

From Group to Patient-Specific Analysis of Brain Function in Arterial Spin Labelling and BOLD Functional MRI

Camille Maumet

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> Camille Maumet PhD Defense, May 29th, 2013

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Director: Christian Barillot, Co-director: Pierre Maurel



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Brain function

Two views of brain function:



[Raichle 2010]

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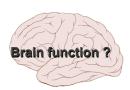
Task-evoked activity







Activation



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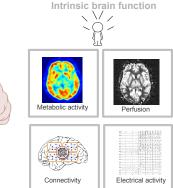
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Activation





[Raichle 2010]

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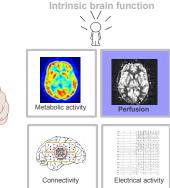
Task-evoked activity





Activation





[Raichle 2010]

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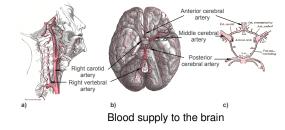
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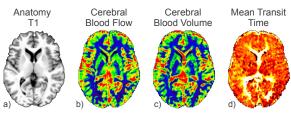
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Brain perfusion



Brain perfusion is the biological process that ensures the delivery of oxygen and nutrients to the cerebral tissues by means of microcirculation.



Example of perfusion parameters

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Labelling

[Detre et al., MRM 1992]

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Readout

[Detre et al., MRM 1992]

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[Detre et al., MRM 1992]

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[Detre et al., MRM 1992]

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Difference 1 pair

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Difference 1 pair



Difference 60 pairs

[Detre et al., MRM 1992]

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Group analyses: definition (1/2)



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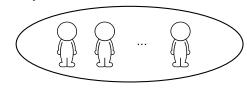
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Group analyses: definition (1/2)

Within-group analyses identify common patterns across a group of subjects.



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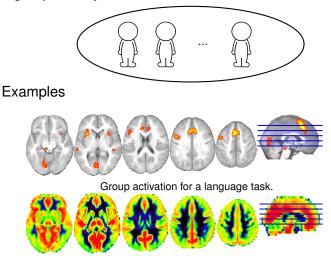
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Group analyses: definition (1/2)

Within-group analyses identify common patterns across a group of subjects.



Group cerebral blood flow.

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Group analyses: definition (2/2)





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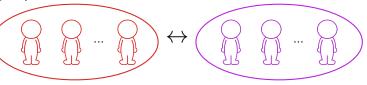
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Group analyses: definition (2/2)

Between-group analyses identify differences at the group level.



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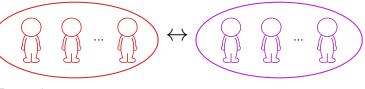
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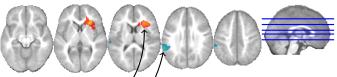
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Group analyses: definition (2/2)

Between-group analyses identify differences at the group level.



Example



Differences of activation between a group of children diagnosed with specific language impairment and a control group during a language task.

- Hyperactivation. /
- Hypoactivation.

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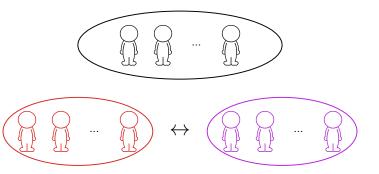
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Group analyses



Neuroimaging group analyses

- focus on the general patterns of brain function observed in the typical or pathological brain.
- are the most widespread type of statistical analysis.

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Patient-specific analyses: definition (1/2)



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Patient-specific analyses: definition (1/2) Patient-specific analyses identify patterns of brain function in a single subject.

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Patient-specific analyses: definition (1/2) Patient-specific analyses identify patterns of brain

function in a single subject.



Examples



Subject activation for a language task.

Cerebral blood flow.

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Patient-specific analyses: definition (2/2)





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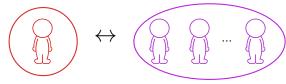
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Patient-specific analyses: definition (2/2)

Patient-specific analyses can also identify deviation from normality in a single subject.



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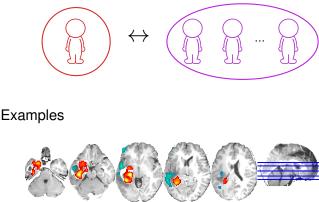
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Patient-specific analyses: definition (2/2)

Patient-specific analyses can also identify deviation from normality in a single subject.



