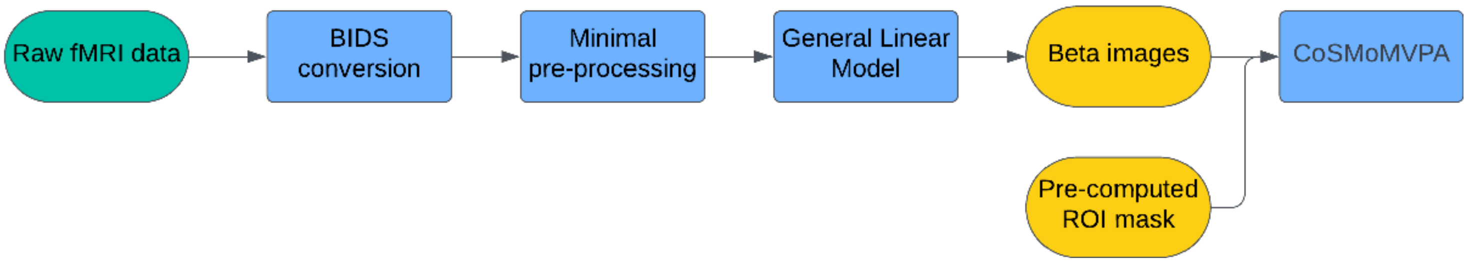
CoSMoMVPA Code Example

Overview

This tutorial shows how to use CoSMoMVPA for Multivariate Pattern Analysis (MVPA) and Representational Similarity Analysis (RSA) in fMRI research. It assumes that you understand basic fMRI concepts and want to learn how to go from raw data to advanced analyses that reveal the structure of neural representations.

Typical Pipeline for Real fMRI Data:



1. **Data Acquisition**: Collect fMRI data as participants perform tasks or view stimuli from different categories.
2. **BIDS Conversion**: Convert raw data into the Brain Imaging Data Structure (BIDS) format. This standardization makes subsequent preprocessing and analysis much easier.
3. **Preprocessing (fMRIPrep)**: Use *minimal* preprocessing to preserve fine-grained voxel-level patterns. fMRIPrep performs standardized alignment and normalization without over-smoothing or aggressive denoising, both of which can destroy subtle patterns critical for MVPA.
4. **GLM Estimation (SPM)**: Fit a General Linear Model to the data, producing:

- **Beta images**: One per condition (category) and run.
- **SPM.mat**: Contains the experiment design and regression coefficients.

Defining Regions of Interest (ROIs):

Use anatomical or functional Regions of Interest (ROI) masks to focus on specific brain regions. Because Linear classifiers struggle with high-dimensional data -- particularly when the number of features (voxels) are significantly higher than the number of observations (beta images), which is often the case with fMRI data --, restricting MVPA analyses on smaller ROIs is generally a good practice.

Here, we focus on

- **IT (Inferotemporal Cortex)**: Associated with more abstract, categorical-level representations.
- **V1 (Primary Visual Cortex)**: Associated with low-level, perceptual representations.

Purpose of This Tutorial

In this example, we will investigate the representational structure of **simulated synthetic data.** We will illustrate the (few) steps required to perform a multi-variate analysis on post GLM data (i.e., beta images produces by SPM).

