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

Camille Maumet PhD Defense, May 29th, 2013

University of Rennes 1, Faculty of medecine, F-35043 Rennes, France INSERM, U746, F-35042 Rennes, France CNRS, IRISA, UMR 6074, F-35042 Rennes, France Inria, VISAGES project-team, F-35042 Rennes, France

Director: Christian Barillot, Co-director: Pierre Maurel









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### Brain function

### Two views of brain function:



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### Brain function

### Two views of brain function:

Task-evoked activity







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### Brain function

### Two views of brain function:

#### Task-evoked activity







# Intrinsic brain function









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### **Brain function**

### Two views of brain function:



















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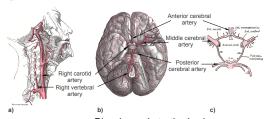
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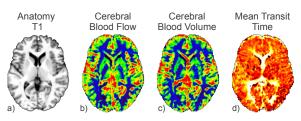
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# Brain perfusion



Blood supply to the brain

**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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1 pair

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1 pair



60 pairs

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# Group analyses: definition (1/2)









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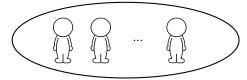
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# Group analyses: definition (1/2)

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



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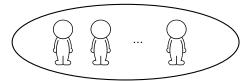
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# Group analyses: definition (1/2)

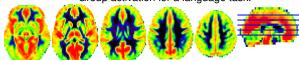
**Within-group** analyses identify common patterns across a group of subjects.



### Examples



Group activation for a language task.



Group cerebral blood flow.

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# Group analyses: definition (2/2)













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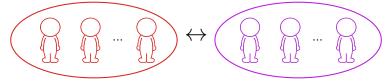
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# Group analyses: definition (2/2)

**Between-group** analyses identify differences at the group level.



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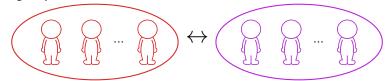
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### Group analyses: definition (2/2)

**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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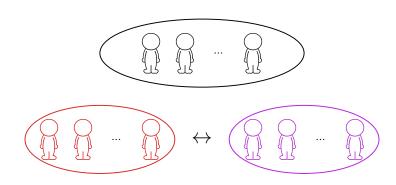
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# Group analyses



### 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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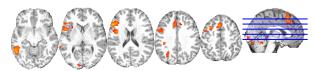
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# Patient-specific analyses: definition (1/2)

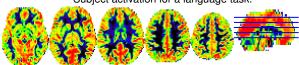
**Patient-specific** analyses identify patterns of brain function in a single subject.



### Examples



Subject activation for a language task.



Cerebral blood flow.

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# Patient-specific analyses: definition (2/2)









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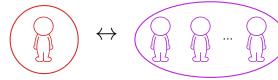
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# Patient-specific analyses: definition (2/2)

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



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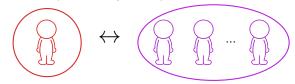
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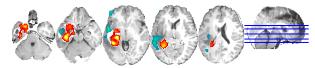
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# Patient-specific analyses: definition (2/2)

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



### Examples



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

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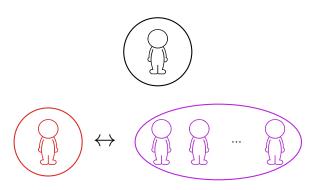
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# Patient-specific analyses



### 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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General Linear Model: homoscedastic and

heteroscedastic models

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### Contributions: overview

	Group analysis	Patient-specific analysis
Within		
Between	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩

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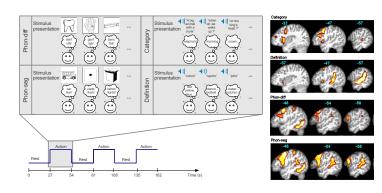
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### Contributions: overview



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



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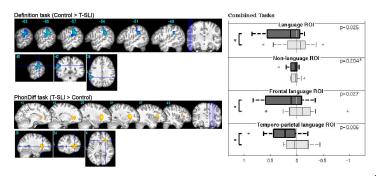
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### Contributions: overview



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



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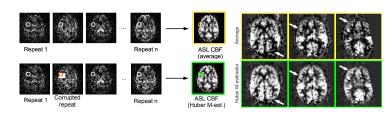
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### Contributions: overview

	Group analysis	Patient-specific analysis
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Robust Estimation of the Cerebral Blood Flow in Arterial Spin Labelling.