Hyper- and hypo-perfusions in a patient diagnosed with brain tumour.

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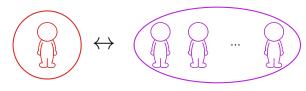
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Patient-specific analyses





Neuroimaging patient-specific analyses

- focus on the specific patterns of brain function observed in a single brain.
- perform based either on a single subject dataset or on a subject and a group of controls.

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Contributions: overview

	Group analysis	Patient-specific analysis
Within		
Between	88-8 + 88 - 8	$(8) \leftrightarrow (8, 8, -, 8)$
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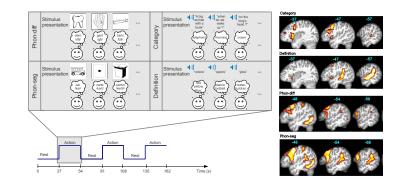
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Contributions: overview

	Group analysis	Patient-specific analysis
Within		
Between		

A panel of 4 fMRI tasks for language mapping in children.



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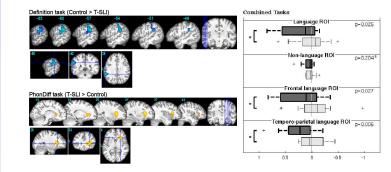
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Contributions: overview



Atypical activity and lateralisation of brain function in children diagnosed with typical specific language impairment.



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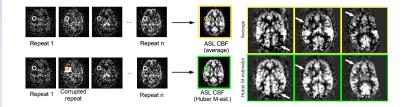
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	Group analysis	Patient-specific analysis
Within		
Between		

Robust Estimation of the Cerebral Blood Flow in Arterial Spin Labelling.



Conclusions and future work

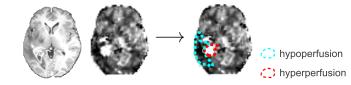
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Contributions: overview

	Group analysis	Patient-specific analysis
Within		
Between		

Objective: Quantitative identification of voxelwise patientspecific perfusion abnormalities.



From group to patient-specific analyses

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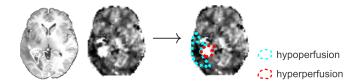
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Materials

25 patients diagnosed with brain tumours and 61 control subjects participated in this study.

Imaging protocol:

- PICORE Q2TIPS Pulsed ASL, 60 repetitions
- MPRAGE T1 3D
- T2 FLAIR

For the patients only:

- T1 3D Gadolinium
- Dynamic Susceptibility Contrast imaging (DSC)

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Validation: Ground Truth

1. Segmentation of the tumour:





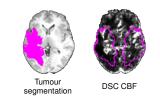
T1 Gadolinium

T2 FLAIR



Tumour and oedema segmentation

2. Combination with T2 perfusion information:





"Ground truth"

3. Visual assessment and manual corrections by a clinician.

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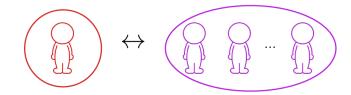
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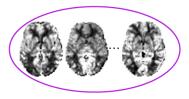
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Massively univariate approaches:

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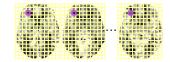
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Massively univariate approaches:





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Massively univariate approaches:



- The standard approach, e.g. [Holmes 1998, Beckmann 2003].
- Computationally efficient.
- No integration of information cross-voxels (pre-smoothing).

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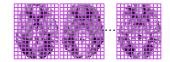
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Multivariate approaches:

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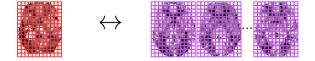
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Multivariate approaches:



- ✓ Combination of voxel information (no smoothing).
- Require specific methods: machine learning, e.g. [Mourão Miranda 2011].
- × Can be time consuming and computationally intensive.

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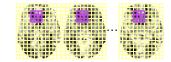
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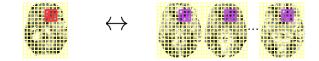
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- ✓ Combination of local voxel information (no smoothing), e.g. [Kriegeskorte 2006].
- ✓ Standard statistics or machine learning.
- Less time consuming than full brain.
- × Can still be time consuming (machine learning).
- × Only local information is combined.

