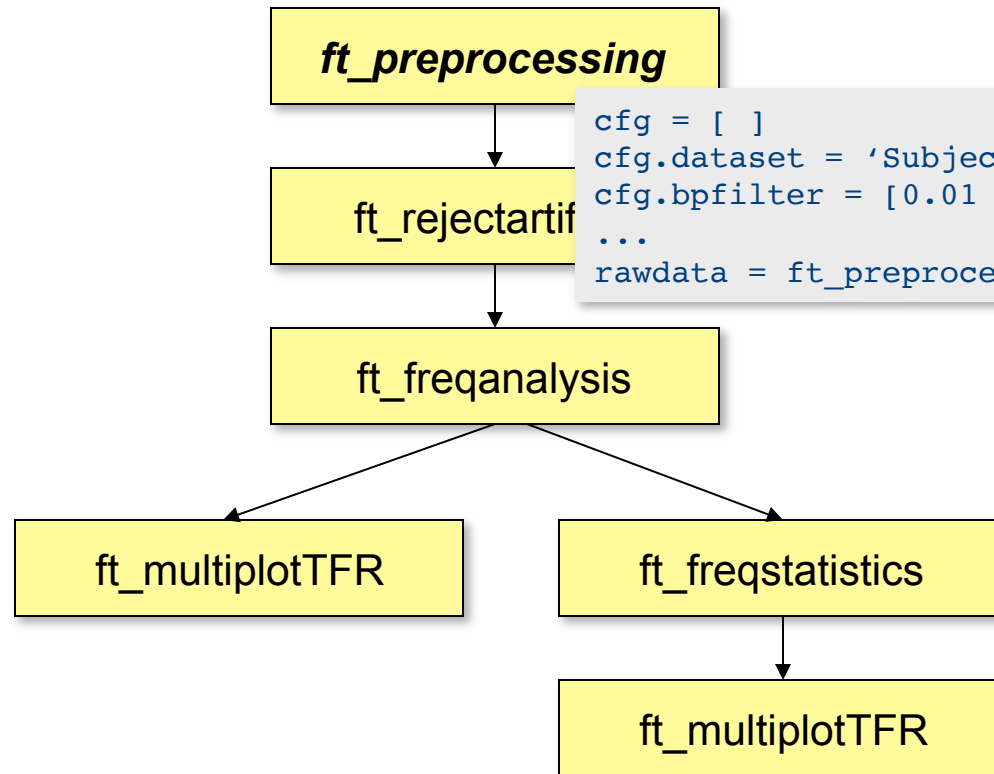
or

```
[data] = ft_preprocessing(cfg, data)
```

The first input argument "cfg" is the configuration structure, which contains all details for the dataset filenames, trials and the preprocessing options. You can only do preprocessing after defining the segments of data to be read from the file (i.e. the trials), which is for example done based on the occurrence of a trigger in the data.

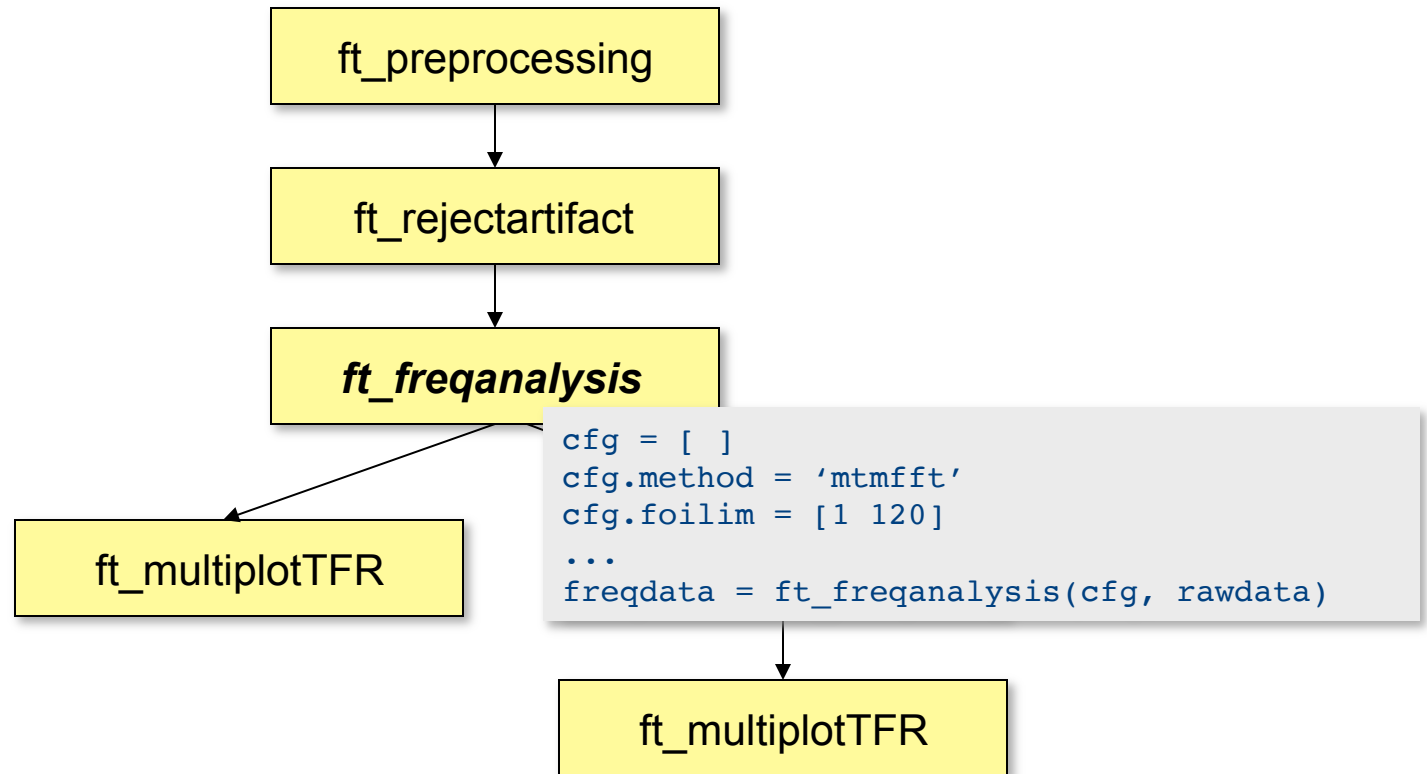
...

