

MRM practical: Repeated measures & multimodal datasets

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Aims of the practical

We will be using the **MRM toolbox** (McFarquhar *et al.*, 2016) to analyse a **repeated measurements** fMRI dataset and a **multimodal** (functional + structural) dataset using the **multivariate GLM**

Multivariate and repeated measures (MRM): A new toolbox for dependent and multimodal group-level neuroimaging data



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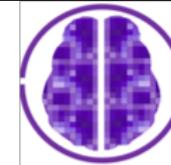
^c Brain Mapping Unit, Herchel Smith Building for Brain and Mind Sciences, University of Cambridge, Robinson Way, Cambridge CB2 0SZ, UK

^d Imaging Sciences, Stopford Building, The University of Manchester, Oxford Road, Manchester M13 9PL, UK

Prerequisites

You will need:

- **MRM v1.0** from <https://github.com/martynmcfarquhar/MRM/releases>
- **SPM12** from <https://www.fil.ion.ucl.ac.uk/spm/software/spm12/>
- The **demo datasets** from <https://tinyurl.com/yxlkqvql>



About the datasets

Repeated measurements dataset

Subjects were:

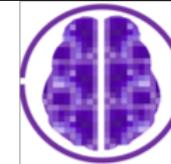
- 12 **older adults** with a **history** of **depression**
- 12 **older adults** with **no history** of **psychiatric disorder**
- 15 **younger adults** with a **history** of **depression**
- 14 **younger adults** with **no history** of **psychiatric disorder**

The **younger** group were aged **35–55** and the **older** group were aged **65–85**

The **between-subject** factorial structure is

- **Age** with **2 levels** — older and younger
- **Diagnosis** with **2 levels** — remitted and controls

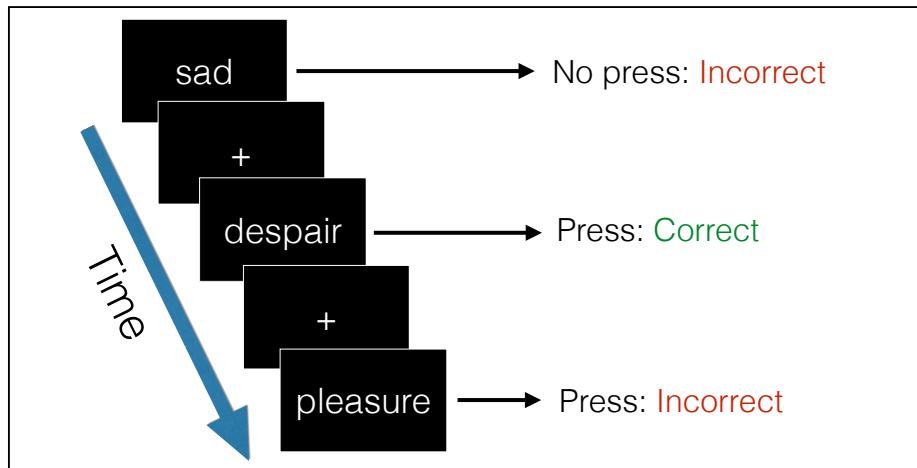
This is a basic **2 x 2 ANOVA** design



About the datasets

Repeated measurements dataset

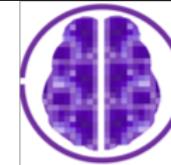
All subjects completed an **Affective Go/No-go** task in the scanner



“Press the button when you see a
SAD word”

3 conditions of the task:

1. **Go Happy No Sad** (GHNS)
2. **Go Sad No Happy** (GSNH)
3. **Neutral** — UPPERCASE and lowercase words



About the datasets

Repeated measurements dataset

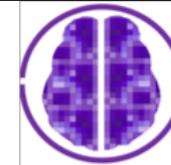
The complete design is therefore a **3 x 2 x 2 mixed-measure ANOVA**:

- One **within-subject** factor (AGN Condition)
- Two **between-subjects** factors (Age, Diagnosis)

The standard SPM approach would be to calculate **contrasts** of the AGN conditions at the **first-level** and then conduct **multiple second-level models**

Instead, we will use **MRM** to analyse the **complete design** at the second-level

The raw data are the **3 AGN condition** estimates for **each subject**, as compared to **rest**



About the datasets

Multi-modal dataset

Subjects were:

- 15 **younger adults** with a **history of depression**
- 13 **younger adults** with **no history of psychiatric disorder**

Subjects completed an **affective picture memory task** in the scanner



Neutral

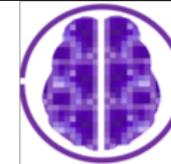


Negative



Positive

We will just focus on the **encoding** phase of the task

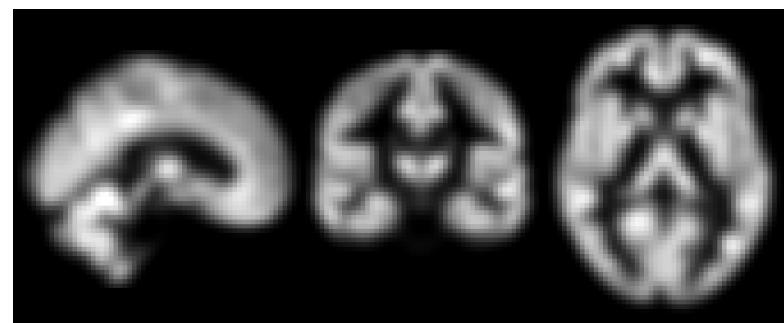


About the datasets

Multi-modal dataset

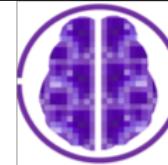
For the **multi-modal** analysis we analyse the **functional data** from the **positive** picture condition as well as **grey-matter volume**

The **structural scans** have already been processed using **DARTEL** to produce maps of grey matter volume



These have been **down-sampled** to match the **functional data** — speeds up the analysis, but usually do it the **other way** (up-sample the functional data) using **nearest-neighbour interpolation**

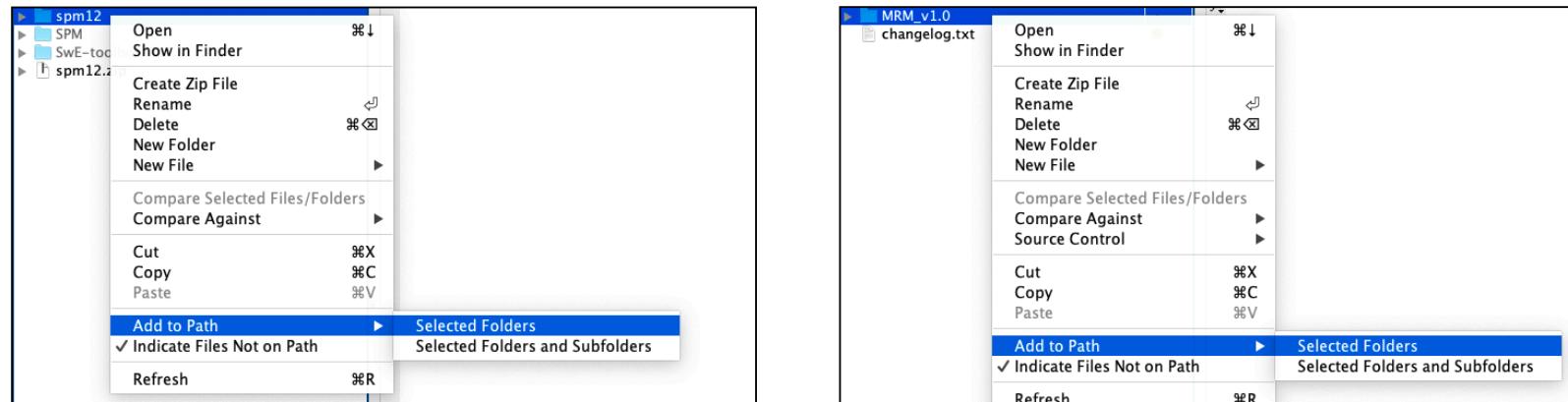
You can use the SPM **Coregister: Estimate & Reslice** tool for this



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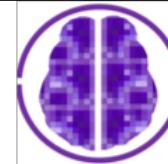
Setup

Add both the **spm12** and **MRM_v1.0** folders to your **MATLAB path** using the **Selected Folders** option



Navigate inside the **MRMdemo** folder and then **launch MRM** by typing **mrm** at the prompt and hitting enter





MRM Launcher

Specify a **MANOVA** model for multi-modal datasets

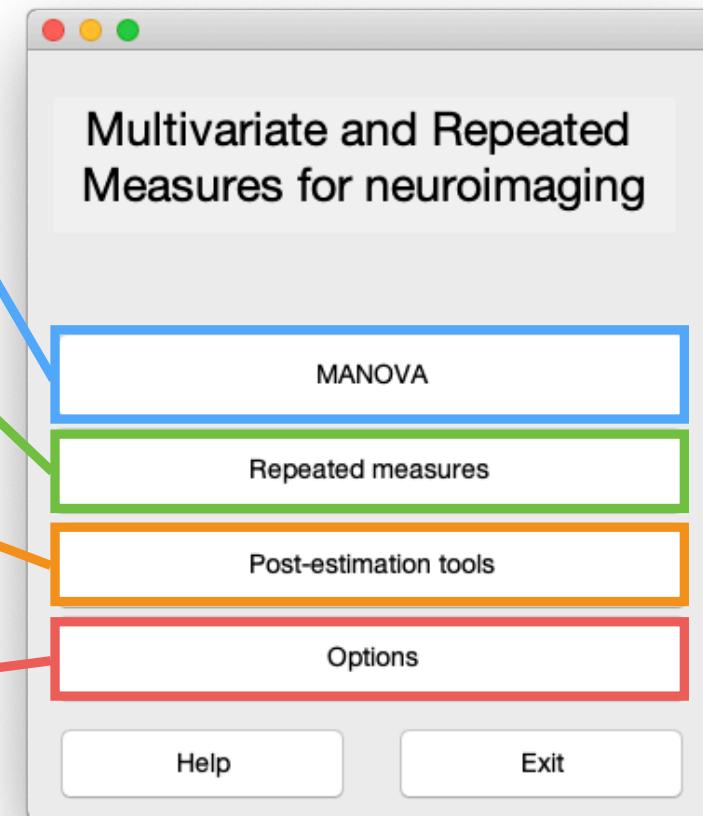
Specify a **repeated measures** model

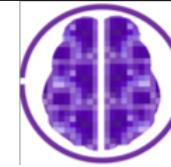
Result exploration tools

General options

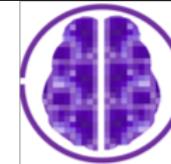
A **MRMoptions.mat** file will be created in the **MRM folder** (can always be deleted)

