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Quality control for the FDG-PET studies in patients with disorders of consciousness

CSG PET workshop

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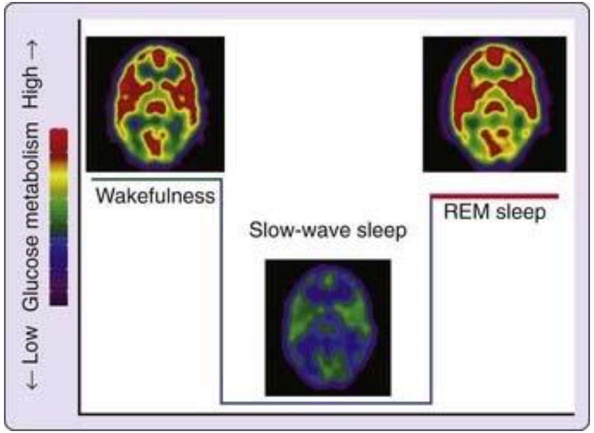
Data quality checks - PET acquisition

- Confounding factors
  - Blood sugar / Glycemia
    - +- 100 mg/dL, below 120 mg/dL
  - Arousal
    - Patient should be awake
  - Least possible stimulation during glucose uptake
    - Lights off, no stimulation unless sleeping

    → Should be assured by following a proper acquisition protocol!
  - Neural inflammation might bias glucose uptake



Adapted from Maquet P, et al. Brain Res 1990.

Boellaard et al., 2009

Data quality checks – PET data analysis

- Data segmentation
  - Isolate cortical grey matter activity from white matter and CSF signal to enhance the detection of metabolic abnormalities
  - Segmentation defines the boundaries of the GLM
- Data normalization
  - Spatial mapping of individual brains to a standard MNI space to enable accurate comparisons of metabolic activity
  - Normalization ensures the data represents the same the anatomical structure

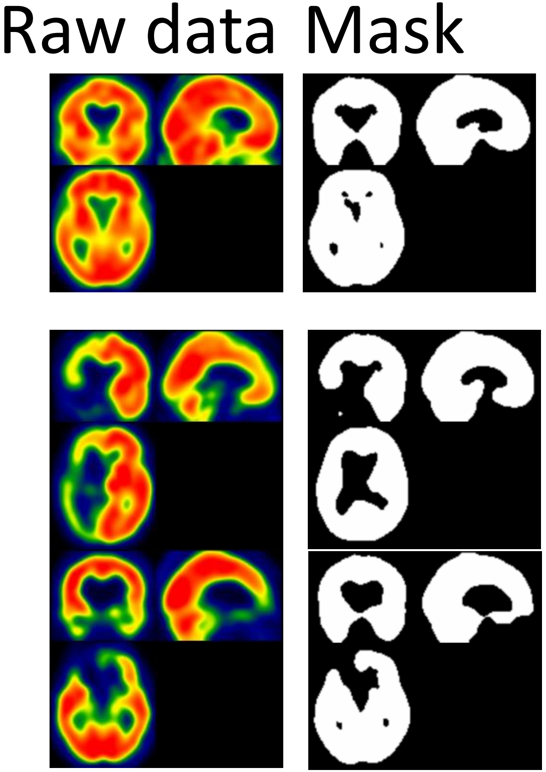
→ Challenge: Low-density structures and atrophy can lead to misinterpretation

→ Solution: careful preprocessing to reduce high variance

Data quality checks – FDG-PET segmentation

single subject

- Healthy Control group
  - Larger is better (>20 subjects)
  - On the same scanner
- The single patient
  - Bad segmentation could bias SPM maps
    - Keep in mind: Will underestimate hypometabolic areas
    - For single subject analysis it is sometimes unavoidable