Using functions in an analysis protocol



```
cfg = [ ]  
cfg.dataset = 'Subject01.ds'  
cfg.bpfilter = [0.01 150]  
...  
rawdata = ft_preprocessing(cfg)
```

Using functions in an analysis protocol



Raw data structure

```
rawData =  
    label: {151x1 cell}  
    trial: {1x80 cell}  
    time: {1x80 cell}  
fsample: 300  
    hdr: [1x1 struct]  
    cfg: [1x1 struct]
```

Event related response

```
timelockData =  
    label: {151x1 cell}  
    avg: [151x900 double]  
    var: [151x900 double]  
    time: [1x900 double]  
dimord: 'chan_time'  
    cfg: [1x1 struct]
```

Keeping track of your analysis

FieldTrip analysis pipeline, Tue 12-Apr-2016 16:30:38

file:///Users/roboos/Desktop/ERF_Stat_Letter_FacevsLetter.html

FieldTrip analysis pipeline, Tue 12-Apr-2016 16:30:38

```
graph TD; P1[ft_preprocessing] --> A[ft_appenddata]; P2[ft_preprocessing] --> A; P3[ft_preprocessing] --> A; P4[ft_preprocessing] --> A; A --> R1[ft_rejectvisual]; R1 --> R2[ft_rejectvisual]; R2 --> R3[ft_redefintrial]; R3 --> R4[ft_rejectartifact]; R4 --> R5[ft_componentanalysis]; R5 --> R6[ft_rejectcomponent]; R6 --> R7[ft_preprocessing]; R7 --> R8[ft_timelockanalysis]; R7 --> R9[ft_timelockanalysis]; R8 --> R10[ft_timelockstatistics]; R9 --> R10;
```

ft_preprocessing

User-specified configuration

```
cfg.dataset = '/home/fanny/Desktop/MEG_Emo_all/practi...';
cfg.trialfun = 'ft_trialfun_general';
cfg.trialdef.eventtype = 'STI101';
cfg.trialdef.eventvalue = [30 31 10 130 131 110];
cfg.trialdef.prestim = 0.7;
cfg.trialdef.poststim = 1.2;
cfg.callinfo.usercfg.dataset = '/home/fanny/Desktop/MEG_Emo_all/practi...';
cfg.callinfo.usercfg.trialf... = 'ft_trialfun_general';
cfg.callinfo.usercfg.triald... = 'STI101';
cfg.callinfo.usercfg.triald... = [30 31 10 130 131 110];
cfg.callinfo.usercfg.triald... = 0.7;
cfg.callinfo.usercfg.triald... = 1.2;
cfg.callinfo.usercfg.trackc... = 'off';
cfg.callinfo.usercfg.checkc... = 'loose';
cfg.callinfo.usercfg.checks... = 100000;
cfg.callinfo.usercfg.showca... = 'yes';
cfg.callinfo.usercfg.debug = 'no';
cfg.callinfo.usercfg.output... = 'overwrite';
cfg.callinfo.usercfg.trackc... = 'yes';
cfg.callinfo.usercfg.trackd... = 'no';
```

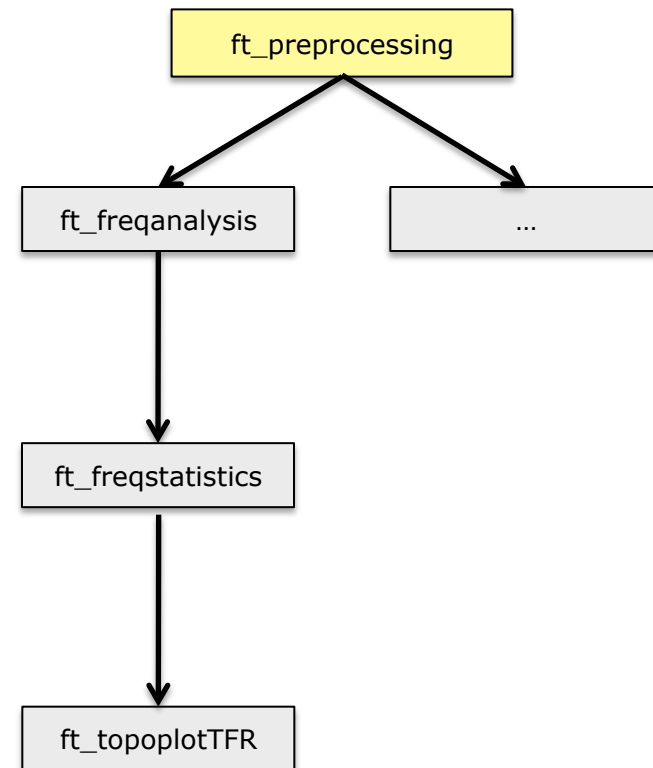
Pipeline HTML generated by roboos on Tue 12-Apr-2016 16:30:38.
Estimated total pipeline processing time: 17.1 minutes.