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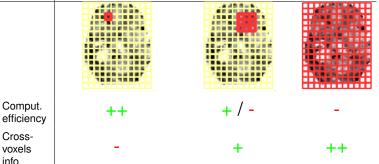
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Univariate / Multivariate - overview

Massively univariate Locally multivariate Multivariate



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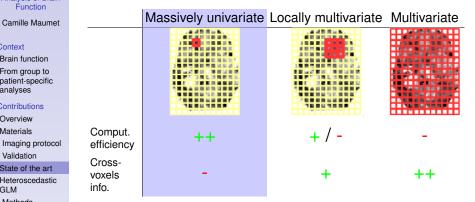
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1. The massively univariate GLM: homoscedastic and heteroscedastic models.

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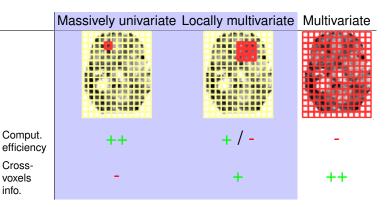
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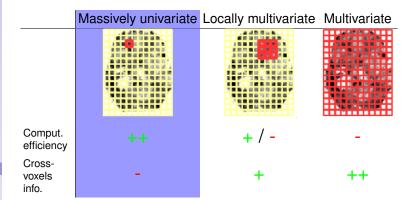
Univariate / Multivariate - overview



1. The massively univariate GLM: homoscedastic and heteroscedastic models.

2. The *a contrario* approach as a new locally multivariate procedure.

Univariate / Multivariate - overview



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- 1. The massively univariate GLM: homoscedastic and heteroscedastic models.
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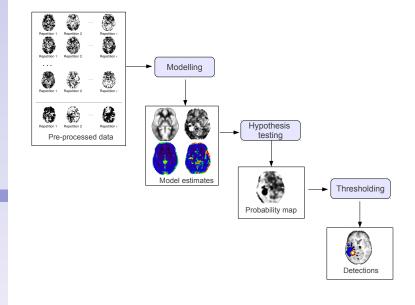
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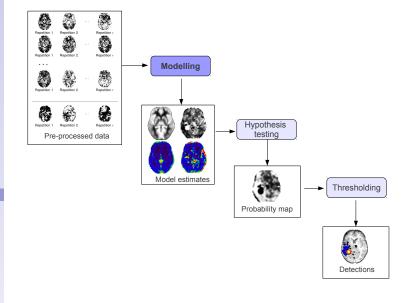
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Modelling: subject level

General Linear Model: subject level







Repetition 1

Repetition 2

Repetition r

Modelling: subject level

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Perfusion estimate in subject 1: $\hat{\beta}_1$

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Repetition 1



Repetition 1

Control Group



Repetition 1

Repetition 2

Repetition 2

Repetition 2



Repetition r



Repetition r



 $\begin{array}{c} \text{Perfusion} \\ \text{estimate in} \\ \text{subject 1: } \hat{\beta}_1 \end{array}$



 $\hat{\beta}_2$

 $\xrightarrow{}$ Repetition r



Modelling: subject level

General Linear Model: subject level

Repetition 2

Repetition 2

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Repetition 1



Repetition 1

Control Group

Patient





Repetition 1



 $\tilde{\mathbf{x}}_{\mathbf{f}}$



Repetition r

Repetition r

Repetition r



Perfusion estimate in subject 1: $\hat{\beta}_1$



 $\hat{\beta}_2$

 $\hat{\beta}_{n-1}$



Repetition 1





Repetition r



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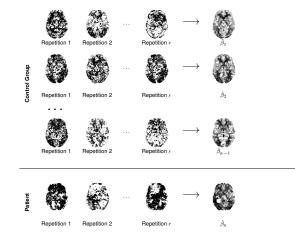
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Modelling: group level

General Linear Model: group level.



Two sources of variation: the **between-subject** variance and the **within-subject** variance.