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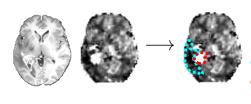
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### Contributions: overview

	Group analysis	Patient-specific analysis
Within	8 - 8	
Between		

Objective: Quantitative identification of voxelwise patientspecific perfusion abnormalities.



hypoperfusion

hyperperfusion

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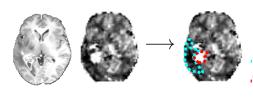
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## Contributions: overview

	Group analysis	Patient-specific analysis
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Objective: Quantitative identification of voxelwise patientspecific perfusion abnormalities.



hypoperfusion

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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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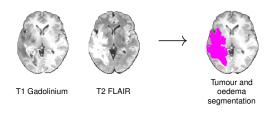
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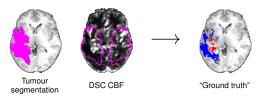
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## Validation: Ground Truth

1. Segmentation of the tumour:



2. Combination with T2 perfusion information:



3. Visual assessment and manual corrections by a clinician.

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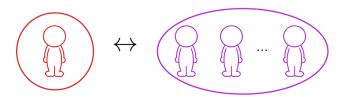
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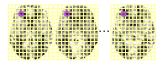
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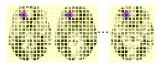
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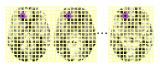
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- √ The standard approach, e.g. [Holmes 1998, Beckmann 2003].
- √ Computationally efficient.
- No integration of information cross-voxels (pre-smoothing).

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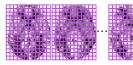
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## **Multivariate** approaches:







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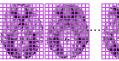
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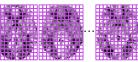
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## **Multivariate** approaches:









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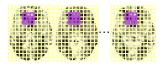
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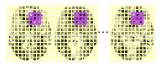
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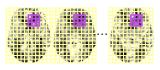
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- Combination of local voxel information (no smoothing), e.g. [Kriegeskorte 2006].
- √ Standard statistics or machine learning.
- √ Less time consuming than full brain.
- × Can still be time consuming (machine learning).
- × Only local information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

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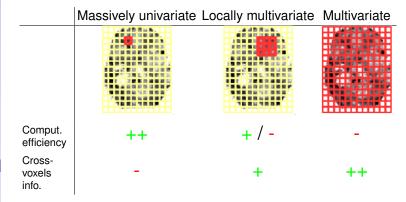
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## Univariate / Multivariate - overview



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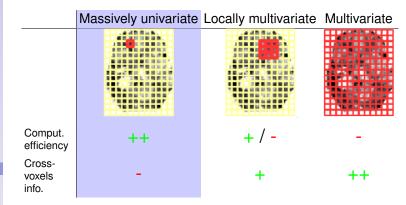
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## Univariate / Multivariate - overview



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

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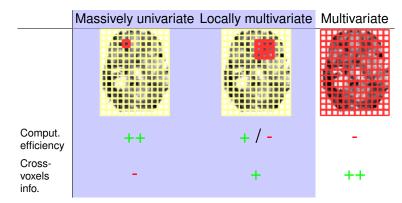
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## Univariate / Multivariate - overview



- 1. The massively univariate GLM: homoscedastic and heteroscedastic models.
- 2. The *a contrario* approach as a new locally multivariate procedure.

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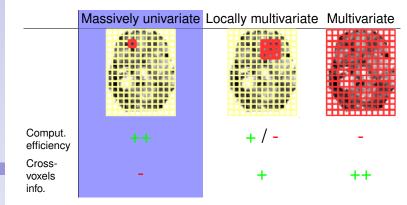
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- 1. The massively univariate GLM: homoscedastic and heteroscedastic models.
- 2. The *a contrario* approach as a new locally multivariate procedure.