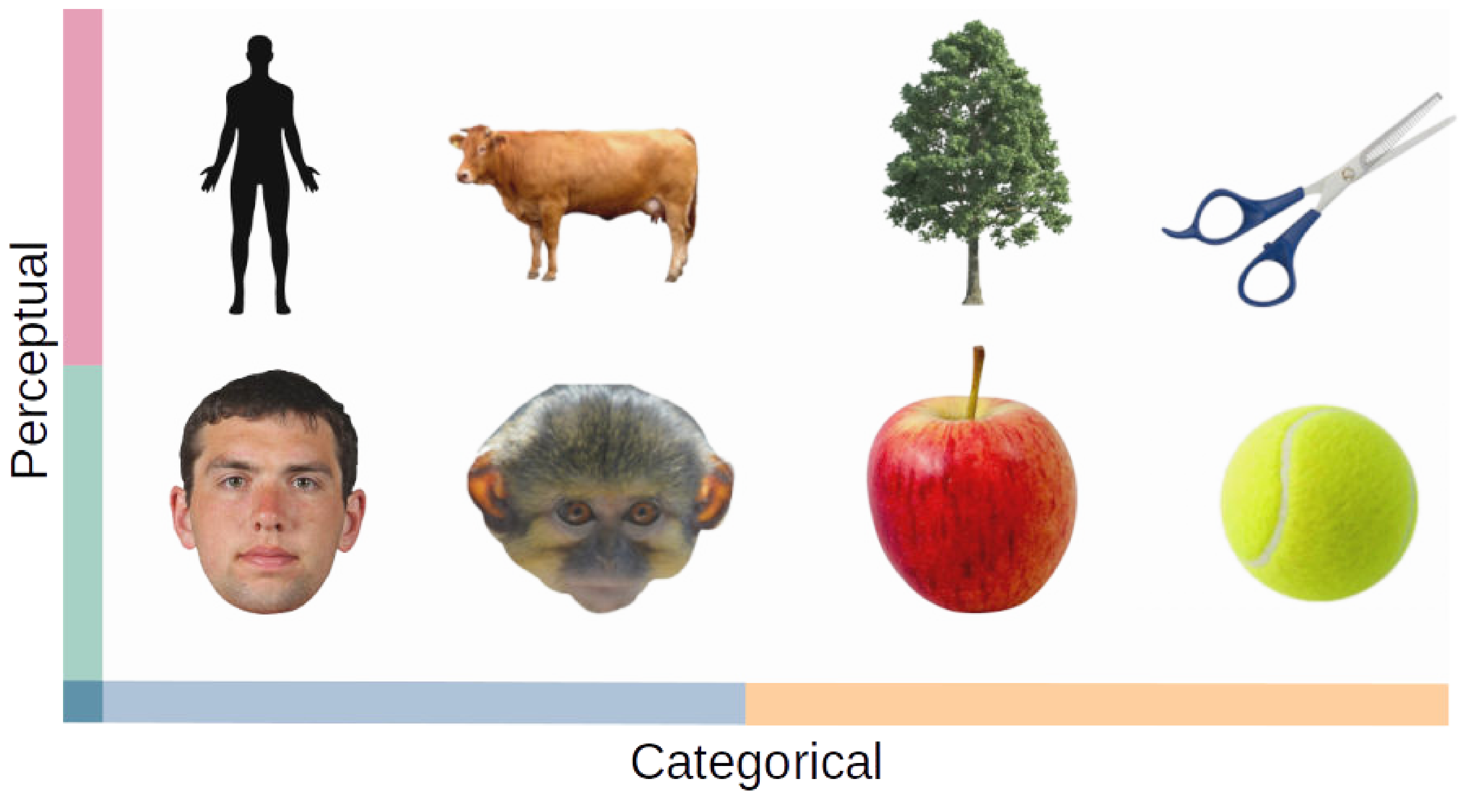
The goal is to investigate the representational geometry of two ROIs, V1 and IT, to determine what properties of the stimuli are represented in these areas.

What We Will Do:

- Generate synthetic fMRI-like data simulating responses in IT or V1.
- Perform MVPA (decoding) to see if the ROI can distinguish between multiple categories above chance.
- Conduct RSA to compare the observed representational geometry with theoretical model RDMs, revealing whether perceptual or categorical features dominate the neural patterns.

Data Structure (Synthetic):

- **Subject(s)**: 1
- **Runs**: 10 runs/subject
- **Categories** (8 total): Human face, Human body, Animal face, Animal body, Natural round object, Natural spiky object, Artificial round object, Artificial spiky object



Hypothesis:

- **V1**: Similarities based on low-level perceptual features (e.g., round vs. spiky).
- **IT**: Similarities based on higher-level conceptual distinctions (e.g., human vs. animal, animate vs. inanimate, natural vs. artificial).