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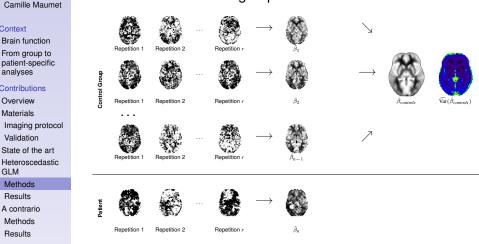
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General Linear Model: group level.



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Two sources of variation: the **between-subject** variance and the within-subject variance.

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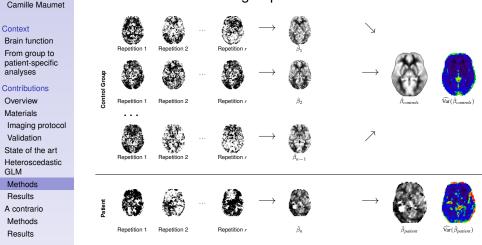
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General Linear Model: group level.



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Two sources of variation: the **between-subject** variance and the within-subject variance.

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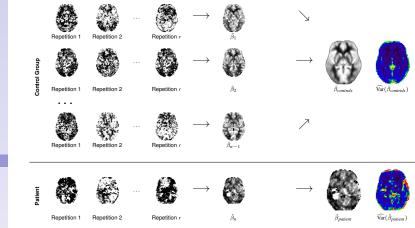
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General Linear Model: group level. The **homoscedastic model**:



Two sources of variation: the **between-subject** variance and the **within-subject** variance.

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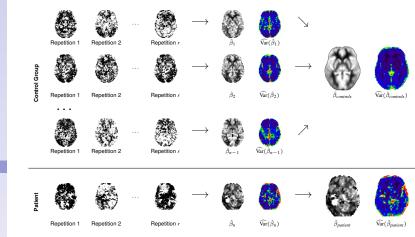
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Modelling: group level

General Linear Model: group level. The **heteroscedastic model**:



Two sources of variation: the **between-subject** variance and the **within-subject** variance.

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Homoscedastic and heteroscedastic GLM

The **homoscedastic model assumes** that the **within-subject variance** is:

- negligible by comparison to the between-subject variance; or
- roughly constant across subjects.

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Homoscedastic and heteroscedastic GLM

In functional MRI there is no consensus:

- Superiority of the heteroscedastic model, [Beckmann 2003, Mumford 2006, Thirion 2007].
- Validity of the homoscedastic model for one-sample t-tests in BOLD fMRI, [Mumford 2009].
- Invalidity of the homoscedastic model [Chen 2012].

Both approaches are in use in the neuroimaging community:

- The homoscedastic approach (SPM¹)
- ► The heteroscedastic approach (FSL², AFNI³).

¹www.fil.ion.ucl.ac.uk/spm/ ²fsl.fmrib.ox.ac.uk/fsl/fslwiki/

³afni.nimh.nih.gov/afni/

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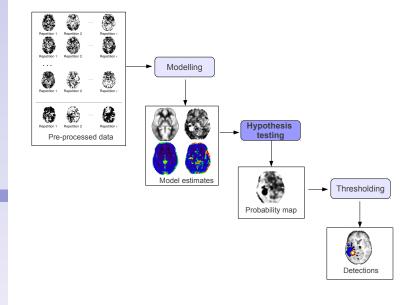
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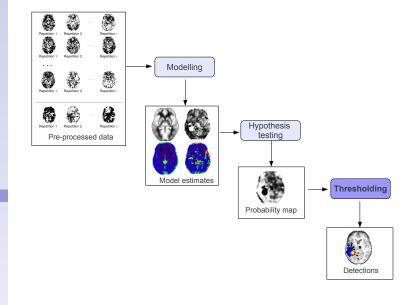
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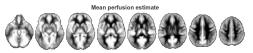
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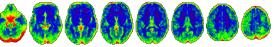
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Results: Perfusion in the control group Mean estimate

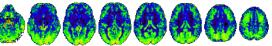


Standard deviation estimates

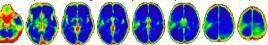
Combined within- and between-subject standard deviation (homoscedastic model)



Between-subject standard deviation (heteroscedastic model)



Root-square of the average within-subject variance (heteroscedastic model)



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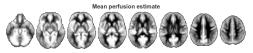
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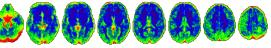
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Results: Perfusion in the control group Mean estimate



Standard deviation estimates

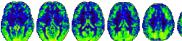
Combined within- and between-subject standard deviation (homoscedastic model)



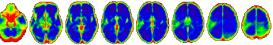
Between-subject standard deviation (heteroscedastic model)







Root-square of the average within-subject variance (heteroscedastic model)





Brain arteries



Brain veins

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Assumptions of the homoscedastic model

Assumption 1: Within-subject variance negligible by comparison to the between-subject variance.