Example use in scripts

```
cfg = []  
cfg.dataset = 'Subject01.ds'  
cfg.bpfiler = [0.01 150]  
...  
rawdata = ft_preprocessing(cfg)
```

```
cfg = []  
cfg.method = 'mtmfft'  
cfg.foylim = [1 120]  
...  
freqdata = ft_freqanalysis(cfg, rawdata)
```

```
cfg = []  
cfg.method = 'montecarlo'  
cfg.statistic = 'indepsamplesT'  
cfg.design = [1 2 1 2 2 1 2 1 1 2 ... ]  
...  
freqstat = ft_freqstatistics(cfg, freqdata)
```

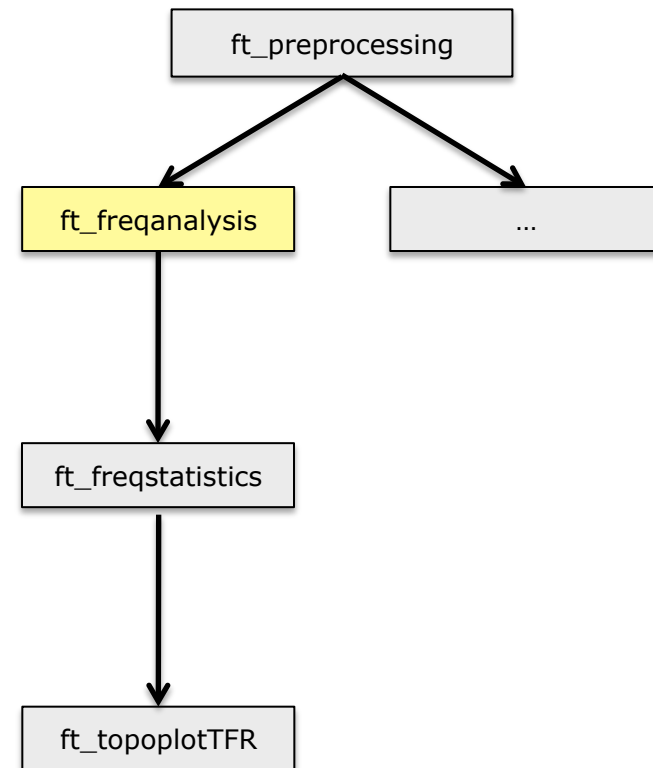


Example use in scripts

```
cfg = []  
cfg.dataset = 'Subject01.ds'  
cfg.bpfiler = [0.01 150]  
...  
rawdata = ft_preprocessing(cfg)
```

```
cfg = []  
cfg.method = 'mtmfft'  
cfg.foylim = [1 120]  
...  
freqdata = ft_freqanalysis(cfg, rawdata)
```

```
cfg = []  
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cfg.statistic = 'indepsamplesT'  
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freqstat = ft_freqstatistics(cfg, freqdata)
```

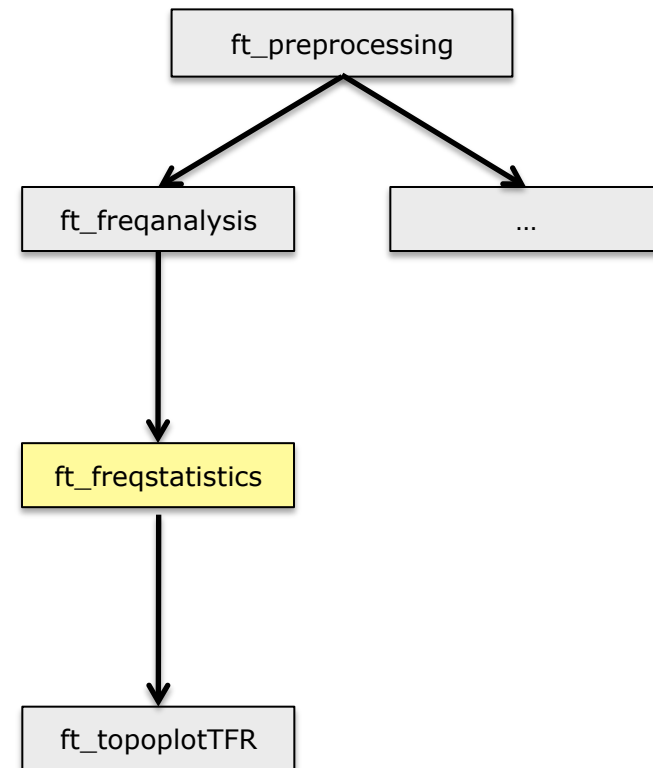


Example use in scripts

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cfg = []  
cfg.dataset = 'Subject01.ds'  
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...  
rawdata = ft_preprocessing(cfg)
```

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cfg = []  
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...  
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```

```
cfg = []  
cfg.method = 'montecarlo'  
cfg.statistic = 'indepsamplesT'  
cfg.design = [1 2 1 2 2 1 2 1 1 2 ... ]  
...  
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```