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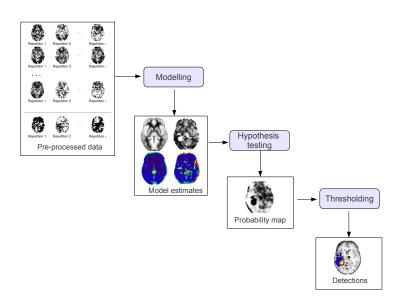
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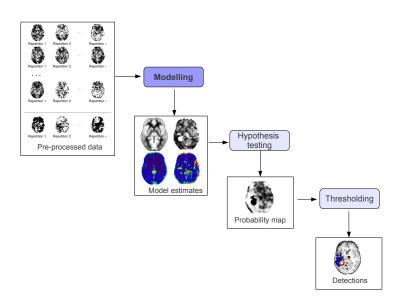
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# Modelling: subject level

## General Linear Model: subject level









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# Modelling: subject level

## General Linear Model: subject level











Perfusion

Repetition 1

Repetition 2

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

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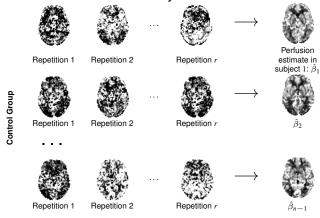
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# Modelling: subject level

## General Linear Model: subject level



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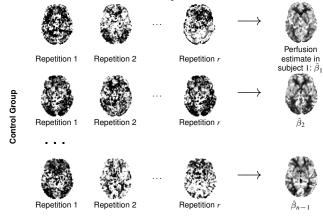
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# Modelling: subject level

## General Linear Model: subject level





Patient

Repetition 1











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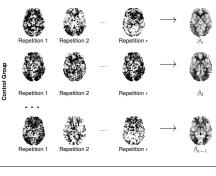
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# Modelling: group level

General Linear Model: group level.





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

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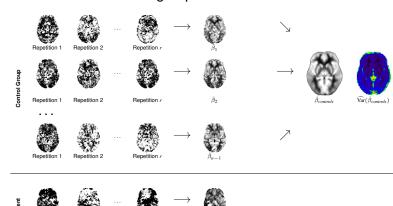
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# Modelling: group level

Repetition 1

Repetition 2

General Linear Model: group level.



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

Repetition /

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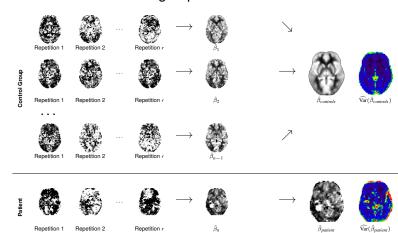
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# Modelling: group level

General Linear Model: group level.



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

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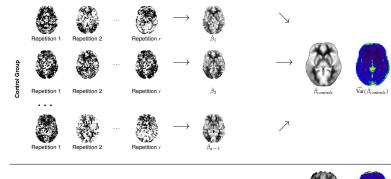
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# Modelling: group level

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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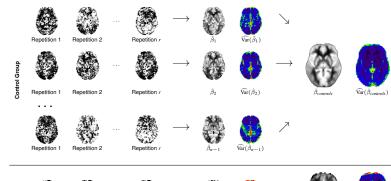
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# Modelling: group level

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).

www.fil.ion.ucl.ac.uk/spm/

<sup>&</sup>lt;sup>2</sup>fsl.fmrib.ox.ac.uk/fsl/fslwiki/

<sup>3</sup>afni.nimh.nih.gov/afni/

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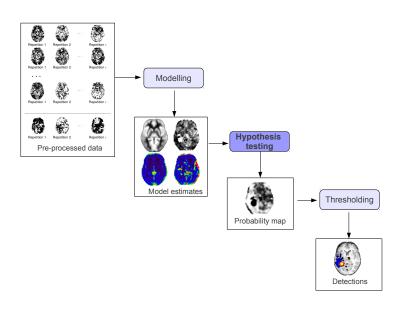
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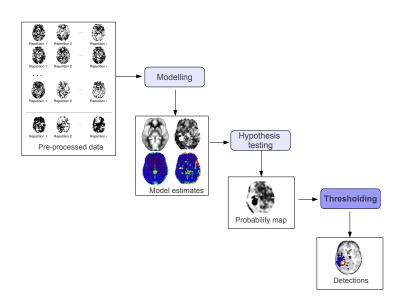
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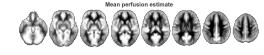
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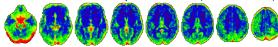
# Results: Perfusion in the control group

