

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

Camille Maumet

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

Camille Maumet PhD Defense, May 29th, 2013

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Director: Christian Barillot, Co-director: Pierre Maurel









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Two views of brain function:



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Task-evoked activity







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Two views of brain function:









Intrinsic brain function









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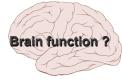
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Two views of brain function:

Task-evoked activity







Intrinsic brain function









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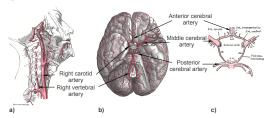
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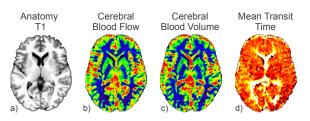
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Brain perfusion



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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Detre et al., MRM 1992

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1 pair

Detre et al., MRM 1992

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1 pair



60 pairs

Detre et al., MRM 1992

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Group analyses: definition (1/2)









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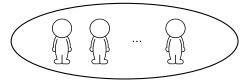
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Group analyses: definition (1/2)

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



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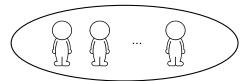
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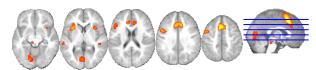
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Group analyses: definition (1/2)

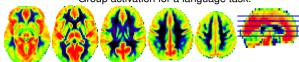
Within-group analyses identify common patterns across a group of subjects.



Examples



Group activation for a language task.



Group cerebral blood flow.

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Group analyses: definition (2/2)













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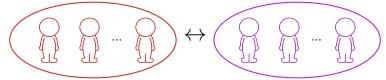
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Group analyses: definition (2/2)

Between-group analyses identify differences at the group level.



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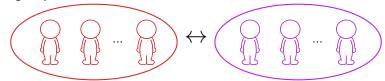
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Group analyses: definition (2/2)

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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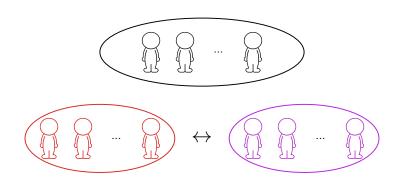
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Group analyses



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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Patient-specific analyses: definition (1/2)

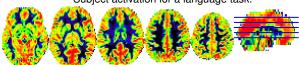
Patient-specific analyses identify patterns of brain function in a single subject.



Examples



Subject activation for a language task.



Cerebral blood flow.

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Patient-specific analyses: definition (2/2)











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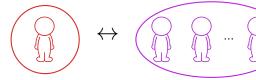
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Patient-specific analyses: definition (2/2)

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



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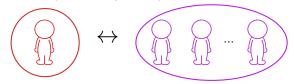
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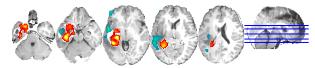
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Patient-specific analyses: definition (2/2)

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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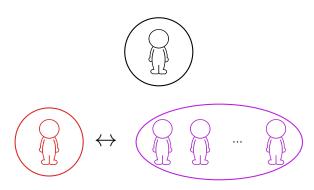
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Patient-specific analyses



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)	(8 - 8)

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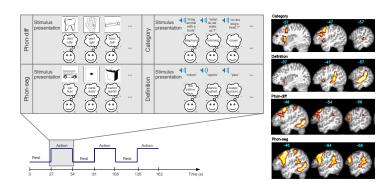
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Contributions: overview

	Group analysis	Patient-specific analysis
Within		
Between	(10 - 10 + (10 - 10)	₩ ₩ ₩ - ₩

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



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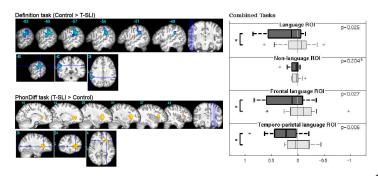
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Atypical activity and lateralisation of brain function in children diagnosed with typical specific language impairment.



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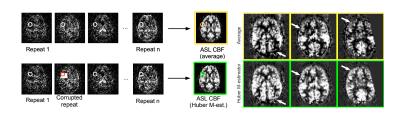
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Robust Estimation of the Cerebral Blood Flow in Arterial Spin Labelling.