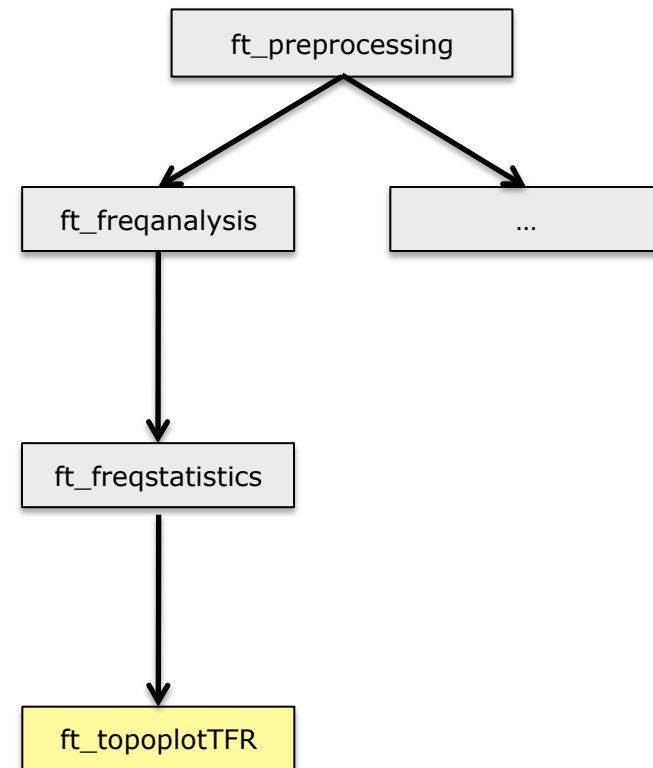


Example use in scripts

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cfg = []  
cfg.dataset = 'Subject01.ds'  
cfg.bpfiler = [0.01 150]  
...  
rawdata = ft_preprocessing(cfg)
```

```
cfg = []  
cfg.method = 'mtmfft'  
cfg.foylim = [1 120]  
...  
freqdata = ft_freqanalysis(cfg, rawdata)
```

```
cfg = []  
cfg.method = 'montecarlo'  
cfg.statistic = 'indepsamplesT'  
cfg.design = [1 2 1 2 2 1 2 1 1 2 ... ]  
...  
freqstat = ft_freqstatistics(cfg, freqdata)
```

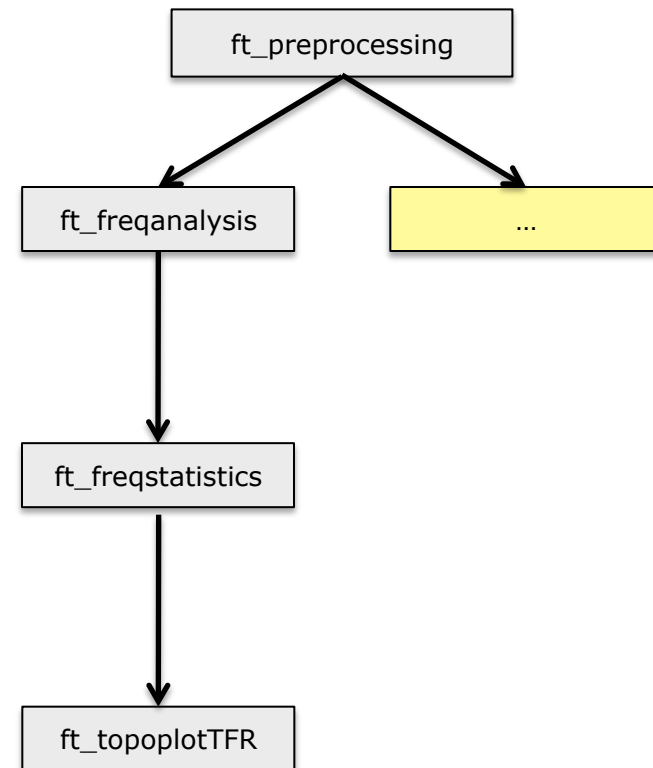


Example use in scripts

```
cfg = []  
cfg.dataset = 'Subject01.ds'  
cfg.bpfiler = [0.01 150]  
...  
rawdata = ft_preprocessing(cfg)
```

```
cfg = []  
cfg.method = 'mtmfft'  
cfg.foylim = [1 120]  
...  
freqdata = ft_freqanalysis(cfg, rawdata)
```

```
cfg = []  
cfg.method = 'montecarlo'  
cfg.statistic = 'indepsamplesT'  
cfg.design = [1 2 1 2 2 1 2 1 1 2 ... ]  
...  
freqstat = ft_freqstatistics(cfg, freqdata)
```



Example use in scripts