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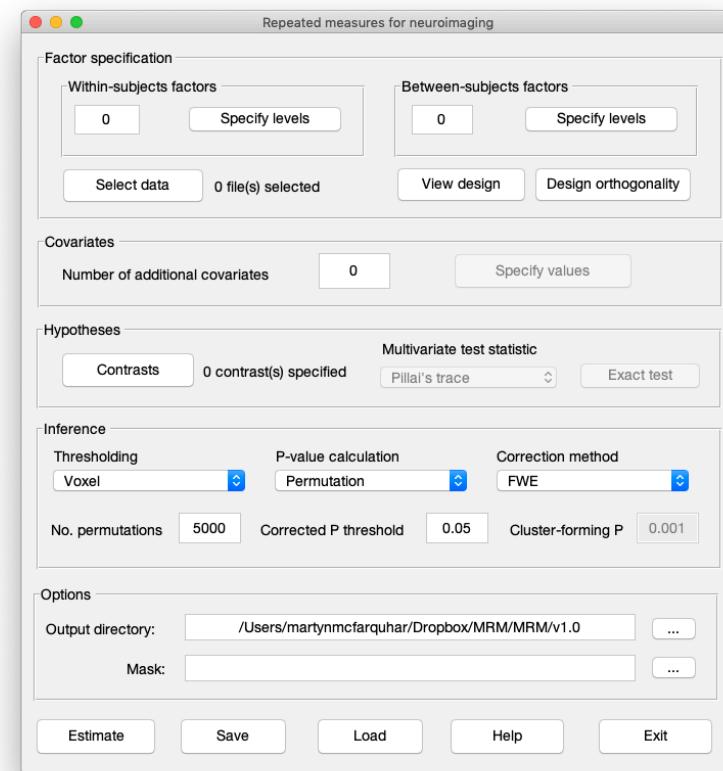
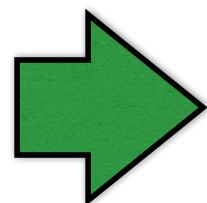
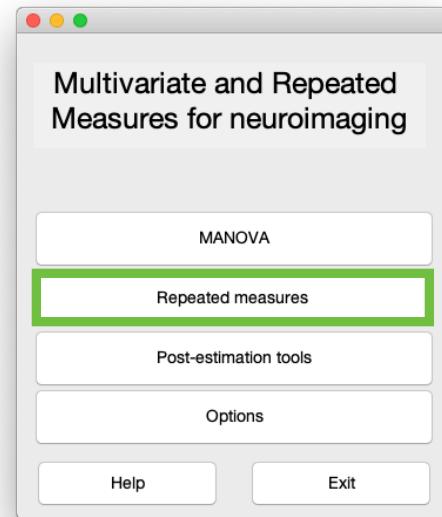
Repeated measurements analysis

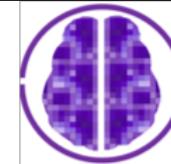


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Repeated measurements analysis

To analyse the **repeated measures** dataset, click the **Repeated measures** button





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Repeated measurements analysis

To specify the model we will work from the **top** of the window to the **bottom**

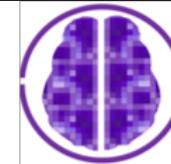
We first need to specify the **factorial structure** of the model

Factor specification

Within-subjects factors	Between-subjects factors
0	0
Specify levels	Specify levels
Select data	0 file(s) selected
View design	
Design orthogonality	

Change the **number** of **within-subject factors** to **1** and change the **number** of **between-subject factors** to **2**

Within-subjects factors	Between-subjects factors
1	2
Specify levels	Specify levels



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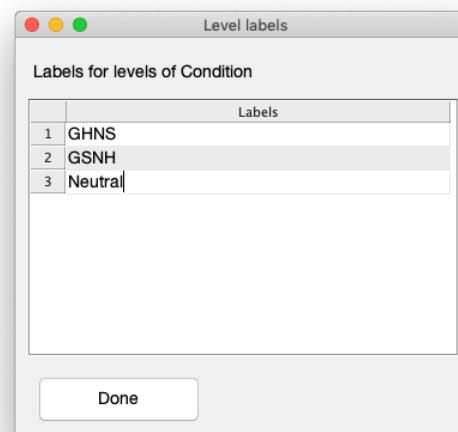
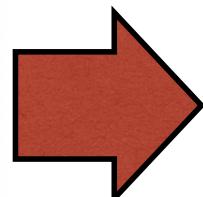
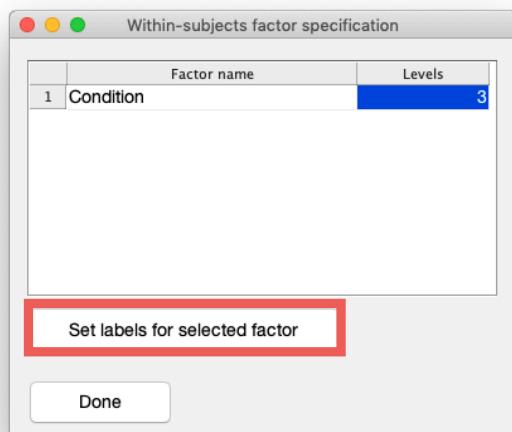
Repeated measurements analysis

Click **Specify levels** for the **Within-subject factors**

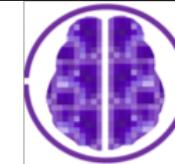


Call the factor **Condition** and set the **number of level** to **3**

Click the **Set labels...** button and name the levels **GHNS**, **GSNH** and **Neutral**



Click **Done** on both windows



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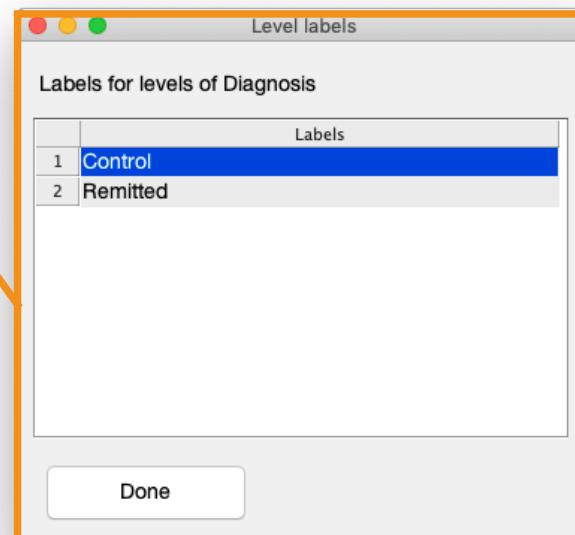
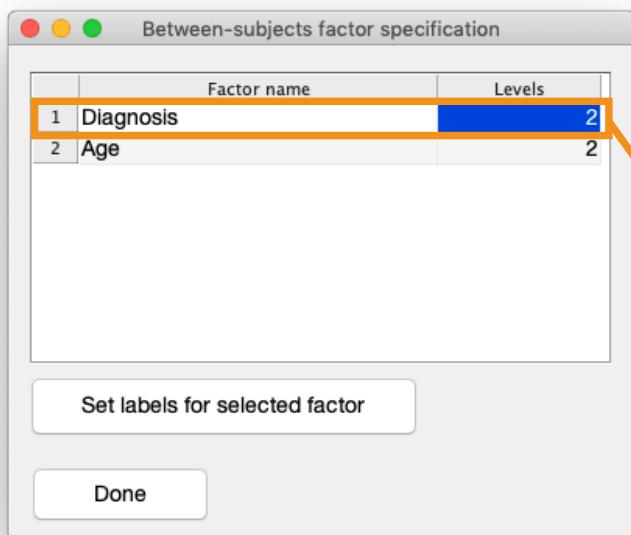
Repeated measurements analysis

Click **Specify levels** for the **Between-subjects factors**



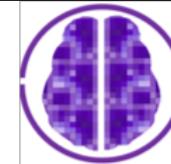
Call the **first** factor **Diagnosis** and with **2 levels**

Call the **second** factor **Age** and with **2 levels**



Complete the **level labels** for **Diagnosis** using **Control** and **Remitted**

Click **Done** on the **labels** windows



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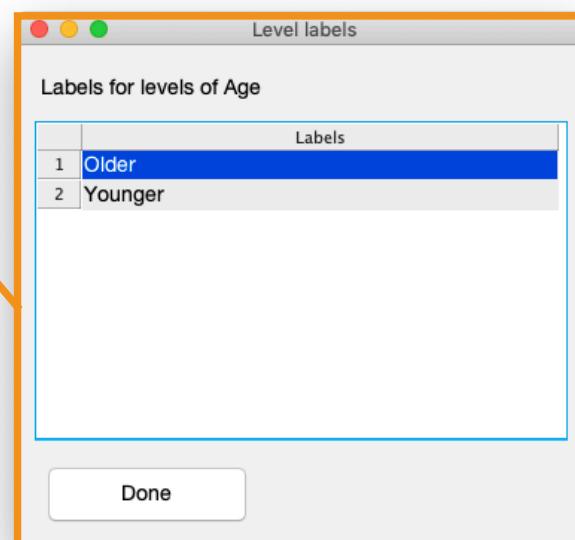
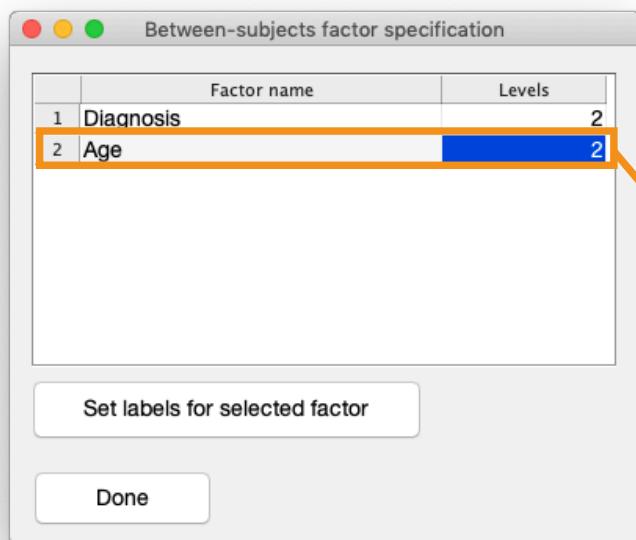
Repeated measurements analysis

Click **Specify levels** for the **Between-subjects factors**



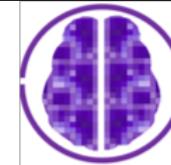
Call the **first** factor **Diagnosis** and with **2 levels**

Call the **second** factor **Age** and with **2 levels**



Complete the **level labels** for **Age** using **Older** and **Younger**

Click **Done** on **both windows**

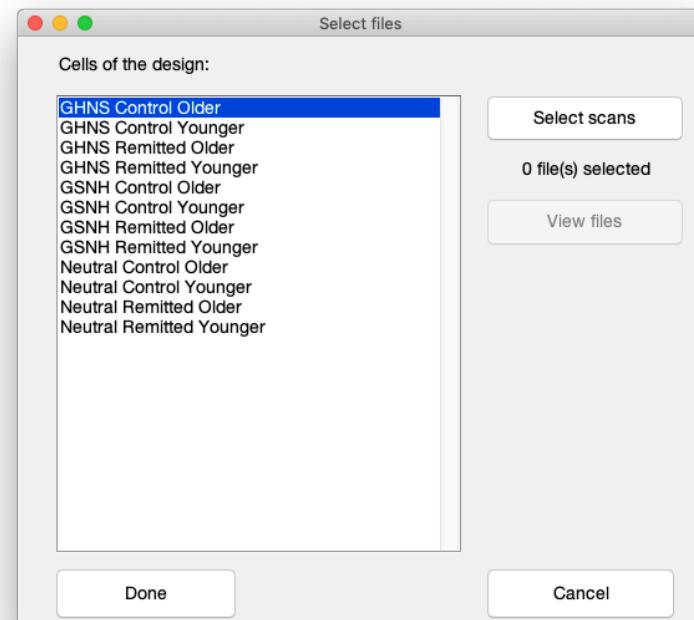


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Repeated measurements analysis



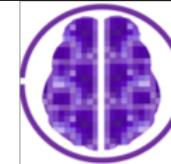
Click **Select data** on the main window