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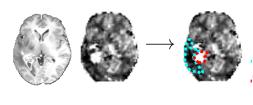
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Between		₩ ₩ ₩ - ₩

Objective: Quantitative identification of voxelwise patientspecific perfusion abnormalities.



hypoperfusion

hyperperfusion

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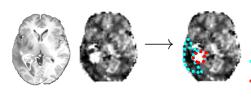
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Objective: Quantitative identification of voxelwise patientspecific perfusion abnormalities.



hypoperfusion

hyperperfusion

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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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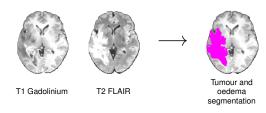
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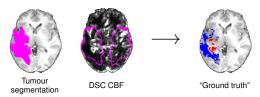
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Validation: Ground Truth

1. Segmentation of the tumour:



2. Combination with T2 perfusion information:



3. Visual assessment and manual corrections by a clinician.

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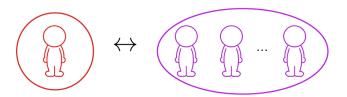
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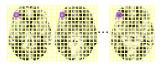
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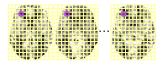
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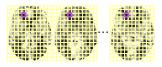
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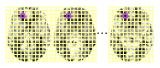
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- √ The standard approach, e.g. [Holmes 1998, Beckmann 2003].
- √ Computationally efficient.
- No integration of information cross-voxels (pre-smoothing).

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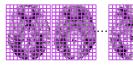
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Multivariate approaches:







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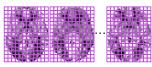
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Multivariate approaches:







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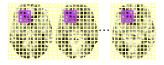
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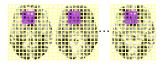
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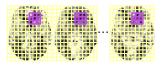
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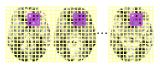
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- Combination of local voxel information (no smoothing), e.g. [Kriegeskorte 2006].
- √ Standard statistics or machine learning.
- √ Less time consuming than full brain.
- × Can still be time consuming (machine learning).
- × Only local information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

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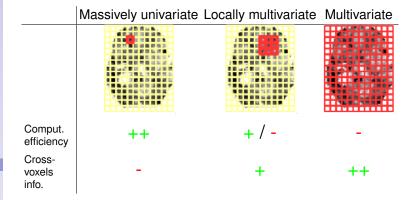
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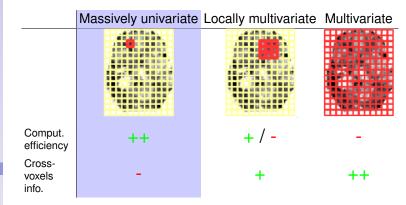
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1. The massively univariate GLM: homoscedastic and heteroscedastic models.

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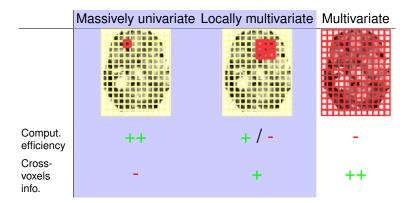
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- 1. The massively univariate GLM: homoscedastic and heteroscedastic models.
- 2. The *a contrario* approach as a new locally multivariate procedure.

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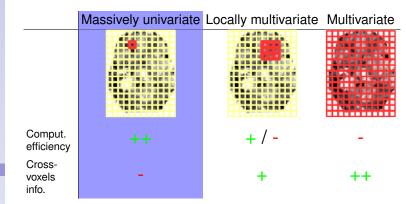
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- 1. The massively univariate GLM: homoscedastic and heteroscedastic models.
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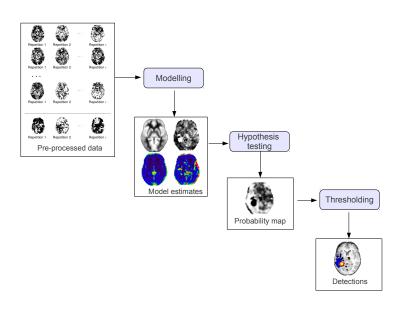
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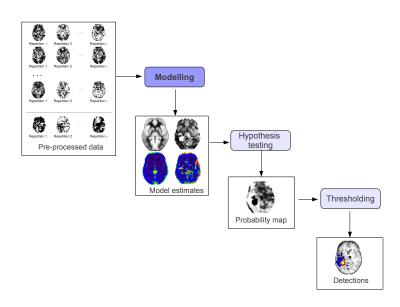
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Modelling: subject level

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

Repetition 2

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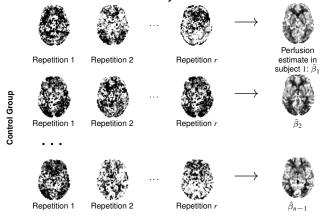
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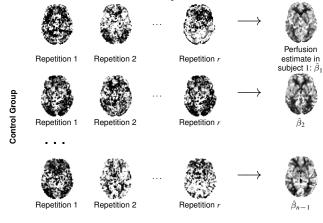
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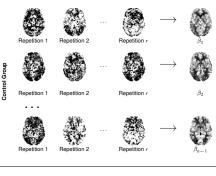
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Modelling: group level

General Linear Model: group level.