Code:

Setup

We set up the MATLAB environment, ensuring reproducibility and proper paths.

```
% Clear workspace, close figures, and reset command window
clear all;
close all;
clc;

% Set random seed for reproducibility
seed = 42;
rng(seed);

% Add paths to required functions
addpath("functions/");
outDir = fullfile(pwd, "results");
```

(Optional) Loading Real Data from SPM

If we had real data, after preprocessing and GLM estimation, we could load it like this:

```
% % Example (not run here):
% spm_path = 'path_to_SPM.mat';
% mask_path = 'path_to_ROI_mask.nii';
% ds = cosmo_fmri_dataset(spm_path, 'mask', mask_path);
```

For this tutorial, we are skipping this step because we use synthetic data.

Synthetic Data Generation

We now generate synthetic data that mimics patterns in IT or V1. You can switch `roiName` between `"V1"` and `"IT"`.

Key Parameters:

- **numCategories** = 8
- **numRuns** = 10
- **numSubjects** = 1
- **numRepetitions** = 1
- **sigma**: Controls data variability.

```
% Parameters for synthetic data generation
numCategories = 8;
numRuns = 10;
numSubjects = 1;
numRepetitions = 1;
size = "normal";
```

```
% Choose ROI
roiName = "IT";  % For abstract, categorical representations
% roiName = "V1"; % For low-level, perceptual representations

sigma = 0.6; % Data variability

% Generate synthetic dataset
ds = generate_clustered_dataset(numCategories, numSubjects, numRuns, ...
    numRepetitions, sigma, seed, roiName, size);
```

```
Generated dataset with the following clusters:
Cluster 1: Animate
  Targets: [1  2  3  4]
  Sigma Level: 0.70

Cluster 2: Humans
  Targets: [1  2]
  Sigma Level: 0.20

Cluster 3: Animals
  Targets: [3  4]
  Sigma Level: 0.20

Cluster 4: Natural
  Targets: [5  6]
  Sigma Level: 0.70

Cluster 5: Artificial
  Targets: [7  8]
  Sigma Level: 0.60
```

Inspecting the Data

Before proceeding, let’s inspect the generated dataset:

- **Target-to-Label Mapping**: Understand which category corresponds to which integer label.
- **Activation Heatmap**: Visualize category-specific activity patterns.

```
% Extract and display unique labels
labelNames = unique(ds.sa.labels, 'stable');
disp('Target to Label Mapping:');
```

```
Target to Label Mapping:
```