```
subj = {'S01.ds', 'S02.ds', ...}
trig = [1 3 7 9]

for s=1:nsubj
for c=1:ncond

    cfg = []
    cfg.dataset = subj{s}
    cfg.trigger = trig(c)
    rawdata{s,c} = ft_preprocessing(cfg)

    cfg = []
    cfg.method = 'mtmfft'
    cfg.foilim = [1 120]
    freqdata{s,c} = ft_freqanalysis(cfg, rawdata{s,c})

end
end
```

Example use in scripts

```
subj = {'S01.ds', 'S02.ds', ...}
trig = [1 3 7 9]

for s=1:nsubj
for c=1:ncond

    cfg = []
    cfg.dataset = subj{s}
    cfg.trigger = trig(c)
    rawdata = ft_preprocessing(cfg)

    filename = sprintf('raw%s_%d.mat', subj{s}, trig(c));
    save(filename, 'rawdata')

end
end
```

Example use in distributed computing

```
subj = {'S01.ds', 'S02.ds', ...}
trig = [1 3 7 9]

for s=1:nsubj
for c=1:ncond

    cfgA{s,c} = []
    cfgA{s,c}.dataset      = subj{s}
    cfgA{s,c}.trigger      = trig(c)
    cfgA{s,c}.outputfile  = sprintf('raw%s_%d.mat', subj{s}, trig(c))

    cfgB{s,c} = []
    cfgB{s,c}.dataset      = subj{s}
    cfgB{s,c}.trigger      = trig(c)
    cfgB{s,c}.inputfile    = sprintf('raw%s_%d.mat', subj{s}, trig(c));
    cfgB{s,c}.outputfile  = sprintf('freq%s_%d.mat', subj{s}, trig(c));

end
end

dfeval(@ft_preprocessing, cfgA)
dfeval(@ft_freqanalysis,  cfgB)
```

Example use in distributed computing

```
subj = {'S01.ds', 'S02.ds', ...}
trig = [1 3 7 9]

for s=1:nsubj
for c=1:ncond

    cfgA{s,c} = []
    cfgA{s,c}.dataset      = subj{s}
    cfgA{s,c}.trigger      = trig(c)
    cfgA{s,c}.outputfile  = sprintf('raw%s_%d.mat', subj{s}, trig(c))

    cfgB{s,c} = []
    cfgB{s,c}.dataset      = subj{s}
    cfgB{s,c}.trigger      = trig(c)
    cfgB{s,c}.inputfile    = sprintf('raw%s_%d.mat', subj{s}, trig(c));
    cfgB{s,c}.outputfile  = sprintf('freq%s_%d.mat', subj{s}, trig(c));