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

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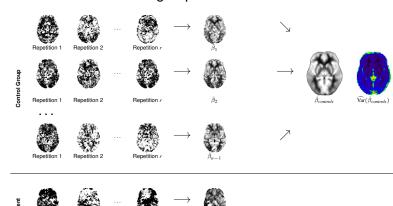
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General Linear Model: group level.



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

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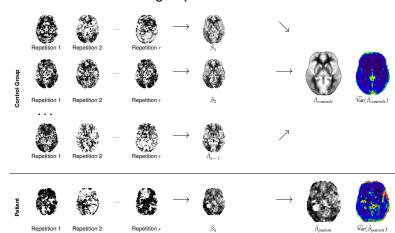
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General Linear Model: group level.



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

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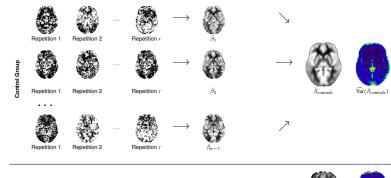
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Modelling: group level

General Linear Model: group level. The homoscedastic model:





Repetition 1















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

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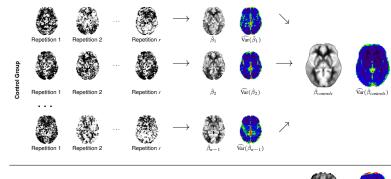
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Modelling: group level

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/

²fsl.fmrib.ox.ac.uk/fsl/fslwiki/

³afni.nimh.nih.gov/afni/

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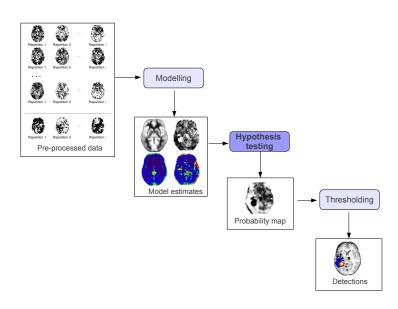
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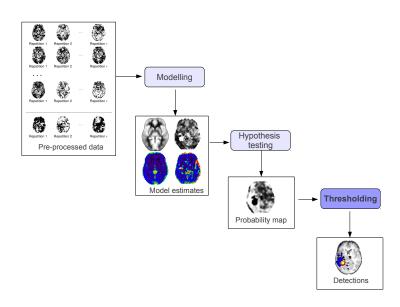
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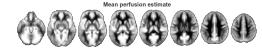
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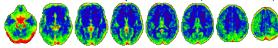
Results: Perfusion in the control group

Mean estimate

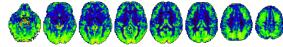


Standard deviation estimates

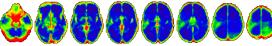
Combined within- and between-subject standard deviation (homoscedastic model)



Between-subject standard deviation (heteroscedastic model)



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



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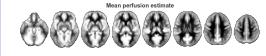
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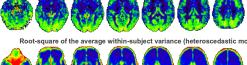
Results: Perfusion in the control group

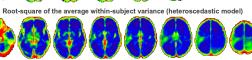
Mean estimate



Standard deviation estimates

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





Anterior cerebral artery Middle cerebral artery Posterior cerebral artery

Brain arteries Sinus



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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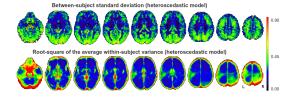
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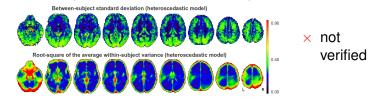
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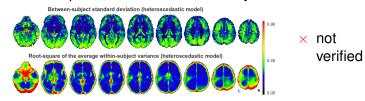
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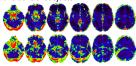
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Within-subject standard deviation in two control subjects:



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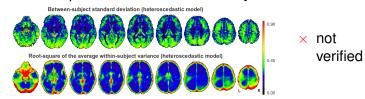
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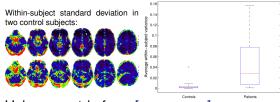
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Assumptions of the homoscedastic model

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Using a metric from [Mumford 2009].

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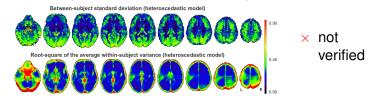
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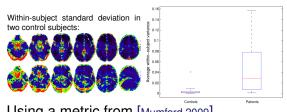
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Assumptions of the homoscedastic model

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



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Using a metric from [Mumford 2009].