The **cells** of the design will now be displayed

We need to work through **each cell** selecting all the appropriate scans

Useful to organise your data **in the same way** to make file selection easier



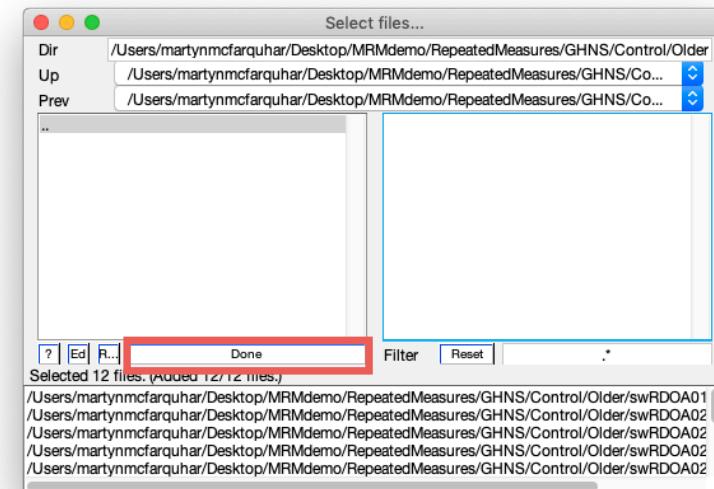
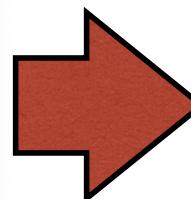
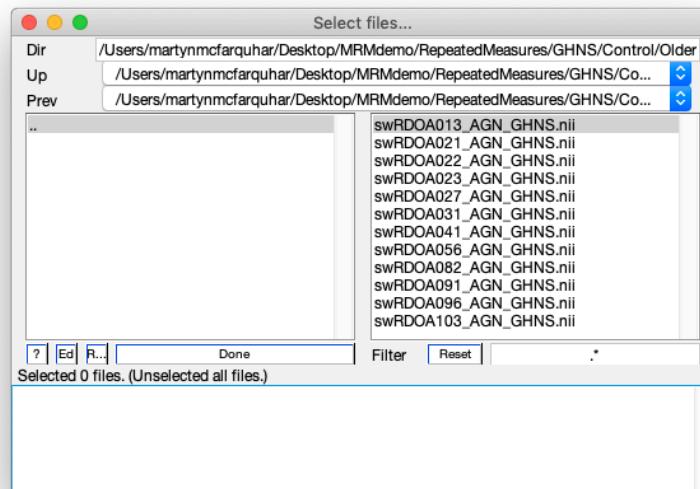
Practical

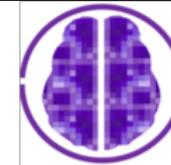
Repeated measurements analysis

With **GHNS Control Older** highlighted, click **Select scans**

Use the **SPM file selector** to navigate to the **demo dataset folder** and then navigate to **RepeatedMeasures/GHNS/Control/Older**

Select the **12 files** inside this folder and click **Done**

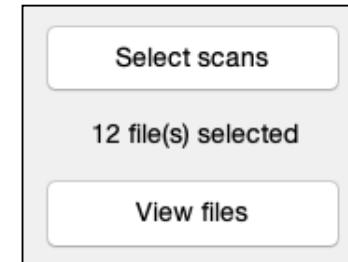




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Repeated measurements analysis

The **Select files** window will update with the **number of files** selected for **this cell**

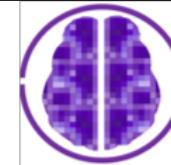


You can click **View files** to see the **paths** of the files you have selected

Repeat this procedure for the remaining **11 cells** using the folder names in the demo dataset to guide you

Once you have finished, click **Done** on the **Select files** window and the main window should **update** to show that **159 files** have been selected





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Repeated measurements analysis

You can now click the **View Design** button to see a **visualisation** of the design

Factor specification

Within-subjects factors

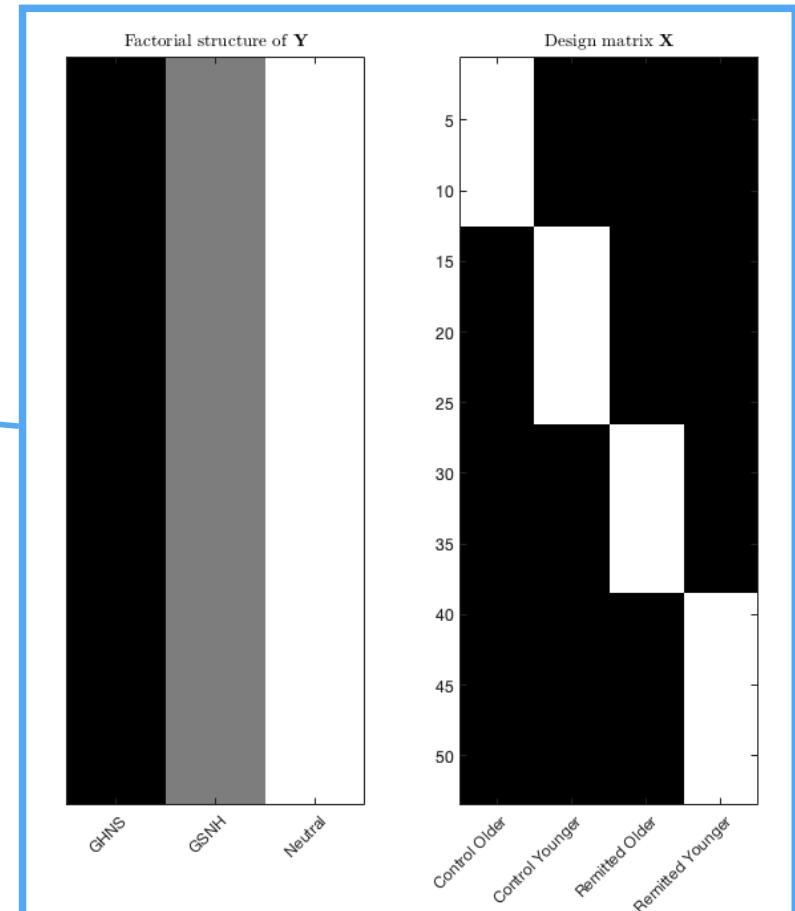
1 Specify levels

Between-subjects factors

2 Specify levels

Select data 159 file(s) selected

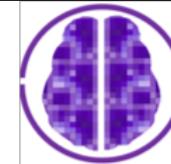
View design Design orthogonality



On the **left** is the **factorial structure** of the **outcome matrix**

On the **right** is the **design matrix**

$$\mathbf{Y} = \mathbf{X}\mathbf{B} + \mathbf{E}$$



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Repeated measurements analysis

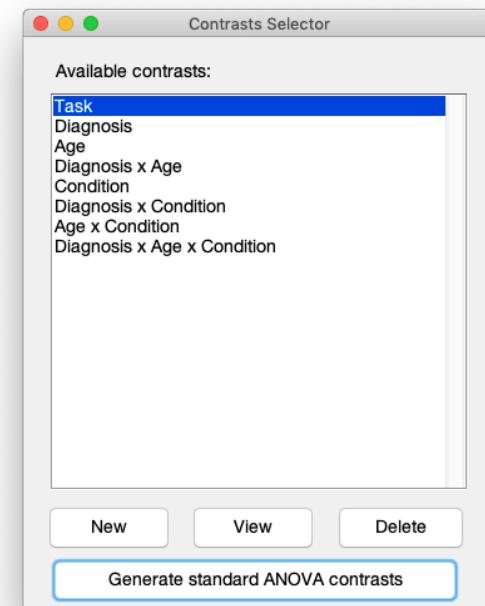
To specify **hypothesis tests** click the **Contrasts** button

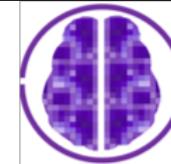


This will open the list of all the currently specified contrasts

For this example, click the **Generate standard ANOVA contrasts** button

This will create **contrasts** for all **main effects** and **interactions** in the design





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Repeated measurements analysis

As an example, select the **Diagnosis x Condition** contrast and click the **View** button

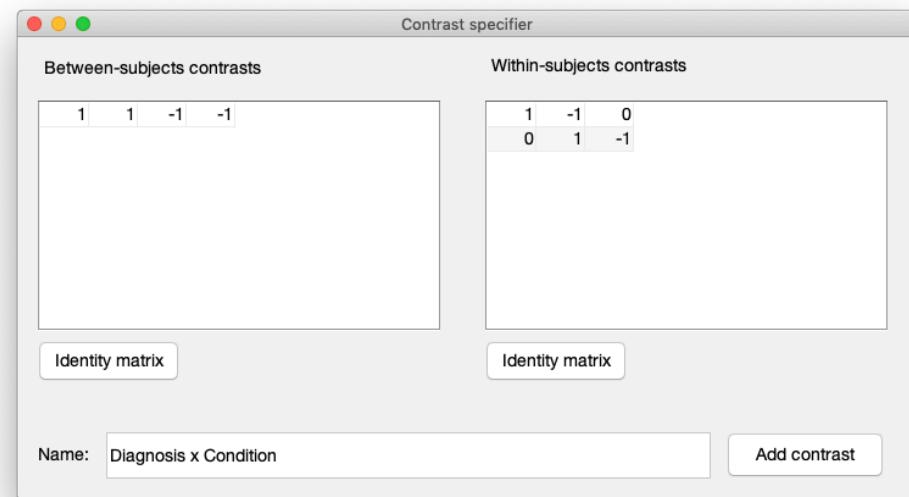
Remember that a **multivariate contrast** is given by

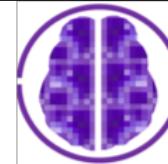
$$\mathbf{c} = \mathbf{L}\hat{\mathbf{B}}\mathbf{M}'$$

The **Between-subjects contrasts** gives the **L** matrix

The **Within-subject contrasts** gives the **M** matrix

Here the **interaction** is a combination of a **between-subject main effect** and a **within-subject main effect**





Practical

Repeated measurements analysis

Close the **contrast** windows and return to the **main window**

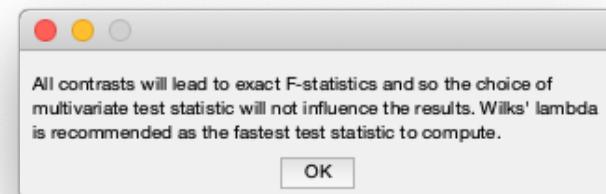


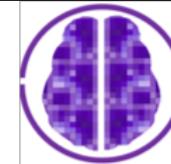
We have a choice of **4** multivariate test statistics to choose from — **Pillai's trace** is the default



Clicking on **Exact test** will tell you whether the **choice of statistic** will make **any difference** to the results

For this example, the choice **does not matter**





Practical

Repeated measurements analysis

The **Inference** section contains all the options for **levels of inference** and **multiple comparisons correct**

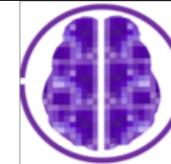
The screenshot shows the 'Inference' settings panel with the following configuration:

- Thresholding:** Voxel
- P-value calculation:** Permutation
- Correction method:** FWE
- No. permutations:** 5000
- Corrected P threshold:** 0.05
- Cluster-forming P:** 0.001

For **final results** you should be using **permutations** to calculate the *p*-values (minimum of 5,000) — ideally with **FWE** correction

For **initial results** you can use a **low number** of **permutations** (e.g. 1,000) or use the **approximate** *p*-values

To save time, we will use the **approximate** approach



Practical

Repeated measurements analysis

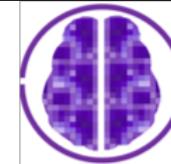
Change the **Thresholding** to **Uncorrected** and change the **P-value calculation** to **Approximate**

Inference		
Thresholding	P-value calculation	Correction method
Uncorrected	Approximate	FDR
No. permutations	1000	Uncorrected P threshold
	0.001	Cluster-forming P
	0.001	

This is the **most liberal** approach that **MRM** provides

We are using it because it is the **fastest** — generally this would **not** be a suitable approach

Useful as a quick **first look** at the data, but nothing more than that



Practical

Repeated measurements analysis

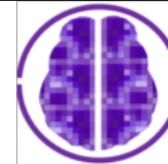
In the **Options** section we set where we want the results saved

We can also set an **analysis mask** to restrict the **voxels** that are analysed

Click ... next to the **Output directory** and select the **RepeatedMeasures** folder from inside the **MRMdemo** folder

Add a folder named **Results** to the end of the path (this will be created by MRM)

The image shows a software interface for setting options. At the top left is a label 'Options'. Below it is a 'Output directory:' label followed by a text input field containing the path '/.../MRMdemo/RepeatedMeasures/Results'. To the right of the input field is a small button with three dots (...). Below this is a 'Mask:' label followed by an empty text input field and another button with three dots (...).