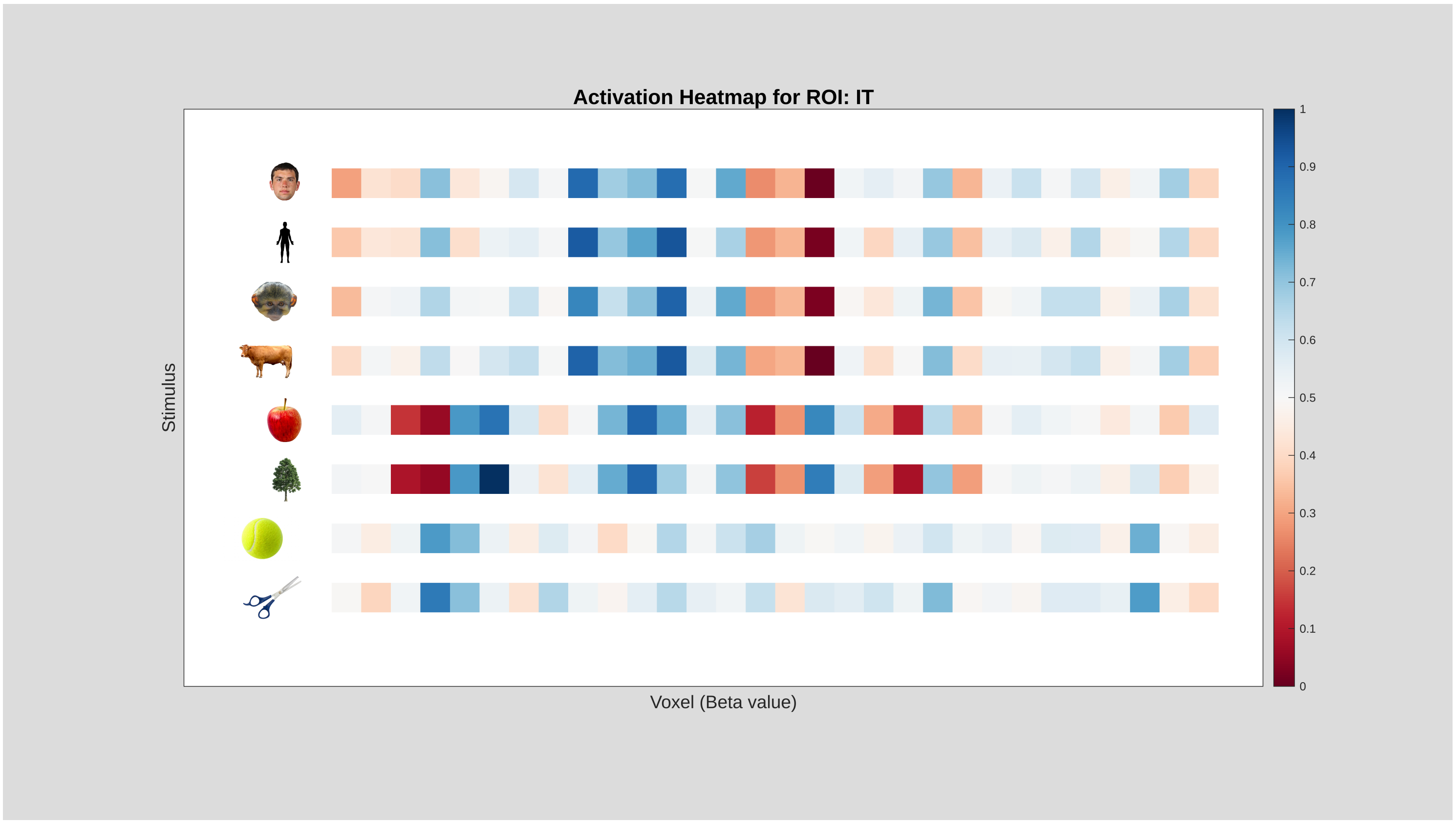
```
disp(table(ds.sa.targets, ds.sa.labels));
```

```
    Var1           Var2
    ____    __________________

     1      {'human face'     }
     2      {'human body'     }
     3      {'animal face'    }
     4      {'animal body'    }
     5      {'natural round'  }
     6      {'natural spiky'  }
     7      {'artificial round'}
```

```
8      {'artificial spiky'}
1      {'human face'      }
2      {'human body'      }
3      {'animal face'     }
4      {'animal body'     }
5      {'natural round'   }
6      {'natural spiky'   }
7      {'artificial round'}
8      {'artificial spiky'}
1      {'human face'      }
2      {'human body'      }
3      {'animal face'     }
4      {'animal body'     }
5      {'natural round'   }
6      {'natural spiky'   }
7      {'artificial round'}
8      {'artificial spiky'}
1      {'human face'      }
2      {'human body'      }
3      {'animal face'     }
4      {'animal body'     }
5      {'natural round'   }
6      {'natural spiky'   }
7      {'artificial round'}
8      {'artificial spiky'}
1      {'human face'      }
2      {'human body'      }
3      {'animal face'     }
4      {'animal body'     }
5      {'natural round'   }
6      {'natural spiky'   }
7      {'artificial round'}
8      {'artificial spiky'}
1      {'human face'      }
2      {'human body'      }
3      {'animal face'     }
4      {'animal body'     }
5      {'natural round'   }
6      {'natural spiky'   }
7      {'artificial round'}
8      {'artificial spiky'}
1      {'human face'      }
2      {'human body'      }
3      {'animal face'     }
4      {'animal body'     }
5      {'natural round'   }
6      {'natural spiky'   }
7      {'artificial round'}
8      {'artificial spiky'}
1      {'human face'      }
2      {'human body'      }
3      {'animal face'     }
4      {'animal body'     }
5      {'natural round'   }
6      {'natural spiky'   }
7      {'artificial round'}
8      {'artificial spiky'}
1      {'human face'      }
2      {'human body'      }
3      {'animal face'     }
4      {'animal body'     }
5      {'natural round'   }
6      {'natural spiky'   }
7      {'artificial round'}
```

```
       8       {'artificial spiky'}
       1       {'human face'      }
       2       {'human body'      }
       3       {'animal face'     }
       4       {'animal body'     }
       5       {'natural round'   }
       6       {'natural spiky'   }
       7       {'artificial round'}
       8       {'artificial spiky'}
```

```
% Plot activation patterns
plot_activation_heatmap(ds, labelNames, roiName, outDir);
```