## Mean estimate

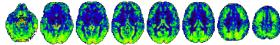


## Standard deviation estimates

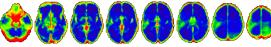
Combined within- and between-subject standard deviation (homoscedastic model)



Between-subject standard deviation (heteroscedastic model)



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



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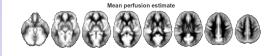
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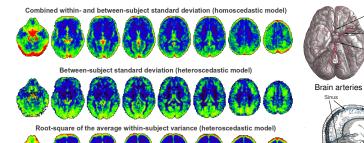
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# Results: Perfusion in the control group

### Mean estimate



### Standard deviation estimates



Brain veins

Anterior cerebral

Middle cerebral

artery

Posterior cerebral artery

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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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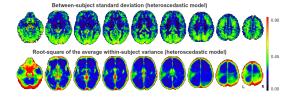
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# Assumptions of the homoscedastic model

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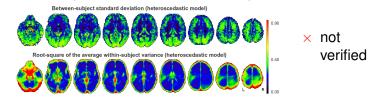
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# Assumptions of the homoscedastic model

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



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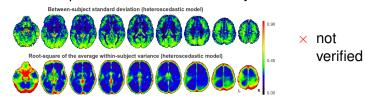
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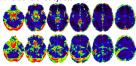
# Assumptions of the homoscedastic model

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



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

Within-subject standard deviation in two control subjects:



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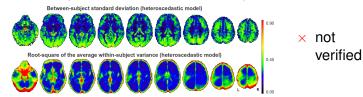
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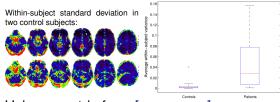
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# Assumptions of the homoscedastic model

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



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



Using a metric from [Mumford 2009].

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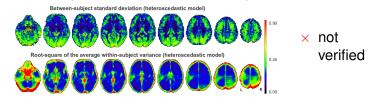
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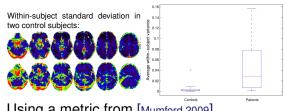
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# Assumptions of the homoscedastic model

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



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



Using a metric from [Mumford 2009].

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verified

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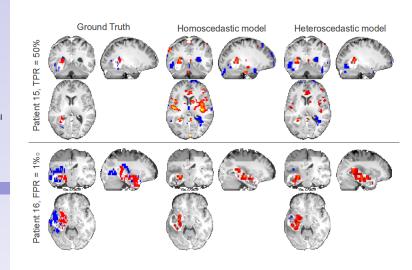
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# Results: homoscedastic versus heteroscedastic GLM



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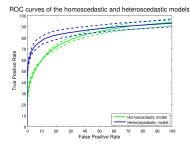
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# Results: homoscedastic versus heteroscedastic GLM



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						
		Heter	oscea	astic r	noaei		
FWHM (mm <sup>3</sup> )	0	Heter 4	oscea 6	astic r	noaei 10	12	
FWHM (mm³) ROC Area		4	6	8	10		

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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 ASI

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

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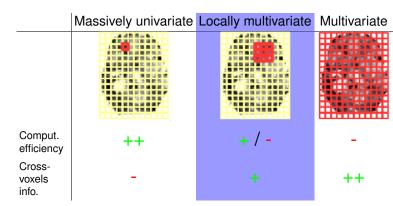
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- The massively univariate GLM: homoscedastic and heteroscedastic models.
- 2. The *a contrario* approach as a new locally multivariate procedure.

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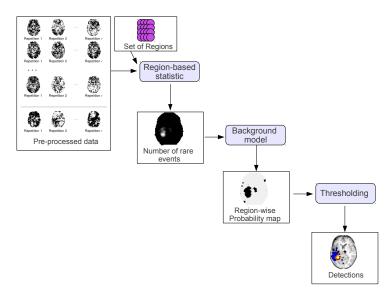
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# A contrario approach

From the computer vision community [Desolneux 2003].