 Assumption 2: Within-subject variance roughly constant across subjects.

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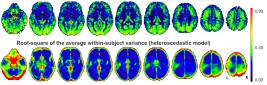
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Between-subject standard deviation (heteroscedastic model)



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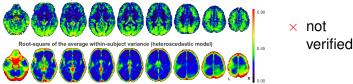
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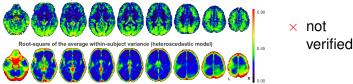
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Assumptions of the homoscedastic model

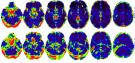
Assumption 1: Within-subject variance negligible by comparison to the between-subject variance.

Between-subject standard deviation (heteroscedastic model)



 Assumption 2: Within-subject variance roughly constant across subjects.

Within-subject standard deviation in two control subjects:



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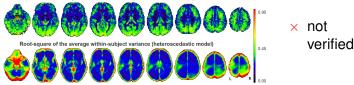
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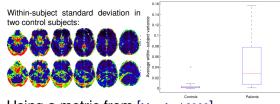
Assumptions of the homoscedastic model

Assumption 1: Within-subject variance negligible by comparison to the between-subject variance.

Between-subject standard deviation (heteroscedastic model)



 Assumption 2: Within-subject variance roughly constant across subjects.



Using a metric from [Mumford 2009].

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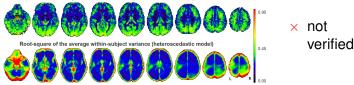
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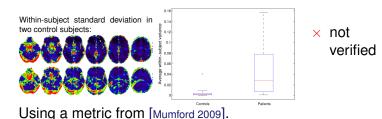
Assumptions of the homoscedastic model

Assumption 1: Within-subject variance negligible by comparison to the between-subject variance.

Between-subject standard deviation (heteroscedastic model)



 Assumption 2: Within-subject variance roughly constant across subjects.



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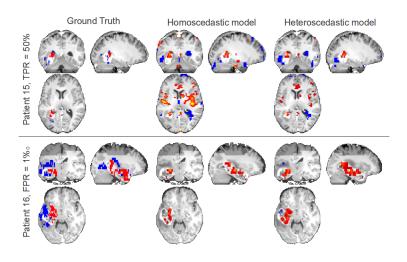
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Results: homoscedastic versus heteroscedastic GLM



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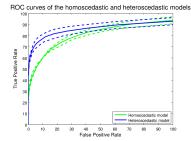
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ROC curves for perfusion abnormality detections.

	Homoscedastic model					
FWHM (mm ³)	0	4	6	8	10	12
ROC Area	0.46	0.49	0.49	0.49	0.48	0.48
	Heteroscedastic model					
FWHM (mm ³)	0	4	6	8	10	12
ROC Area	0.63	0.70	0.72	0.72	0.69	0.65
	Area under the ROC curve.					

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Conclusion: homoscedastic versus heteroscedastic GLM

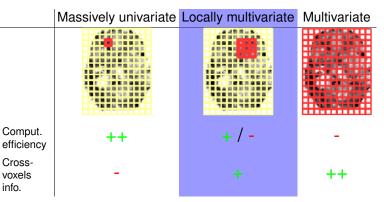
- The assumption of homoscedasticity is violated in ASL studies.
- Modelling heteroscedasticity is essential in the detection of patient-specific perfusion abnormalities with ASL.

Related publication: [Maumet et al., NeuroImage 2013].

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- 2. The *a contrario* approach as a new locally multivariate procedure.

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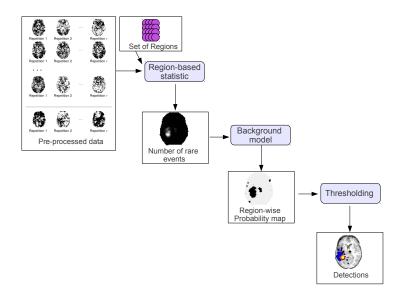
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A contrario approach

From the computer vision community [Desolneux 2003].