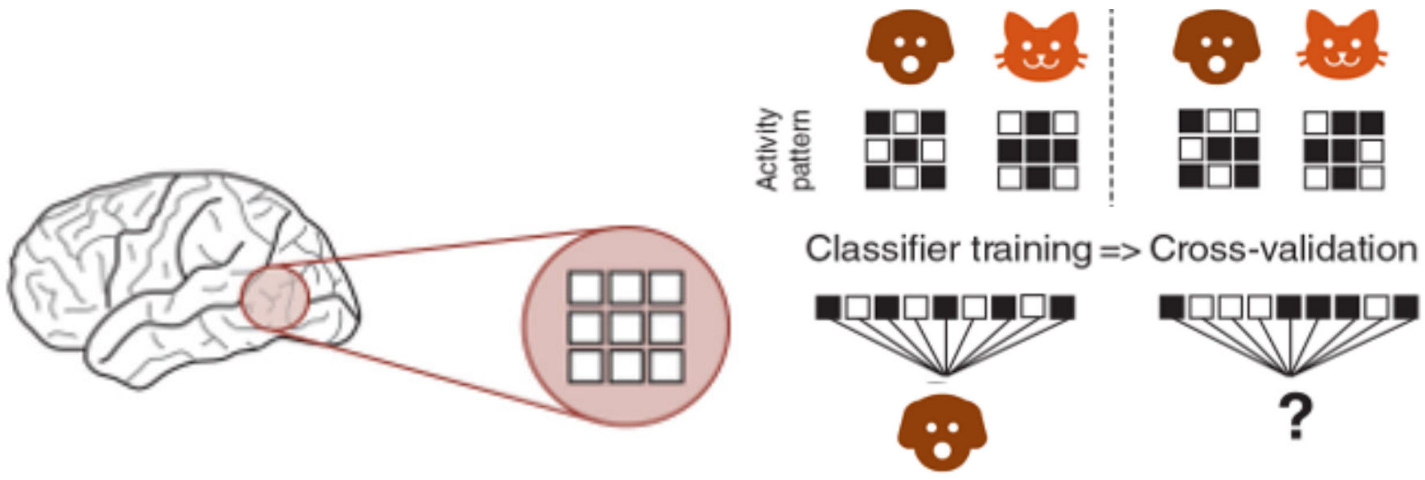
```
    "Activation heatmap created and saved to: "    "/home/eik-tb/OneDrive_andreaivan.costantino@kuleuven.b
```

This step helps confirm that our dataset looks reasonable and visualize the underlying data patterns.

MVPA: Classification Analysis

We use a simple Linear Discriminant Analysis (LDA) classifier with cross-validation to decode category information.

The central idea is that **if differences between categories are present, the classifier will be able to pick that signal up**. When we use an MVPA classifier to brain data, we are testing whether the neural patterns (represented as voxel activity) for different categories contain distinct, systematic differences. If the brain region being analyzed encodes information about the categories in its activity patterns, the classifier will achieve accuracy above chance.



In other words, the classifier looks at the activity from multiple voxels and tries to find **consistent differences between patterns** for different categories (e.g., cats vs. dogs). If those patterns are different enough, the classifier can "learn" to predict the category based on the brain activity by **identifying separable representations** in a high-dimensional space of neural activity.

This works because the brain encodes information about what we see or think in these patterns—like a unique "signature" for each category. If the classifier succeeds, it shows that the brain region we're analyzing contains information relevant to distinguishing those categories.