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Repeated measurements analysis

The model is now ready to be **estimated**

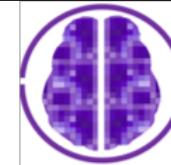
All the **options** will be saved into an **MRM.mat** file which you can use to **reload** the **model specification** (can also save this separately)



When you are ready, click **Estimate** and wait for **MRM** to finish

```
Command Window
Initialising files ...

=====
Model estimation
=====
Estimating parameters and saving images for DV 1 slice 52/52
Estimating parameters and saving images for DV 2 slice 52/52
Estimating parameters and saving images for DV 3 slice 52/52
Estimating and writing covariance structure for slice 52/52
Saving design images ...
```



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Repeated measurements analysis

Once the **model** and the **contrasts** have been estimated, all the output files will be saved in the **Results** folder

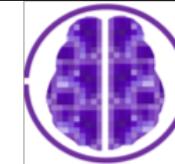


This folder contains **pictures** of the **design** and the model **orthogonality**

This folder also contains all the **parameter estimate** and **covariance matrix** images

- The numbers are given as **matrix indices** e.g.
MRM_PE_2_3.nii means **row 2 column 3**

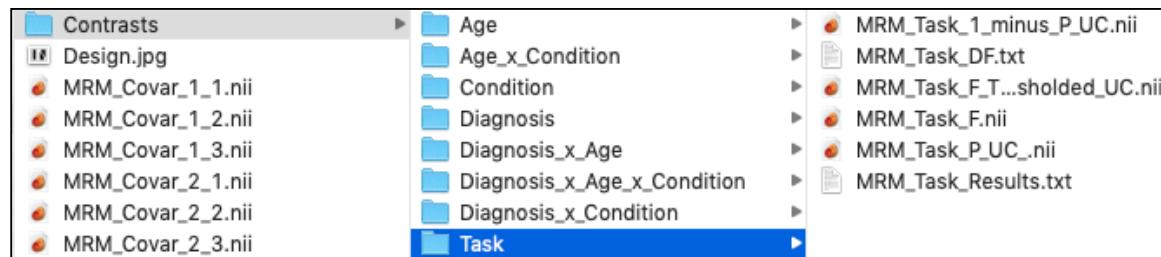
The **MRM.mat** file can be used to **reload** the **model specification** in the interface



Practical

Repeated measurements analysis

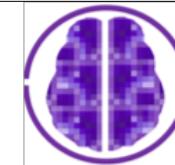
Inside the **Contrasts** folder are **sub-folders** for each of the contrasts we specified



Each **sub-folder** contains

- **Thresholded** and **un-thresholded** images of the **F-statistics**
- Images of the **p-values** and **1-p** (useful for visualising)
- The **degrees of freedom**
- The **results table** as a **text file**

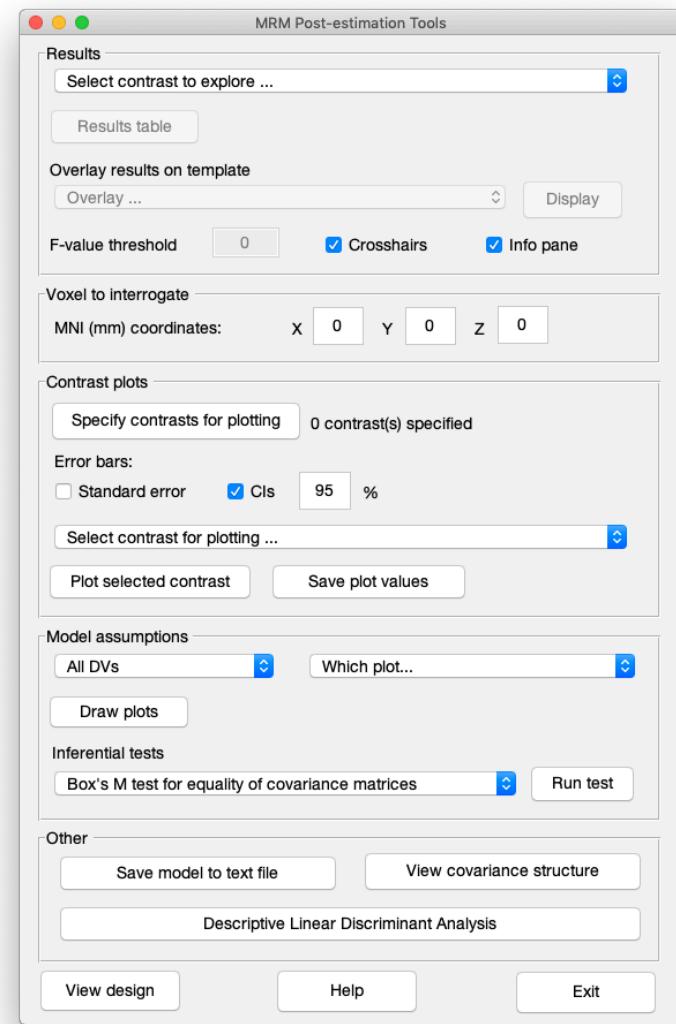
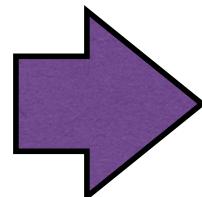
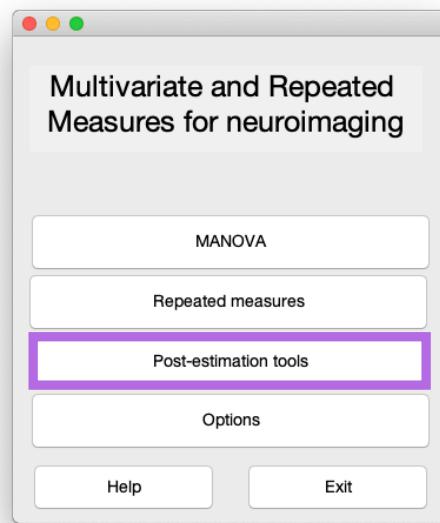
The content will differ depending on the **thresholding options** chosen

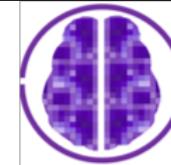


Practical

Repeated measurements analysis

To examine the results **interactively** click the **Post-estimation tools** button and select the **MRM.mat** file from the **Results** folder

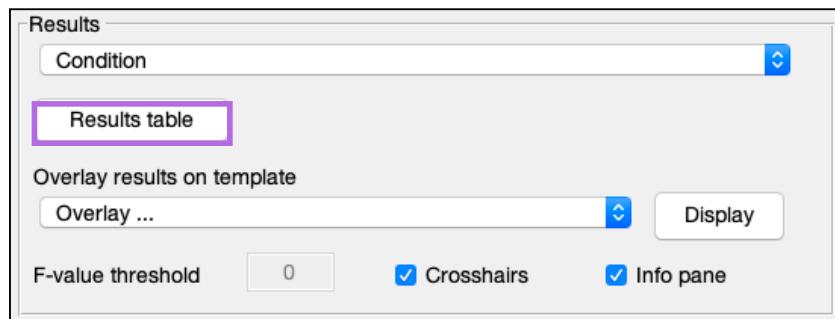




Practical

Repeated measurements analysis

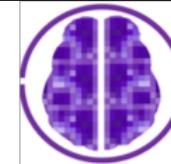
We can **explore** the results of a contrast by **selecting** it from the **drop-down menu** at the top of the window



For example, select the **Condition** contrast from the menu and then click **Results table**

Region	Cluster	Extent	F-value	Uncorrected p-value (voxel)	X	Y	Z
Declive R	1	78	18.012	< 0.001	9	-73	-28
Tuber R	1	78	8.676	0.001	27	-76	-37
Culmen R	2	13	10.099	< 0.001	27	-64	-34
Middle Temporal Gyrus R	3	1	8.098	0.001	45	-1	-34
L	4	4	8.660	0.001	-18	-16	-25
Inferior Frontal Gyrus L	5	559	35.824	< 0.001	-51	29	5
Sub-Gyral L	5	559	34.608	< 0.001	-39	17	23
Inferior Frontal Gyrus BA45...	5	559	31.348	< 0.001	-54	26	8
Inferior Frontal Gyrus L	5	559	26.052	< 0.001	-51	26	-4
Inferior Frontal Gyrus L	5	559	26.037	< 0.001	-48	23	-7
Insula L	5	559	13.647	< 0.001	-30	20	5
Insula BA13 L	5	559	12.157	< 0.001	-39	17	2
Middle Frontal Gyrus L	5	559	11.327	< 0.001	-42	5	44
Sub-Gyral L	5	559	10.091	< 0.001	-33	29	-1
Superior Temporal Gyrus L	6	12.200	< 0.001		51	11	16

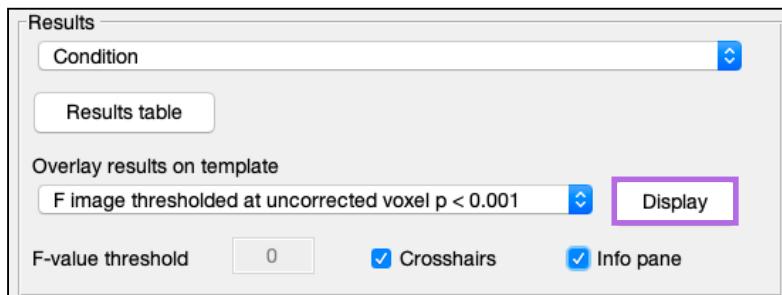
This will give the table of **peak voxels** within **each cluster of results**



Practical

Repeated measurements analysis

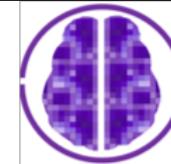
You can now select **F image thresholded...** from the **Overlay...** drop-down menu and click **Display**



You can **click** in the image and use the **Tools** menu to navigate

You can also click the **rows** of the **results table** to update the **crosshair** location

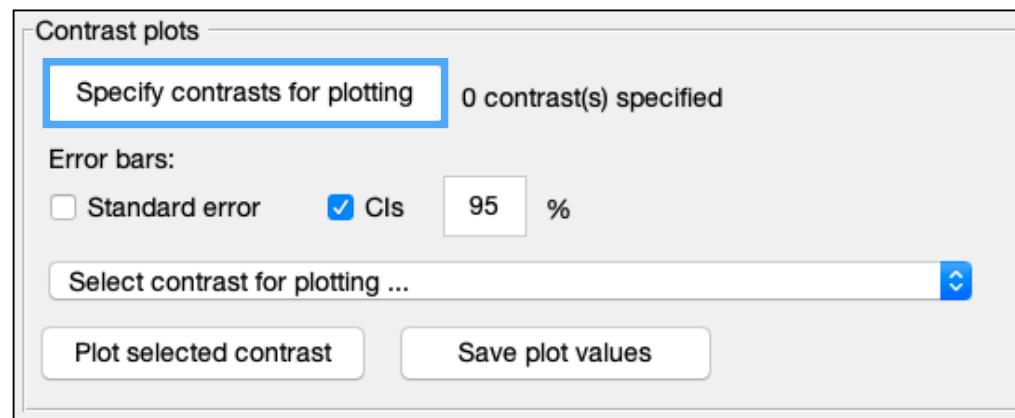




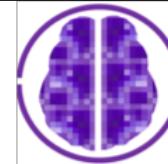
Practical

Repeated measurements analysis

To **plots** results at a single voxel we use a similar scheme to **SPM** where you use a **contrast** to define the values to plot