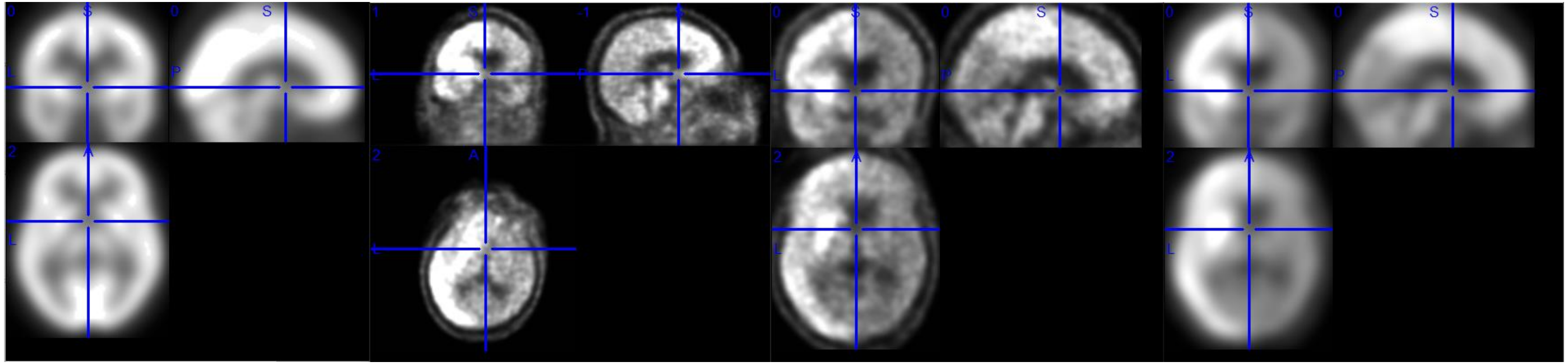


Data quality checks – FDG-PET segmentation

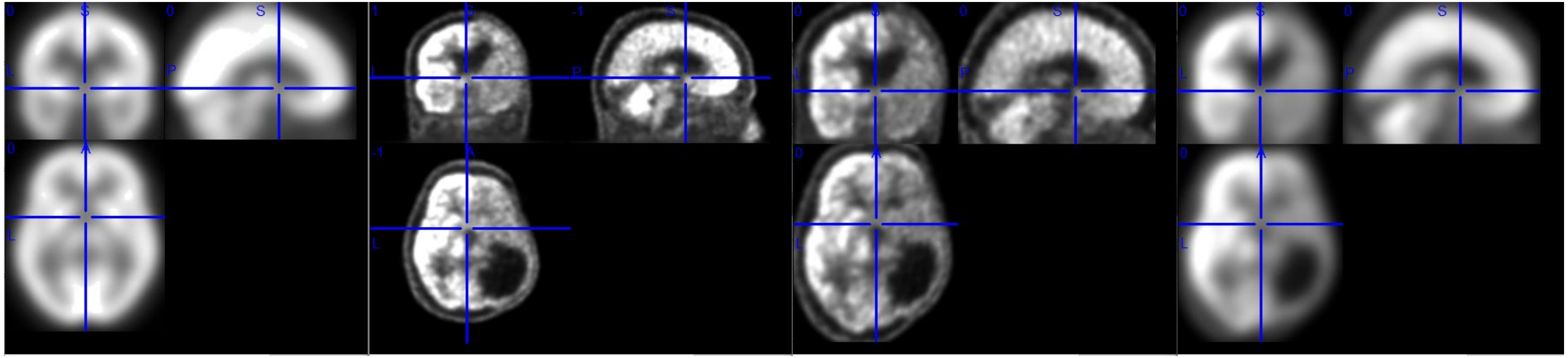
Group analysis

- Healthy Controls: same pipeline as single-subject analysis
- Group of DoC patients: mask quality evaluated individually
  - Subjects with poor segmentation should be excluded, as mask defects can create holes in the grey matter mask and lead to missing statistical tests in affected regions
  - Apparent “non-significant” areas may otherwise reflect absence of analysis rather than true null effects

Data quality checks - Evaluate normalization of **single subjects**


Template
PET Image (native space)
Normalized PET image (w)
Smoothed PET image (sw)

✓


Template
PET Image (native space)
Normalized PET image (w)
Smoothed PET image (sw)

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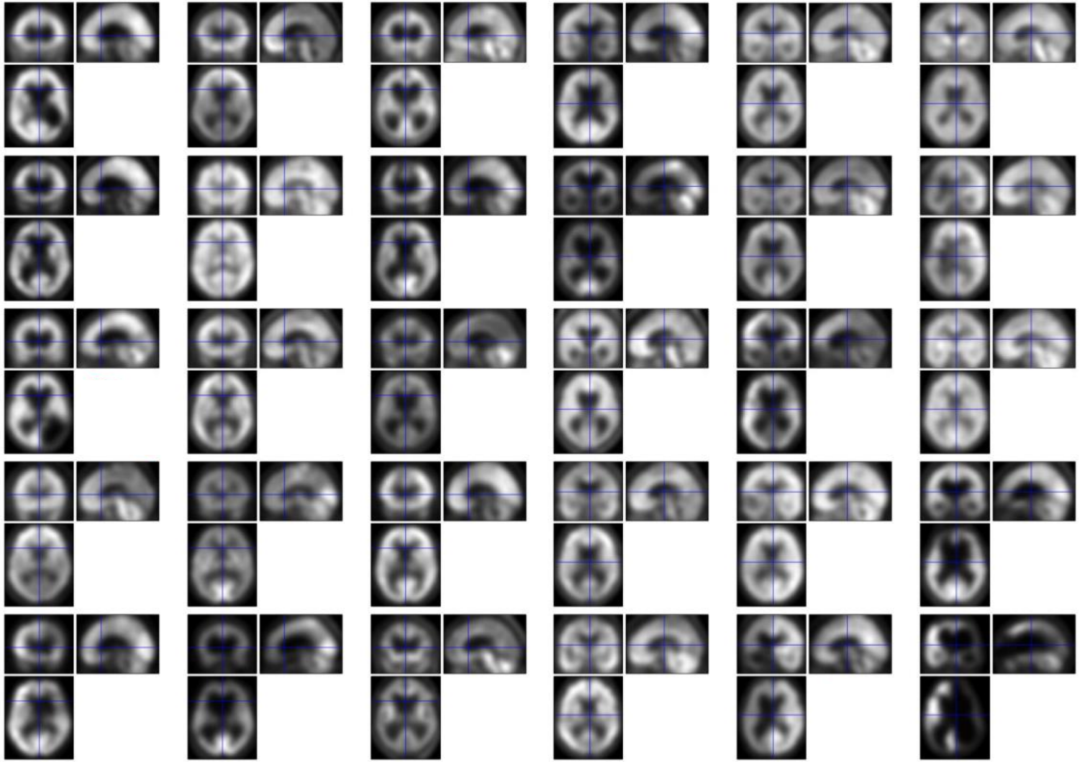
Data quality checks - Normalization in a **group analysis**



Check your statistical model **for group analysis**

- If your Mask and Normalization looks good, check the statistical model!

- Check statistical fit by the RPV image → independent "resolution element"
    - Should be smooth in brain tissue, except in some specific places, e.g. ventricles or brainstem

- Keep in mind: Lesion/heterogeneous images negatively affect the GLM, as the model may not be fitting there
    - Leads to → high false-positive rates, low statistical power, and non-reproducible results

- Consult experienced SPM user or developer for help.
    - Big thanks to Prof. Christophe Phillips & Dr. Mohamed Ali Bahri!

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Thank you for your attention.

Questions?

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