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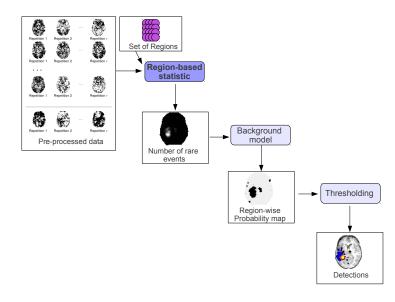
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From the computer vision community [Desolneux 2003].



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A contrario approach

Rare event count per sphere as region-based statistic:



1. Voxel-based probability

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A contrario approach

Rare event count per sphere as region-based statistic:







-based 2. Th bility

2. Thresholding

$$k_{(v)} = egin{cases} 1, & ext{if} \ \pi_v^{GLM} \leq p_{\scriptscriptstyle PRE}\,, \ 0, & ext{otherwise}. \end{cases}$$

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A contrario approach

Rare event count per sphere as region-based statistic:



1. Voxel-based probability

 $k_{(v)}$

2. Thresholding



3. Rare event count per region

$$= \begin{cases} 1, & \text{if } \pi_{v}^{GLM} \leq p_{PRE}, \quad l_{(r)} = \sum_{v \in R} k_{(v)} \\ 0, & \text{otherwise.} \end{cases}$$

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Context

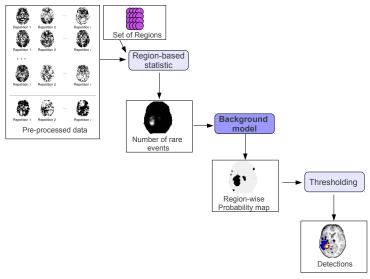
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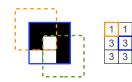
From the computer vision community [Desloneux 2003].



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A contrario approach

From region-based statistic to region-based probability:



3. Rare event count per region



 Region-based probability

$$L_{(r)} = \sum_{v \in R} K_{(v)}$$
 with $K_{(v)} \sim \operatorname{Bern}(p_{\scriptscriptstyle PRE})$

The original *a contrario* approach assumes **white noise**, i.e. the events are **independent**:

$$\pi_{(r)} = \Pr(L_{(r)} \ge l_{(r)})$$
, where $L_{(r)} \sim \mathrm{B}(e, p_{\scriptscriptstyle PRE})$,

where e is the number of voxel per region.

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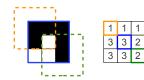
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From region-based statistic to region-based probability:





3. Rare event count per region

 Region-based probability

$$L_{(r)} = \sum_{v \in R} K_{(v)}$$
 with $K_{(v)} \sim \operatorname{Bern}(p_{\scriptscriptstyle PRE})$

In MRI, spatial **autocorrelation of the noise** has been described (e.g. [Chumbley 2009]) and the independance assumption is therefore questionned.

We proposed a **non-independent probability** based on the joint distribution of a multivariate Gaussian distribution.

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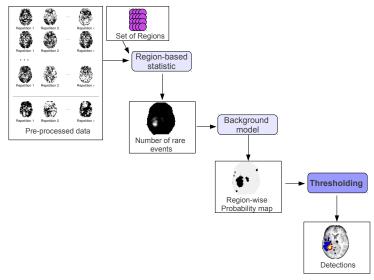
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From the computer vision community [Desloneux 2003].



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A contrario approach: thresholding

The correction for multiple testing is usually done by computing the Number of False Alarms:

$$NFA_{(r)} = numReg \pi_{(r)},$$

and the detections are outlined with:

$$NFA_{(r)} < \epsilon.$$

where ϵ , is the average number of false detections that are tolerated.

The NFA is related to Bonferroni correction [Rousseau 2007].