end
end

qsubcellfun(@ft_preprocessing, cfgA)
qsubcellfun(@ft_freqanalysis,  cfgB)
```

FieldTrip is a toolbox

the data and the separate functions are in
your hands

the scripts depend on the data properties,
your computer and on your programming
skills and style

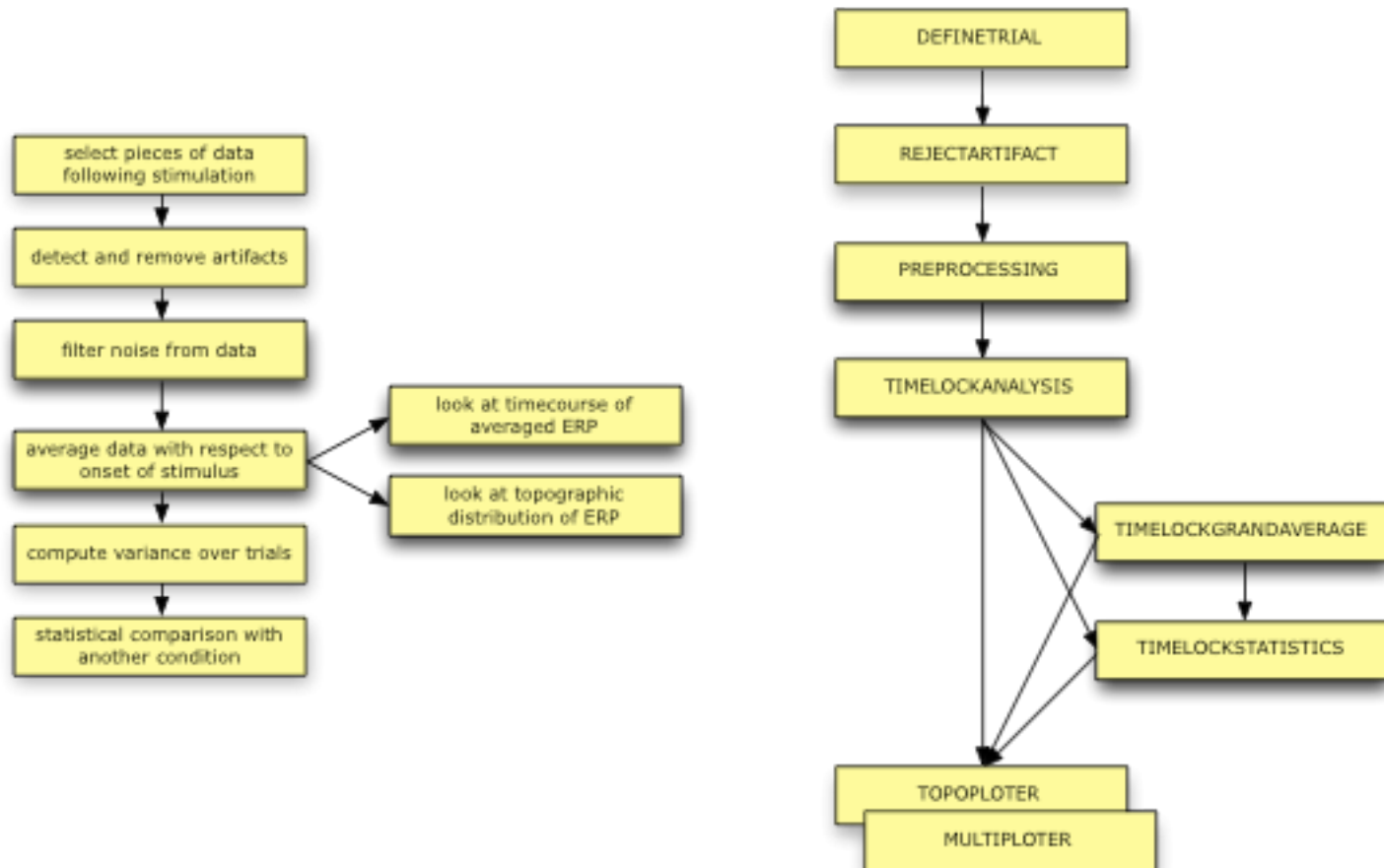
scripts correspond to analysis protocols

- scripts can be reviewed by supervisors

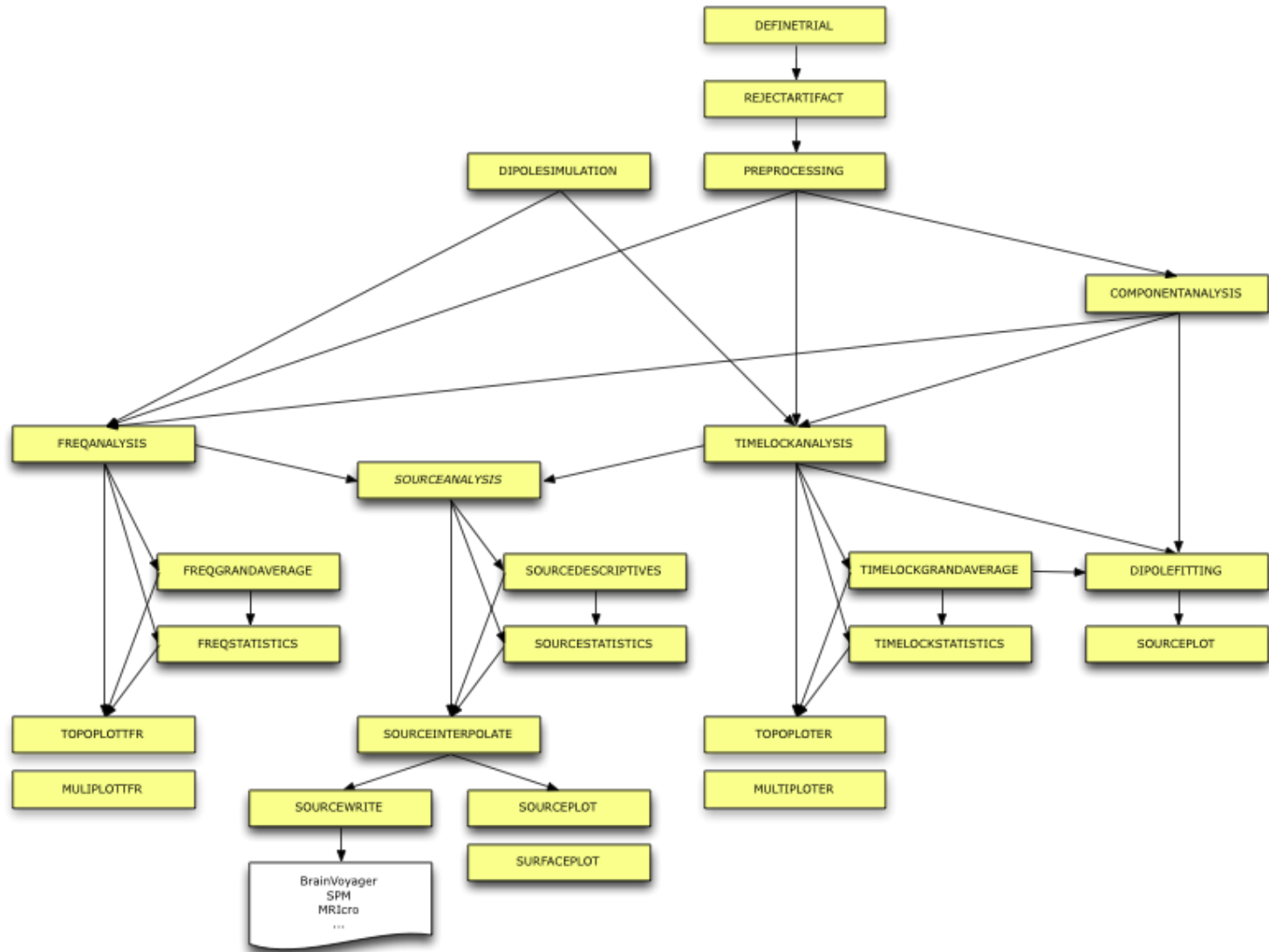
- scripts are often shared with colleagues

- scripts can be published/released

One-to-one mapping between analysis steps and toolbox functions



Overview of main functions