For example, select the **peak voxel** for the **Condition** contrast (**Tools** ▶ **Go to global maximum** in the viewer window) and click the **Specify contrasts for plotting** button



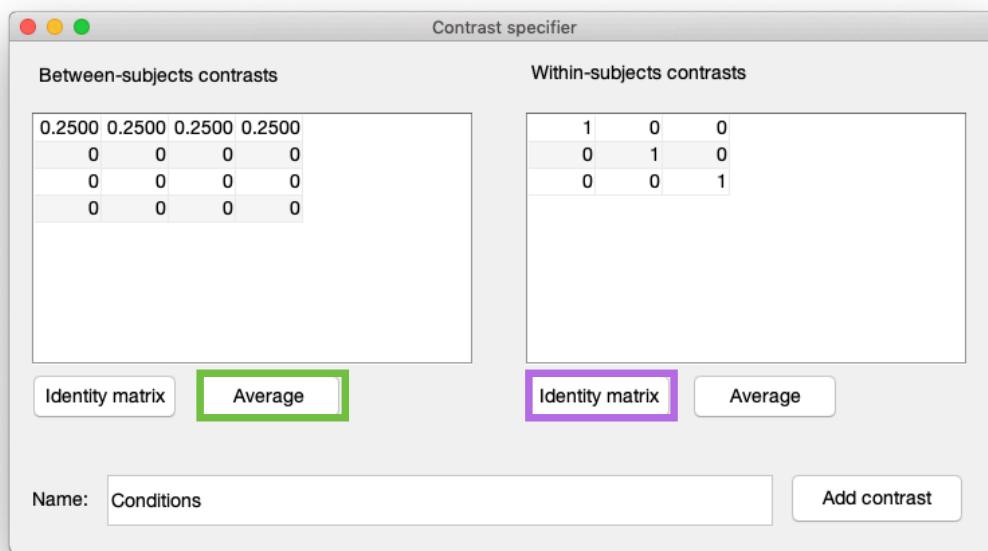
Practical

Repeated measurements analysis

This will open a **similar** contrast list to the **model specification** tool

Click **New** to open the **Contrast specifier**

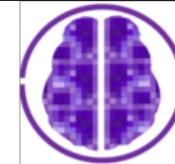
Click the **Average** button for the **Between-subjects contrasts** and the **Identity...** button for the **Within-subject contrasts**



This will plot **each** within-subject cell, **averaged over** the between-subject cells

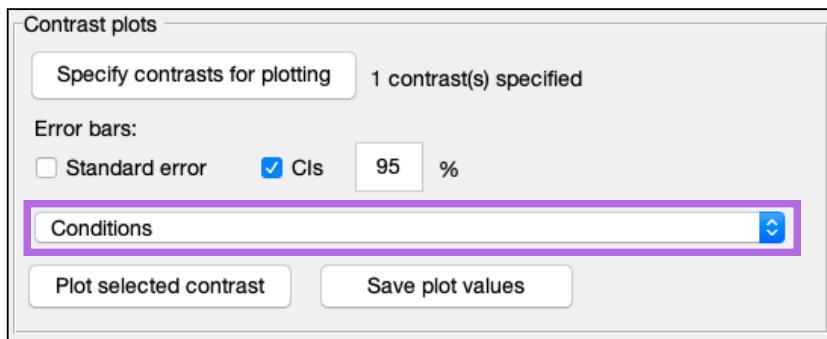
Call this **Conditions** and click **Add contrast**

Close the **contrasts list**



Practical

Repeated measurements analysis

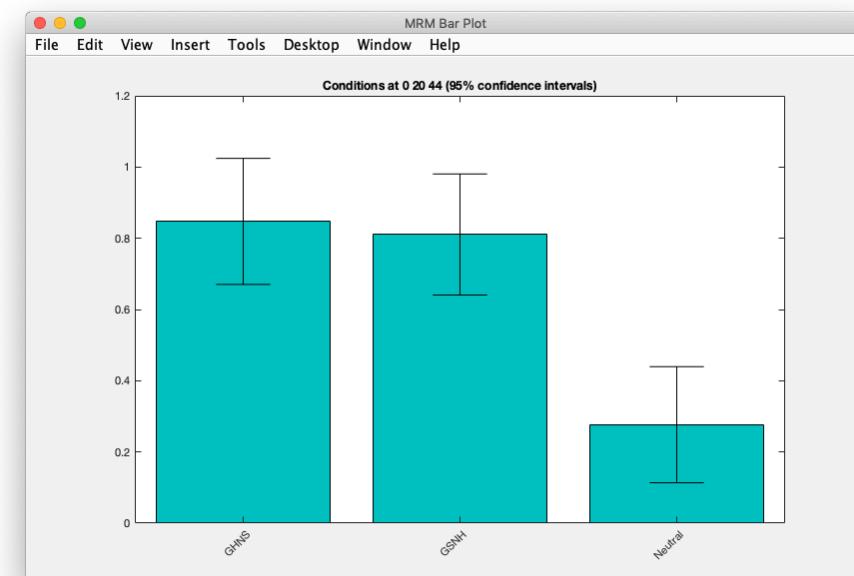


The **Conditions** contrast should now be available in the **menu**

Click **Plot selected contrast**

A bar plot of the **parameter estimates** for the **3 conditions** should now appear

This will **update** as you click around in the **results image** and when you select **rows** in the **results table**

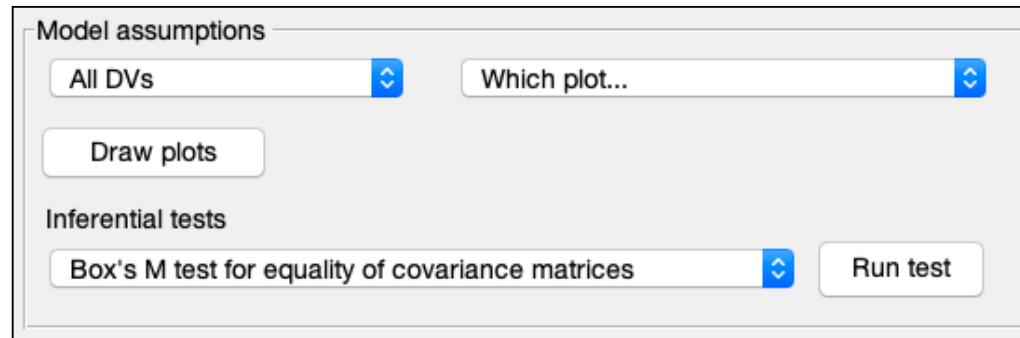




Practical

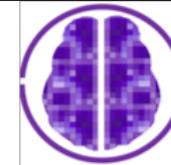
Repeated measurements analysis

MRM also has facilities for assessing the **model assumptions** for **peak voxels of interest**



The multivariate GLM has **two** core assumptions that we assess in a variety of ways:

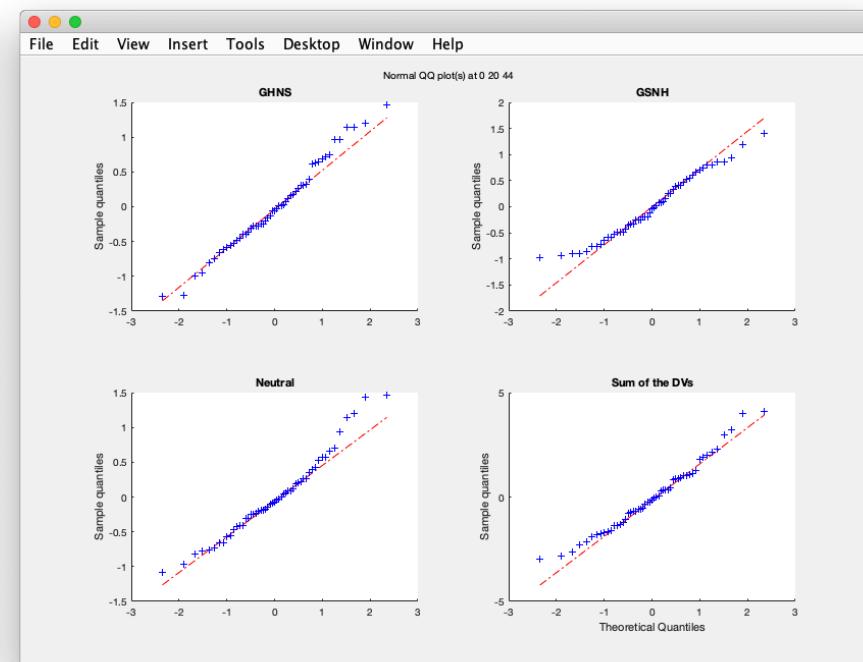
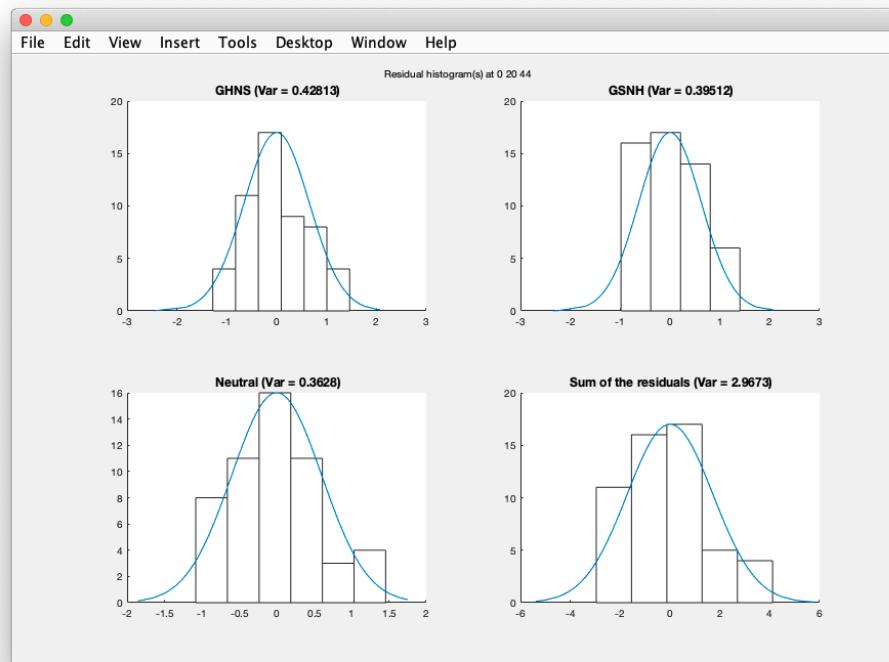
- Multivariate normality of the residuals
- Equality of the variance-covariance matrix across groups

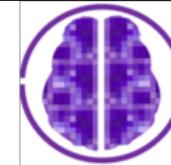


Practical

Repeated measurements analysis

Multivariate normality can be assessed with the **residual histograms** and **QQ-plots**