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verified

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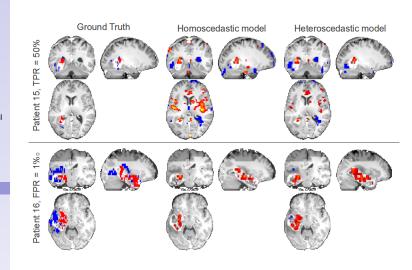
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Results: homoscedastic versus heteroscedastic GLM



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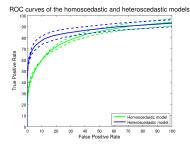
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Results: homoscedastic versus heteroscedastic GLM



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	osced	lastic r	nodel			
FWHM (mm ³)	0	Heter 4	osced 6	lastic r 8	nodel 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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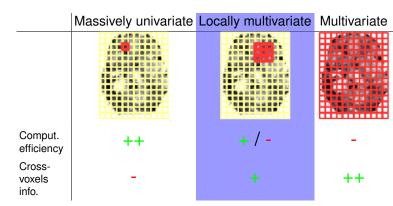
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Univariate / Multivariate - overview



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

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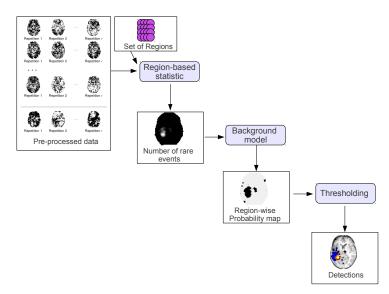
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From the computer vision community [Desolneux 2003].



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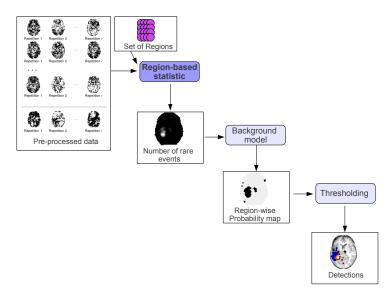
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From the computer vision community [Desolneux 2003].



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Rare event count per sphere as region-based statistic:



 Voxel-based probability

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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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Rare event count per sphere as region-based statistic:







 Voxel-based probability 2. Thresholding

3. Rare event count per region

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

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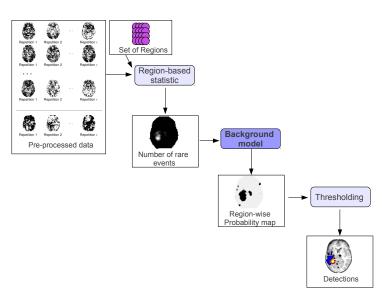
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From the computer vision community [Desloneux 2003].



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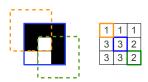
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A contrario approach

From region-based statistic to region-based probability:





3. Rare event count per region

4. 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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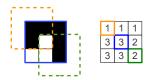
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From region-based statistic to region-based probability:





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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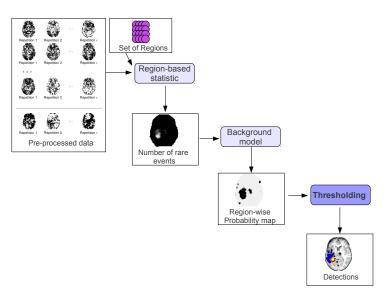
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From the computer vision community [Desloneux 2003].



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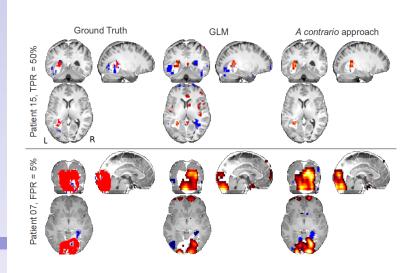
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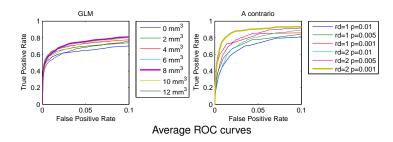
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GLM 0 2 8 10 12 w 6 ROC area 0.70 0.72 0.73 0.63 0.67 0.70 0.65

-	a contrario								
	rd = 1				rd = 2				
$p_{\it PRE}$	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			
A									

Area under the ROC curves

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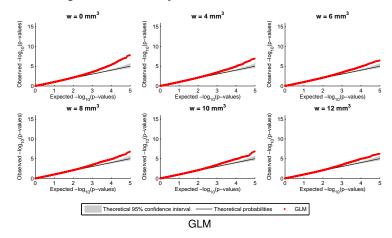
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Checking the test validity



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

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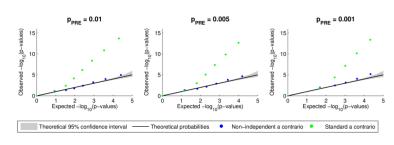
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Conclusion: a contrario

- ► 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.

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Contributions (1/2)

Patient-specific analysis in BOLD fMRI and ASL:

- Comparison of the homoscedastic and heteroscedastic GLM
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- ► 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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Q & A