Finding your way around in the FieldTrip toolbox

Matlab

help functionname

edit functionname

Website

<http://www.fieldtriptoolbox.org>

Email discussion list

Expertise in your local group

Talk outline

What kind of signals are generated in the brain

How do we record those signals

Analyzing those signals with FieldTrip

Background on the FieldTrip toolbox

Who is the audience?

experimental neuroscientists

no graphical user interface

more dedicated and ambitious researchers

developers of other software packages

SPM

EEGLAB

BESA

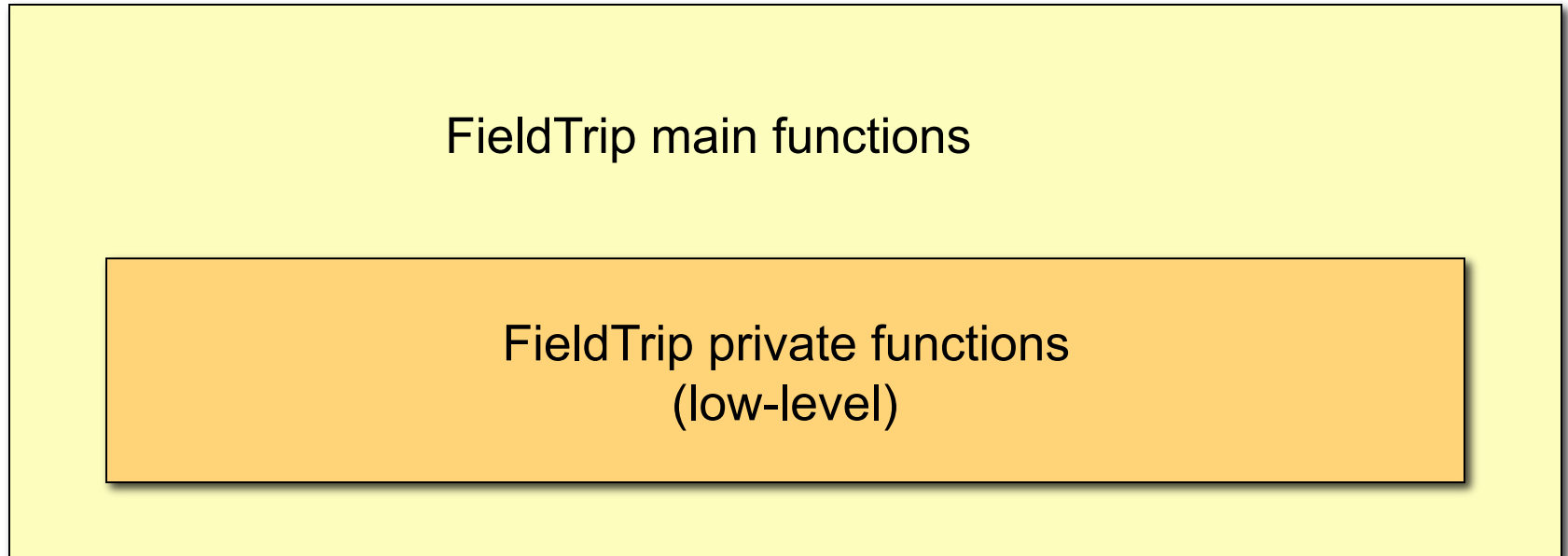