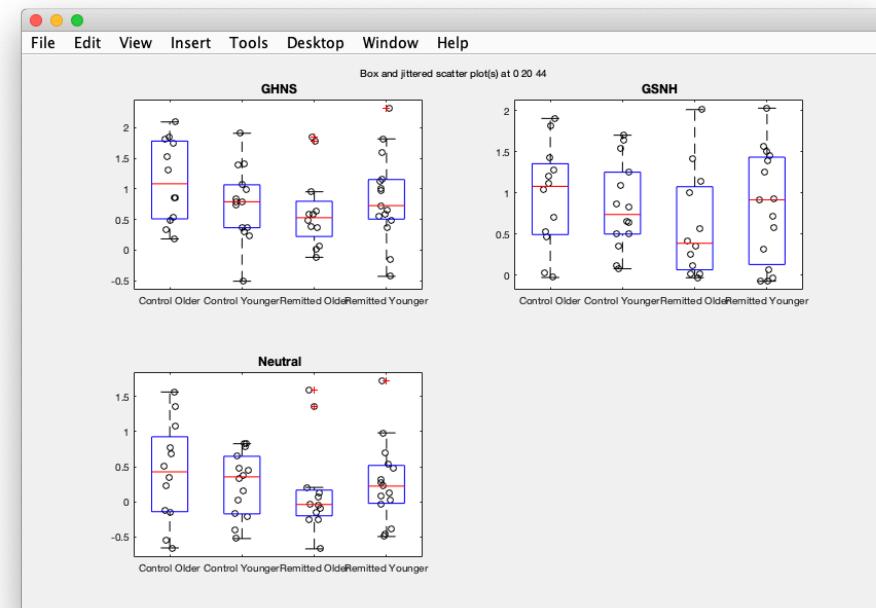
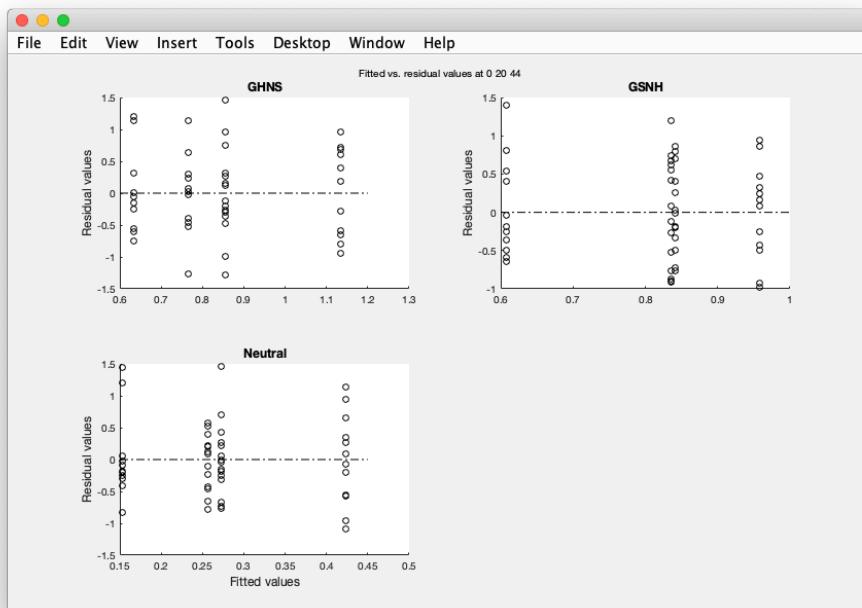


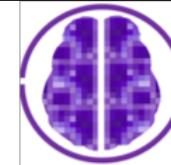


Practical

Repeated measurements analysis

Homogeneity of variance can be assessed using the **fitted vs residuals** and **box plots**

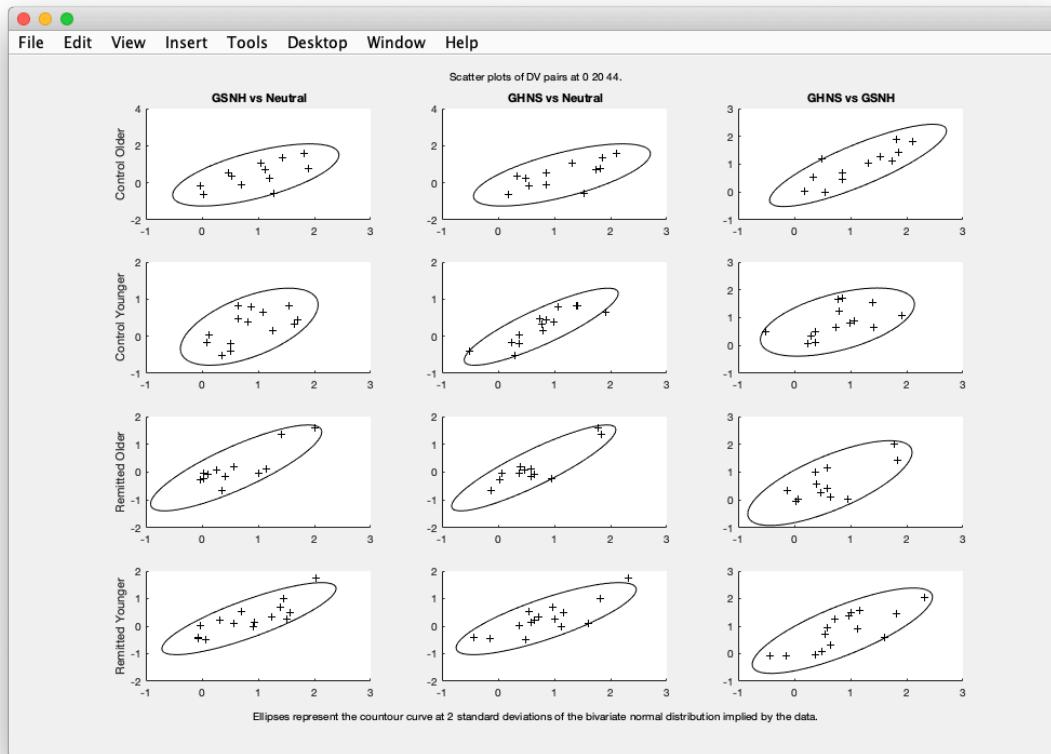




Practical

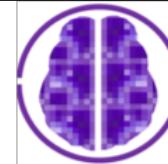
Repeated measurements analysis

Homogeneity of covariance can be assessed using the **DV pairs** plot



The **rows of each column** should look **roughly similar**

Demonstrates that the **correlation** between the **dependent variables** is roughly equivalent across the **between-subject** cells



Practical

Repeated measurements analysis

Assumptions about the **covariance structure** can also be assessed **inferentially**

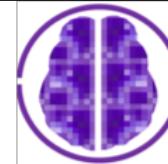
Inferential tests

Box's M test for equality of covariance matrices

Results are returned in the **main MATLAB window**

```
Box's M Test for equality of covariance matrices
-----
Results for voxel: 0 20 44
    Box's M |      F |      df1 |      df2 |      p-value
    18.2976 | 0.900485 |      18 | 7809.96 | 0.577998
Tests the null hypothesis that the population covariance
matrices are equal across the cells of the design.

NOTE: This test can be notoriously sensitive to departures
from normality. It is also usual to evaluate the test at
an alpha of 0.001.
```



Practical

Repeated measurements analysis

Assumptions about the **covariance structure** can also be assessed **inferentially**

Inferential tests

Levene's test for homogeneity of variance

Results are returned in the **main MATLAB window**

```
Levene's test for equality of variance
-----
Results for voxel: 0 20 44
    F |      df1 |      df2 |      p-value
GHNS | 0.463174 |      3 |      49 | 0.709285
GSNH | 0.473083 |      3 |      49 | 0.702442
Neutral | 0.652895 |      3 |      49 | 0.58497
Tests the null hypothesis that the population variances are equal
across the cells of the design for each DV.
NOTE: This test uses the mean as the center of each group, and so
can be sensitive to outliers. It is also usual to evaluate the
test at an alpha of 0.001.
```



Practical

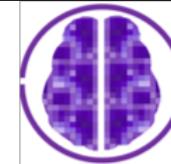
Repeated measurements analysis

If **assumptions are violated**:

- **Multivariate normality** — use **permutation tests** as these do not depend on the distribution
- **Equality of variance/covariance** — use **Pillai's trace** as it is the **more conservative** test statistic

Best to run these tests on **peak voxels** in regions you are interested in — obviously can't be run at **every** voxel but checking a **few** is a good idea to give **confidence** to your findings

Plots work well for **small numbers** of DVs, but soon get out of hand for more than **4-5**



Practical

Repeated measurements analysis

There a few other things you can do with the **Post-estimation tools**

Save model to text file

Save the **raw data, fitted values** and **residuals** for the current voxel to a **text file**

Specify the **exact coordinates** of the voxel of interest

Voxel to interrogate
MNI (mm) coordinates: X 0 Y 20 Z 44

View covariance structure

Visualise the **estimated covariance structure** at the current voxel

Overlay results on template

Unthresholded F image

Display

F-value threshold

5

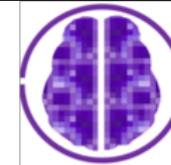
Crosshairs

Info pane

Manually **threshold** the image and switch **on/off** the **crosshairs** and **info display**



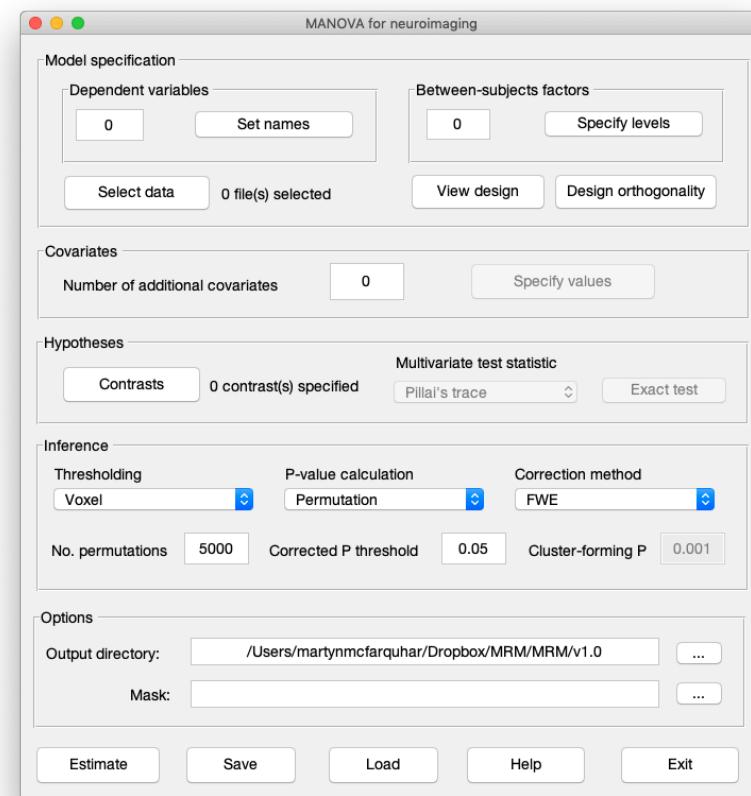
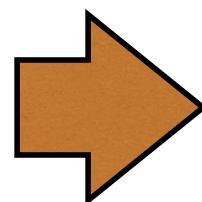
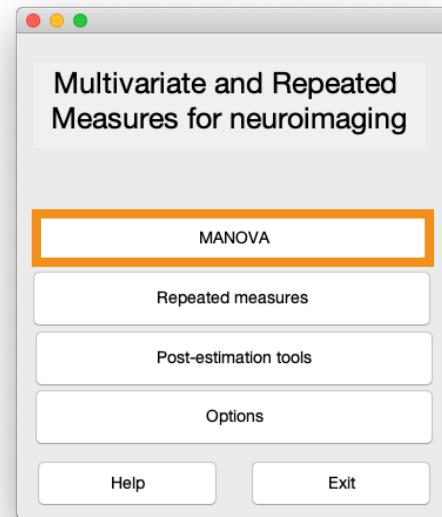
Multi-modal analysis

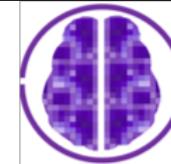


Practical

Multi-modal analysis

To analyse the **multi-modal** dataset, click the **MANOVA** button





Practical

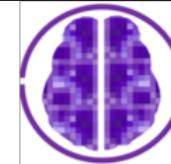
Multi-modal analysis

Model specification is **very similar** to the **repeated measurements** model

The screenshot shows a software interface for model specification. It has two main sections: 'Dependent variables' and 'Between-subjects factors'. In the 'Dependent variables' section, there is a text input field containing '0' and a button labeled 'Set names'. Below these are buttons for 'Select data' and 'View design'. A status message indicates '0 file(s) selected'. In the 'Between-subjects factors' section, there is a text input field containing '0' and a button labeled 'Specify levels'. Below these are buttons for 'Design orthogonality'.