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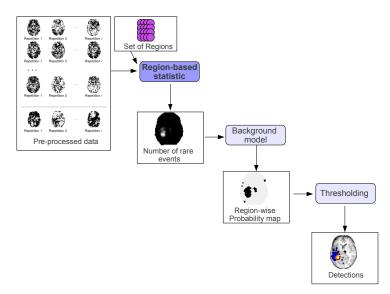
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# A contrario approach

From the computer vision community [Desolneux 2003].



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# A contrario approach

Rare event count per sphere as region-based statistic:



Voxel-based probability

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# A contrario approach

### Rare event count per sphere as region-based statistic:





 Voxel-based probability

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:







 Voxel-based probability 2. Thresholding

3. Rare event count per region

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

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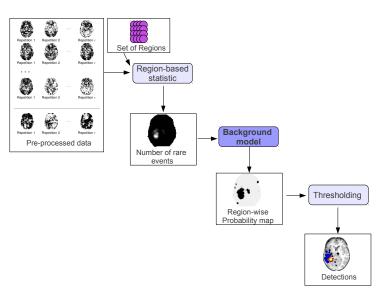
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# A contrario approach

From the computer vision community [Desloneux 2003].



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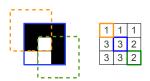
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# A contrario approach

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  $K_{(v)} \sim \text{Bern}(p_{PRE})$ 

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

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

where e is the number of voxel per region.

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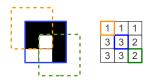
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# A contrario approach

From region-based statistic to region-based probability:





3. Rare event count per region

Region-based probability

$$L_{(r)} = \sum_{v \in R} K_{(v)} \quad ext{with} \quad K_{(v)} \sim ext{Bern}(p_{ ext{\tiny PRE}})$$

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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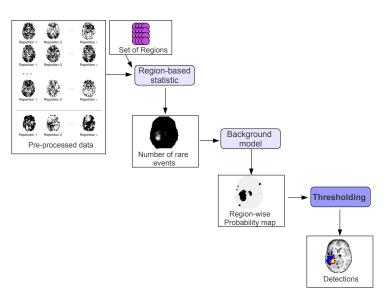
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# A contrario approach

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  $\epsilon$ , is the average number of false detections that are tolerated.

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

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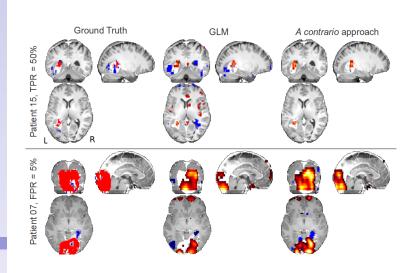
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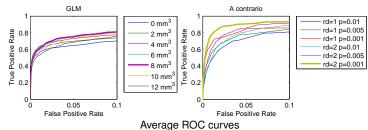
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# Results: a contrario



Average ROC curves

CL M

	GLIM							
w	0	2	4	6	8	10	12	
ROC area	0.63	0.67	0.70	0.72	0.73	0.70	0.65	

	a contrario					
		rd = 1 $rd = 2$				
$p_{PRE}$	0.01	0.005	0.001	0.01	0.005	0.001
ROC area	0.68	0.73	0.79	0.75	0.80	0.87

Area under the ROC curves

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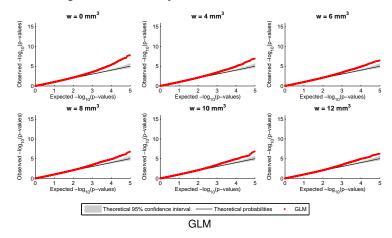
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## Checking the test validity



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

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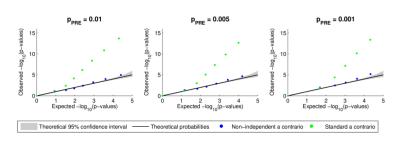
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# Checking the test validity



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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 ASI

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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.

#### Camille Maumet

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# Contributions (1/2)

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- Comparison of the homoscedastic and heteroscedastic GLM
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  - 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.



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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