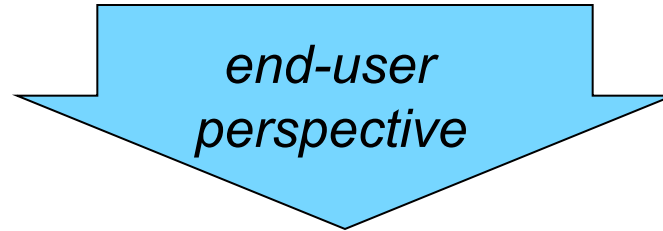
BCI2000

developers of analysis tools and methods

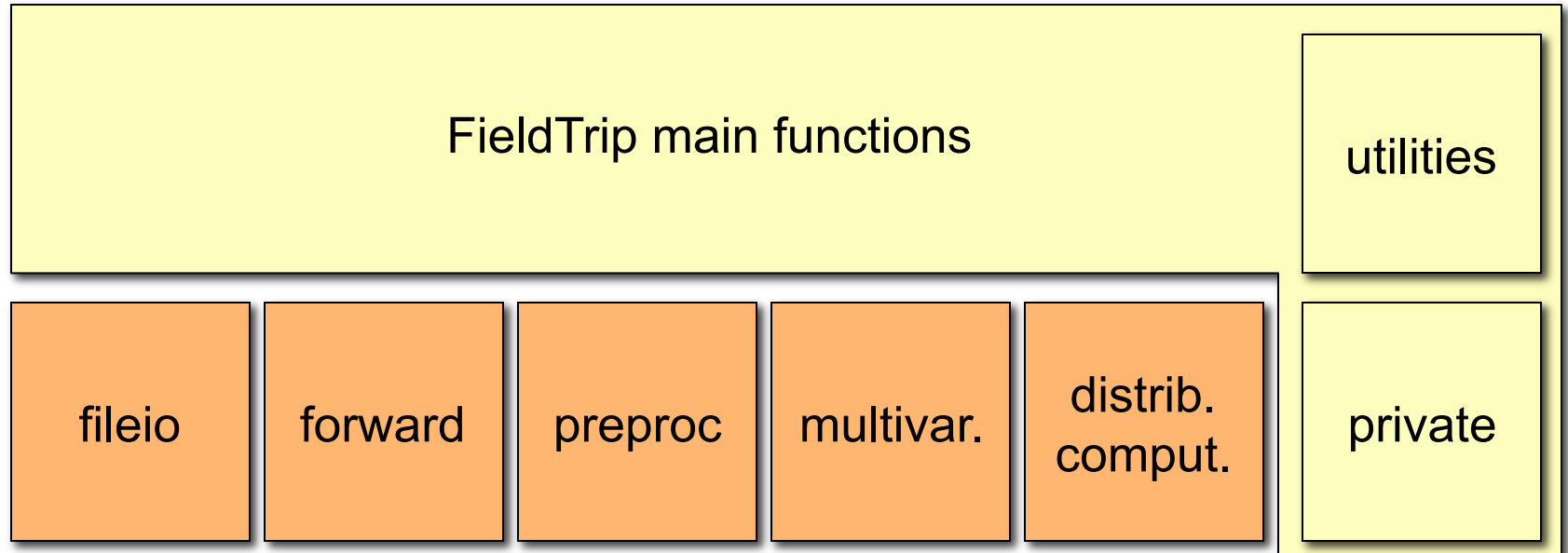
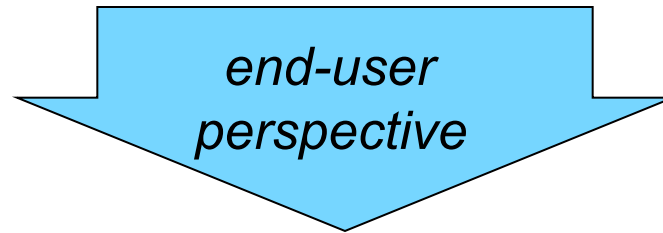
SIMBIO

OpenMEEG

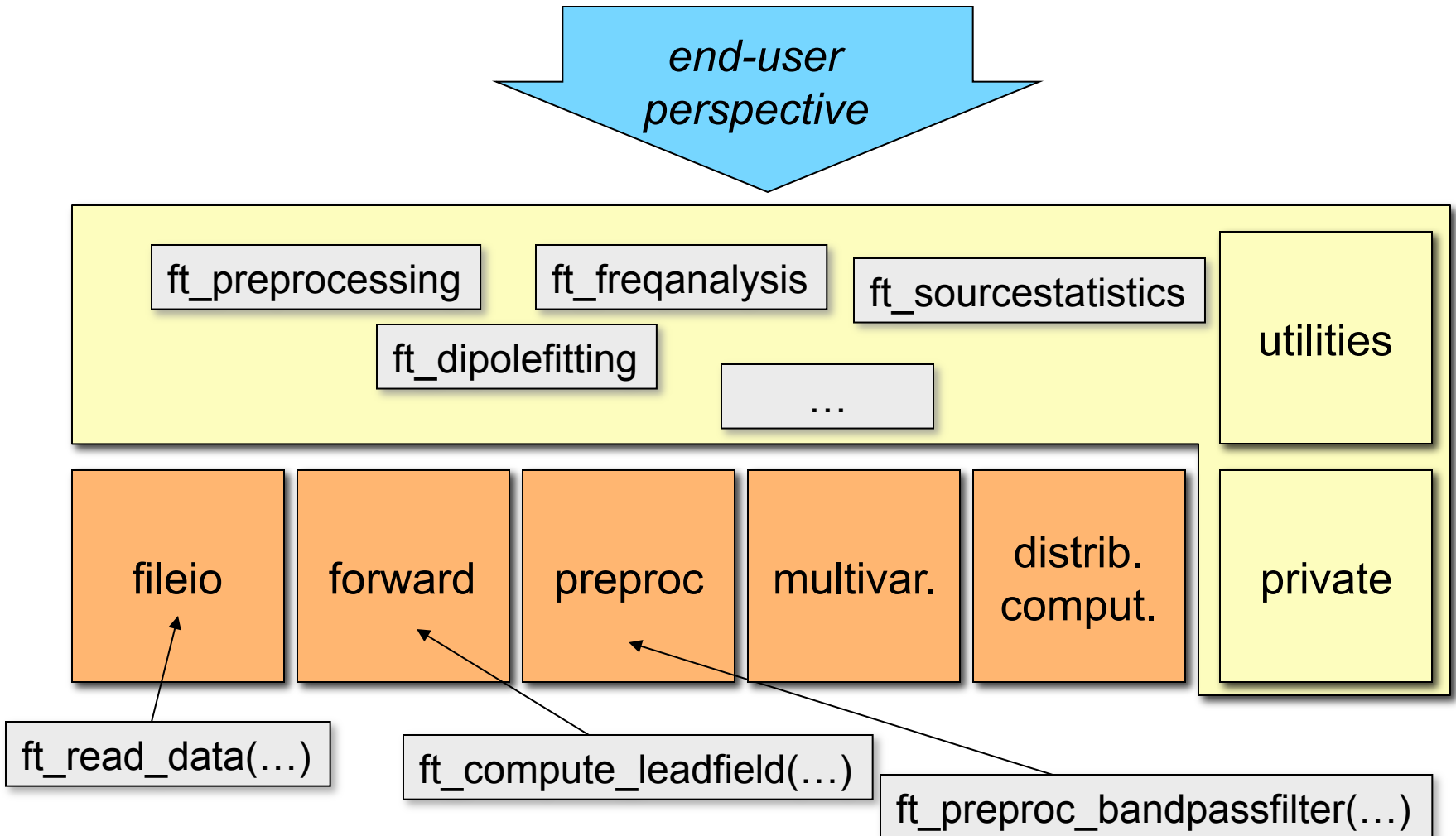
FieldTrip toolbox structure - at a glance



FieldTrip toolbox structure - a closer look



FieldTrip toolbox structure - a closer look



Summary

What kind of signals are generated in the brain

How do we record those signals

Analyzing those signals with FieldTrip

Background on the FieldTrip project

hands-on

Selecting segments of data

Reading and preprocessing

Averaging

Plotting