The main difference is that we specify the number of **dependent variables**, rather than **within-subject factors**

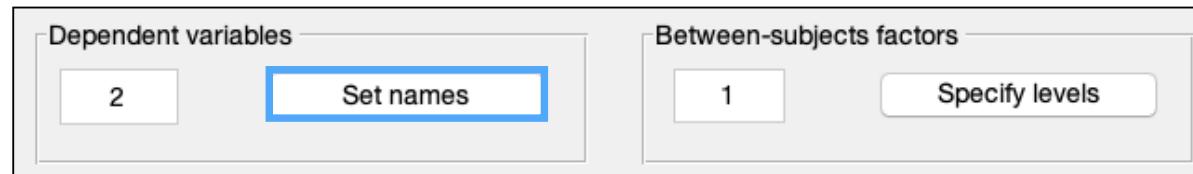
The number of **dependent variables** can be set to **1** for a **traditional univariate analysis** with **permutation tests**



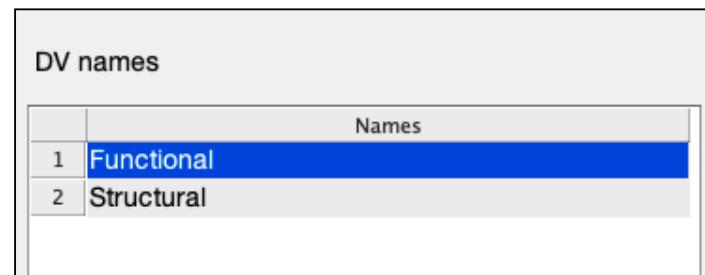
Practical

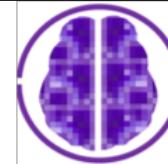
Multi-modal analysis

Change the **number** of **dependent variables** to **2** and change the **number** of **between-subject factors** to **1**



Click the **Set names** button and call the dependent variables **Functional** and **Structural**





Practical

Multi-modal analysis

Click the **Specify levels** button and call the factor **Diagnosis** with **2** levels called **Controls** and **Remitted**

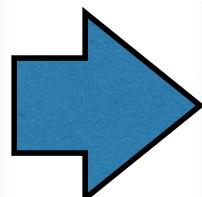
Dependent variables	
2	Set names
Between-subjects factors	
1	Specify levels

Between-subjects factor specification

	Factor name	Levels
1	Diagnosis	2

Set labels for selected factor

Done

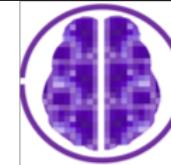


Level labels

Labels for levels of Diagnosis

	Labels
1	Controls
2	Remitted

Done

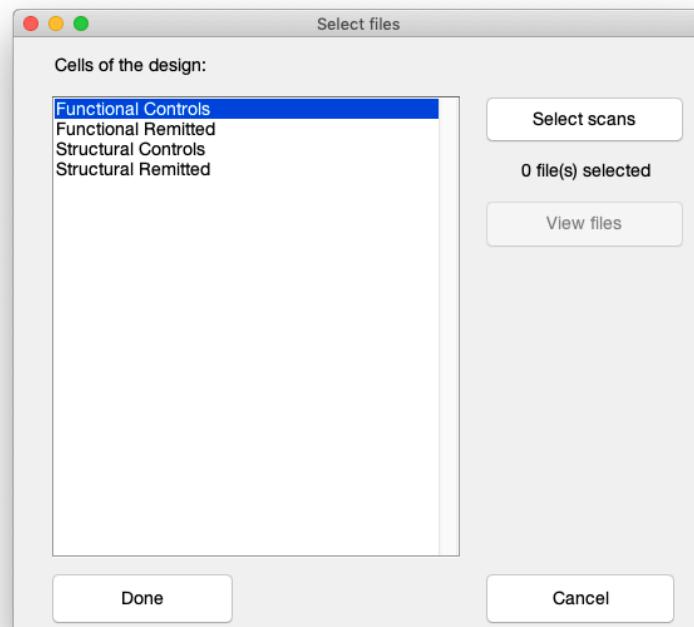


Practical

Multi-modal analysis

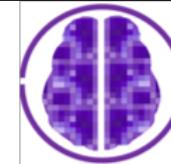


Click **Select data** on the main window



As with the **repeated measures** model, we need to work through **each cell** of the design, selecting all the appropriate scans

The scans in **MRMdemo/Multimodal/** have been organised **in this order**, so **select them all** as we did previously



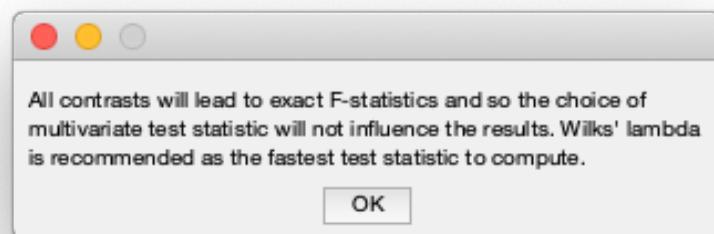
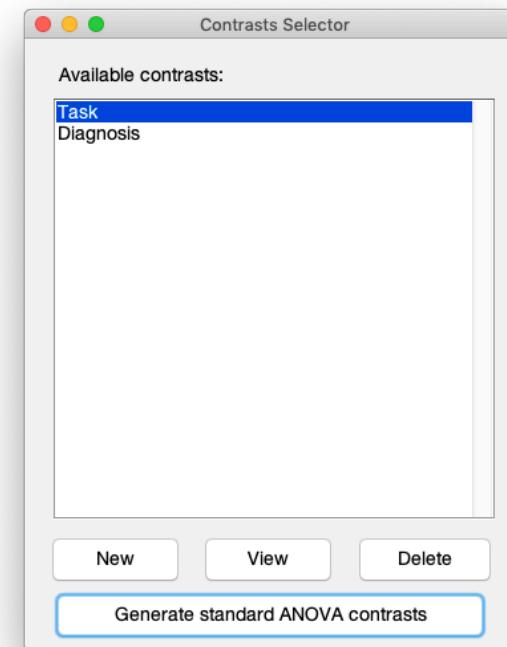
Practical

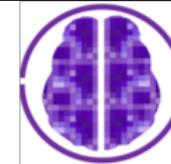
Multi-modal analysis

Once you have finished, click **Done** on the **Select files** window and the main window should **update** to show that **56 files** have been selected



Contrasts can again be automatically generated and are still **exact**, meaning we don't need to worry about the choice of **multivariate test statistic**





Practical

Multi-modal analysis

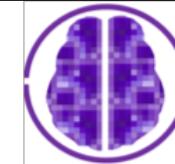
For the **thresholding** we will again choose **Uncorrected** with **Approximate** p -value calculation and a threshold of $p < 0.001$

Inference
Thresholding: Uncorrected
P-value calculation: Approximate
Correction method: FDR
No. permutations: 1000
Uncorrected P threshold: 0.001
Cluster-forming P: 0.001

Again, this is for the sake of **speed** and **not accuracy**

Specify an **Output directory** inside the **MRMdemo/Multimodal/** folder and the model setup should be complete

Output directory:	/.../MRMdemo/Multimodal/Results	...
-------------------	---------------------------------	-----



Practical

Multi-modal analysis

Your model specification should now look like this:

With **structural** images, a **grey matter mask** can be a good idea
(we will skip that step)

Click **Estimate** and wait for
MRM to finish

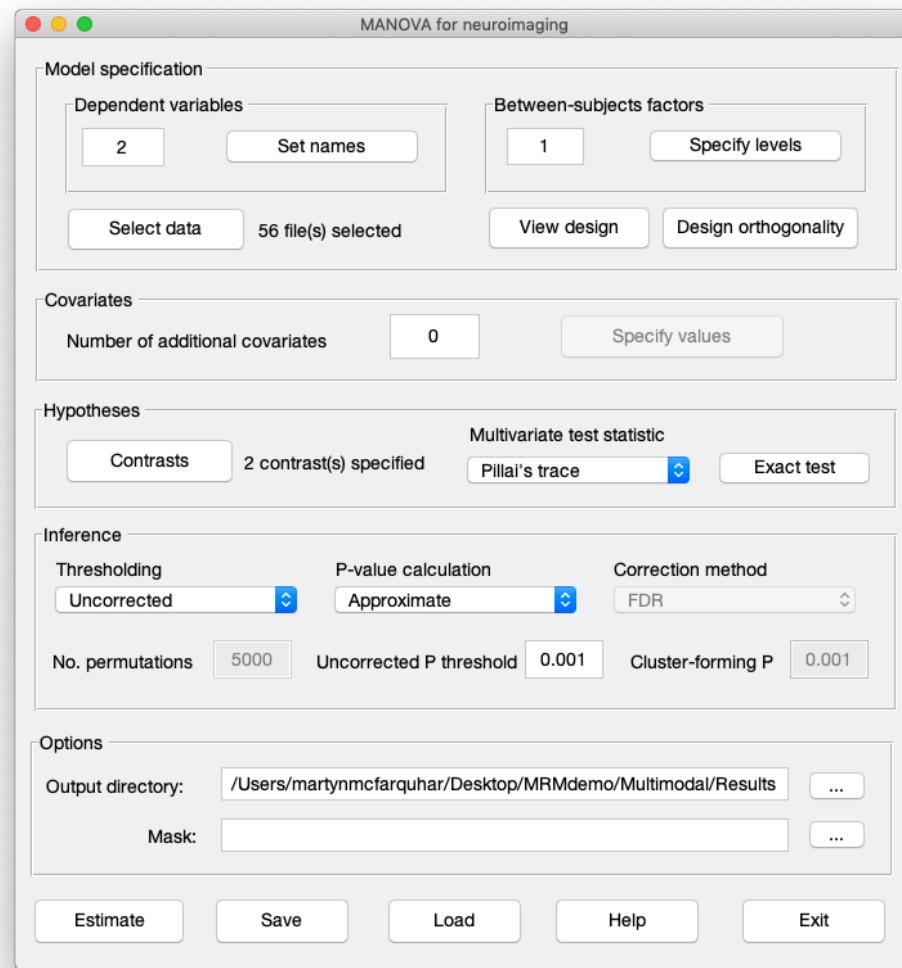
Initialising files ...

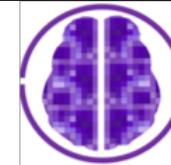
=====
Model estimation
=====

Estimating parameters and saving images for DV 1 slice 52/52
Estimating parameters and saving images for DV 2 slice 52/52

Estimating and writing covariance structure for slice 52/52

Saving design images ...