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Results: a contrario

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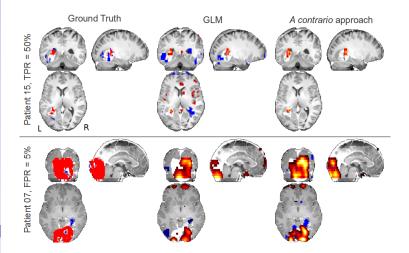
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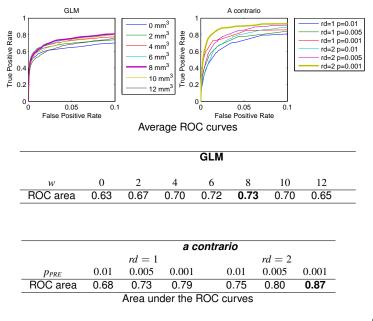
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Results: a contrario



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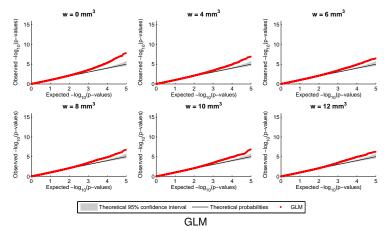
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Results: *a contrario* Checking the test validity



- Invalidity of the GLM.
- This invalidity was also observed in voxel-based morphometry [Scarpazza 2013, Viviani 2007].

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Context

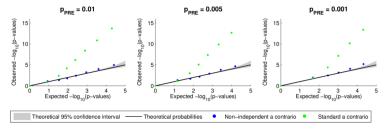
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Results: a contrario

Checking the test validity



A contrario

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Conclusion: a contrario

- The a contrario approach outperforms the standard General Linear Model.
- Non-independent probabilities provide more valid statistics in the context of MRI data analysis.

Related publications: [Maumet et al., ISBI 2012], [Maumet et al., MICCAI 2012], a journal paper submitted to NeuroImage.

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Contributions(1/2)

Patient-specific analysis in BOLD fMRI and ASL:

- Comparison of the homoscedastic and heteroscedastic GLM
 - Heteroscedasticity of Arterial Spin Labelling data.
 - Modelling heteroscedasticity is essential in the detection of patient-specific perfusion abnormalities with ASL.

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Patient-specific analysis in BOLD fMRI and ASL:

- Comparison of the homoscedastic and heteroscedastic GLM
 - Heteroscedasticity of Arterial Spin Labelling data.
 - Modelling heteroscedasticity is essential in the detection of patient-specific perfusion abnormalities with ASL.
- The a contrario locally multivariate procedure
 - Superiority onto the massively univariate GLM.
 - Two applications: the detection of patient-specific perfusion abnormalities and the detection of activation patterns in task-evoked analyses.

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Contributions(1/2)

Patient-specific analysis in BOLD fMRI and ASL:

- Comparison of the homoscedastic and heteroscedastic GLM
 - Heteroscedasticity of Arterial Spin Labelling data.
 - Modelling heteroscedasticity is essential in the detection of patient-specific perfusion abnormalities with ASL.
- The a contrario locally multivariate procedure
 - Superiority onto the massively univariate GLM.
 - Two applications: the detection of patient-specific perfusion abnormalities and the detection of activation patterns in task-evoked analyses.
- Robust computation (using M-estimators) of cerebral blood flow maps from a series of Arterial Spin Labelling acquisitions.

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Contributions (2/2)

Group analyses in BOLD functional MRI.

- An original panel of four tasks for language mapping in children.
- Atypical patterns of activity and lateralisation in children diagnosed with specific language impairment.

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Software

autoMRI: SPM-based automation tools for anatomical and functional MRI data, Matlab scripts

- Used in other clinical projects.
- Registered at the APP.
- Open source (GPL), available on request.

aut@fMRI

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Discussion and future work (1/2)

Atypical brain function in specific language impairment:

- Extend the preliminary results of the *a contrario* approach in fMRI to this context.
- Take advantage of ASL sequences.

Robust statistics to compute cerebral blood flow maps:

 Compare current results with other M-estimators and complementary robust approaches.

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Discussion and future work (2/2)

Arterial Spin Labelling

- More advanced ASL sequences, such as pseudo-continuous ASL with 3D readouts, provide a better signal-to-noise ratio.
- How does the conclusion on heteroscedasticity extend to these datasets ?

The a contrario approach

- Provide a more thorough validation in BOLD fMRI.
- Extend the approach to group analyses.

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Questions

Q & A