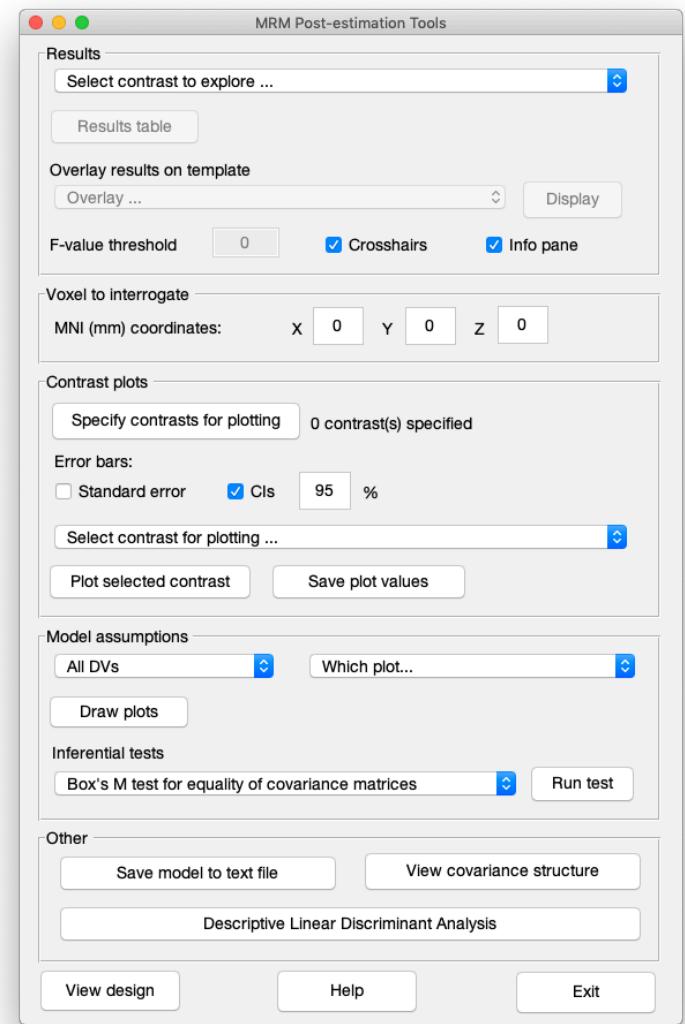
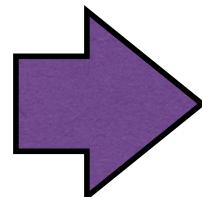
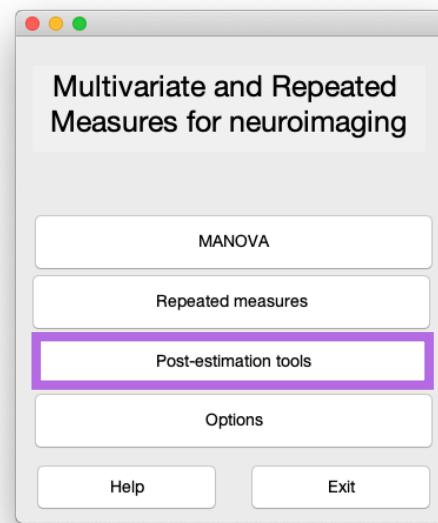


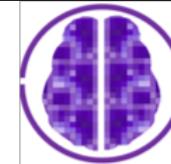


Practical

Multi-modal analysis

To examine the results **interactively** click the **Post-estimation tools** button and select the **MRM.mat** file from the **Results** folder

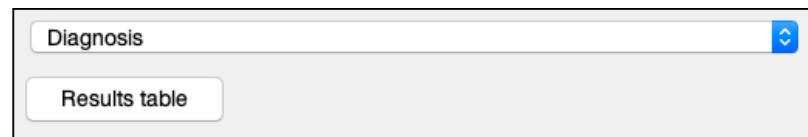




Practical

Multi-modal analysis

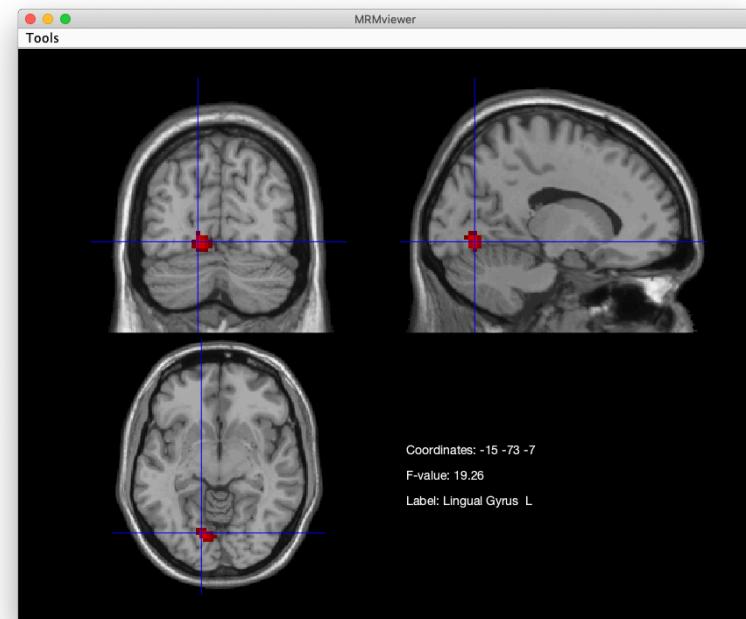
The **Task** contrast is not very useful (the **whole brain** will be **significant**) so select the **Diagnosis** contrast from the **menu**

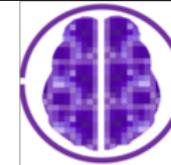


We shall explore the **peak voxel** from the **Lingual Gyrus** cluster

Results Table

Region	Cluster	Extent	F-value	Uncorrected p-value (voxel)	X	Y	Z
Declive L	1	5	10.430	0.001	-27	-67	-19
Lingual Gyrus L	2	48	19.260	< 0.001	-15	-73	-7
Extra-Nuclear R	3	1	9.667	0.001	18	-10	-1
Precentral Gyrus R	4	1	9.273	0.001	33	14	38





Practical

Multi-modal analysis

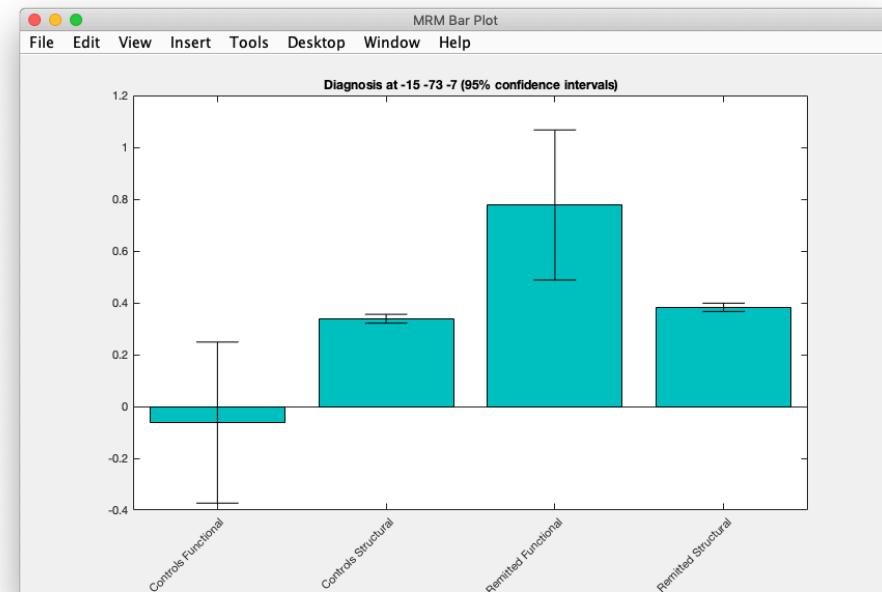
We can use the **plot** tools to get some idea about what is going on

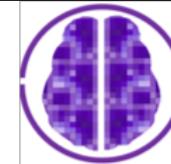
Specify the following **plotting contrast**

The plot of the **peak voxel** suggests that **Remitted > Controls** in **both modalities**

Because these are on **different scales** the effects are **difficult to see**

Between-subjects contrasts		Within-subject contrasts	
1	0	1	0
0	1	0	1



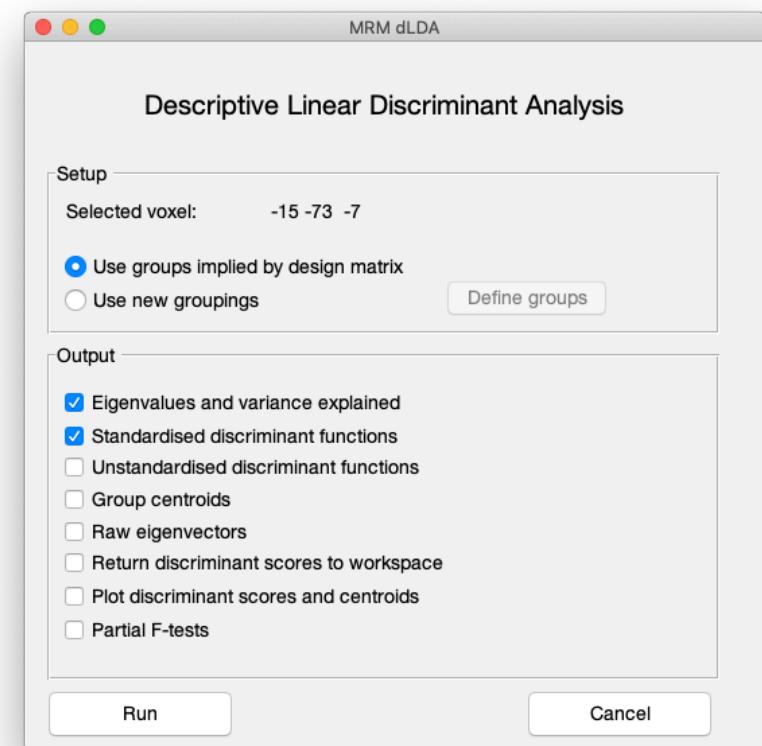
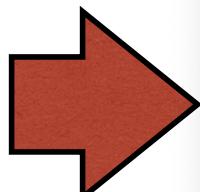
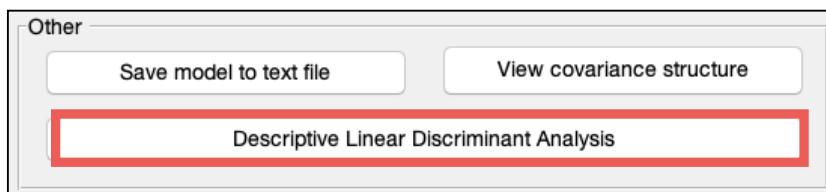


Practical

Multi-modal analysis

To make things **clearer** we can use **Descriptive Linear Discriminant Analysis** (dLDA)

Click the **Descriptive Linear Discriminant Analysis** button to launch the **dLDA tool**



Make sure that the **selected voxel** matches the **peak voxel of interest**

Practical

Multi-modal analysis

Variety of options available here

Output

- Eigenvalues and variance explained
- Standardised discriminant functions
- Unstandardised discriminant functions
- Group centroids
- Raw eigenvectors
- Return discriminant scores to workspace
- Plot discriminant scores and centroids
- Partial F-tests

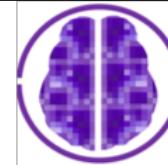
Most useful for this example is the **Partial F-tests** option

Note that you need a **minimum** of **2** discriminant functions to produce the **plots**

The **Use new groupings** options is useful for exploring a **main effect** in a model containing **interactions** — by default dLDA will be performed on **all the cells of the design**

Use groups implied by design matrix
 Use new groupings

Define groups



Practical

Multi-modal analysis

The **dLDA** results will be returned in the **MATLAB** window

Descriptive Linear Discriminant Analysis						
Results for voxel: -15 -73 -7						
Eigenvalues and variance explained						
Eigenvalues	Variance %	F	df1	df2	p	
1.5408	100	19.26	2	25	8.66711e-06	
Standardised discriminant functions						
	Function 1					
Functional	0.850116					
Structural	0.825928					
Partial F-tests for the dependent variables						
	F	df1	df2		p	
Functional	16.7943	1	25	0.000384976		
Structural	15.2766	1	25	0.000626419		

As there is only one function, 100% of the variance is explained

Equivalent weights suggest an almost equal balance of functional and structural group differences leading to the multivariate effect

As both partial F-tests are significant, we can conclude that both modalities are significantly contributing to the group difference