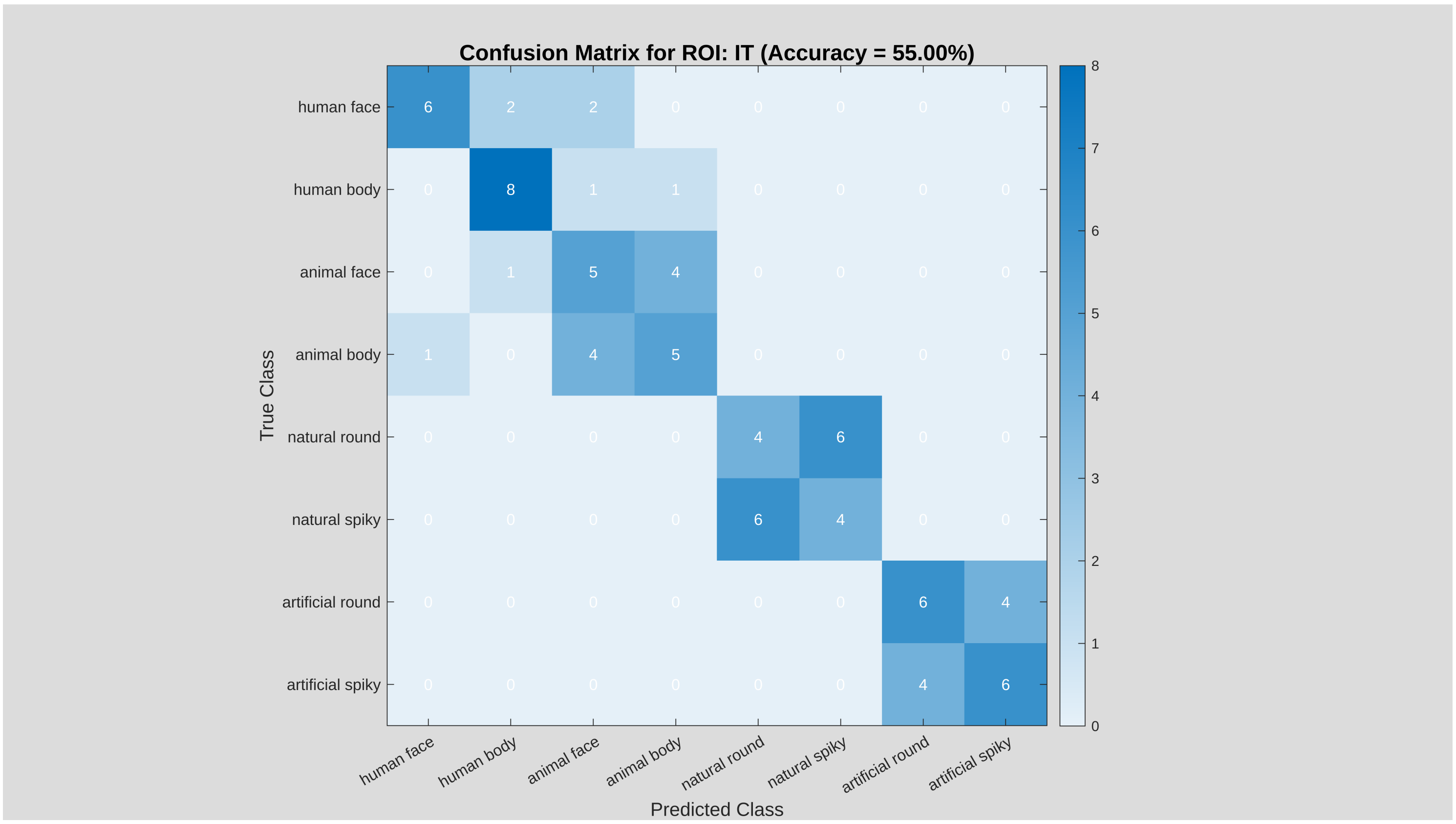
Steps:

1. **Partitioning**: Divide the data into folds based on runs (e.g., leave-one-run-out).
2. **Training & Testing**: Train on some runs, test on another run.
3. **Evaluate Accuracy**: Compare accuracy to chance (1/8 = 12.5%).

```
% Define the classifier
classifier = @cosmo_classify_lda;

% Set up cross-validation partitions
partitions = cosmo_nfold_partitioner(ds);

% Perform cross-validation decoding
[predictedLabels, accuracy] = cosmo_crossvalidate(ds, classifier,
partitions);

% Compute chance level
chanceLevel = 1 / numCategories;

% Display the decoding results
fprintf('Classification accuracy: %.2f%% (chance level: %.2f%%)\n', ...
    accuracy * 100, chanceLevel * 100);
```

```
Classification accuracy: 55.00% (chance level: 12.50%)
```

```
% Plot confusion matrix
plot_confusion_matrix(ds.sa.targets, predictedLabels, numCategories,
accuracy, ...
    labelNames, roiName, outDir);
```

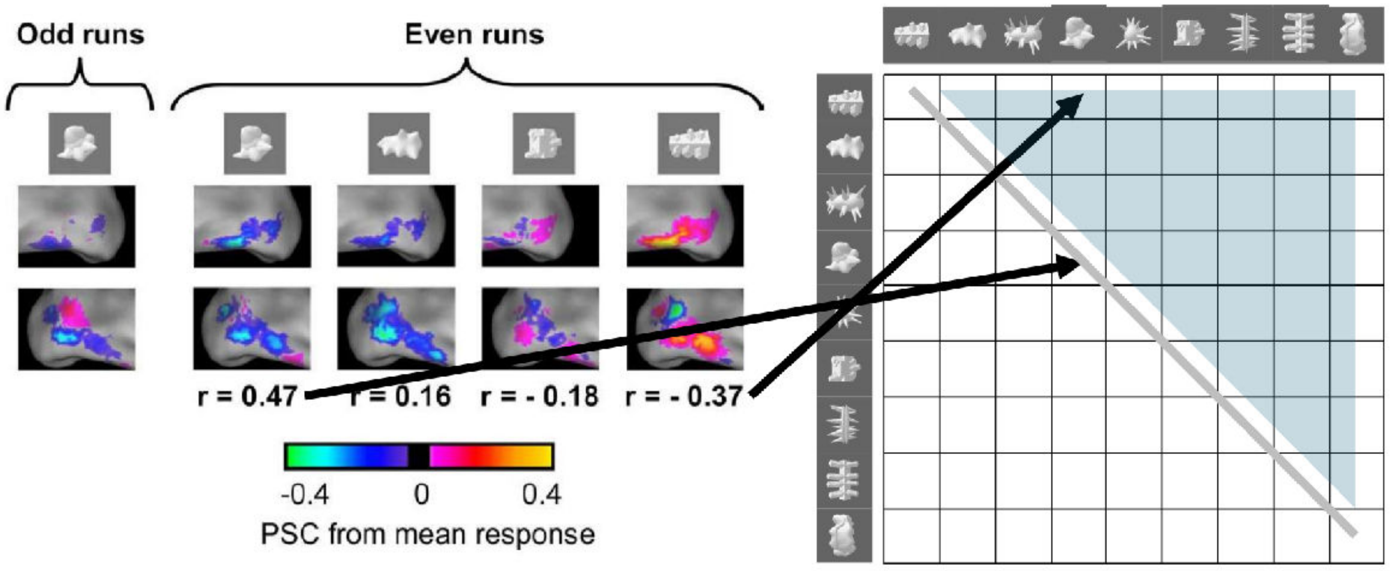


	human face	human body	animal face	animal body	natural round	natural spiky	artificial round	artificial spiky
human face	6	2	2	0	0	0	0	0
human body	0	8	1	1	0	0	0	0
animal face	0	1	5	4	0	0	0	0
animal body	1	0	4	5	0	0	0	0
natural round	0	0	0	0	4	6	0	0
natural spiky	0	0	0	0	6	4	0	0
artificial round	0	0	0	0	0	0	6	4
artificial spiky	0	0	0	0	0	0	4	6

```
    "Confusion matrix plot created and saved to: "    "/home/eik-tb/OneDrive_andreaivan.costantino@kuleuve
```

A confusion matrix helps identify which categories are easily distinguishable and which are often confounded.

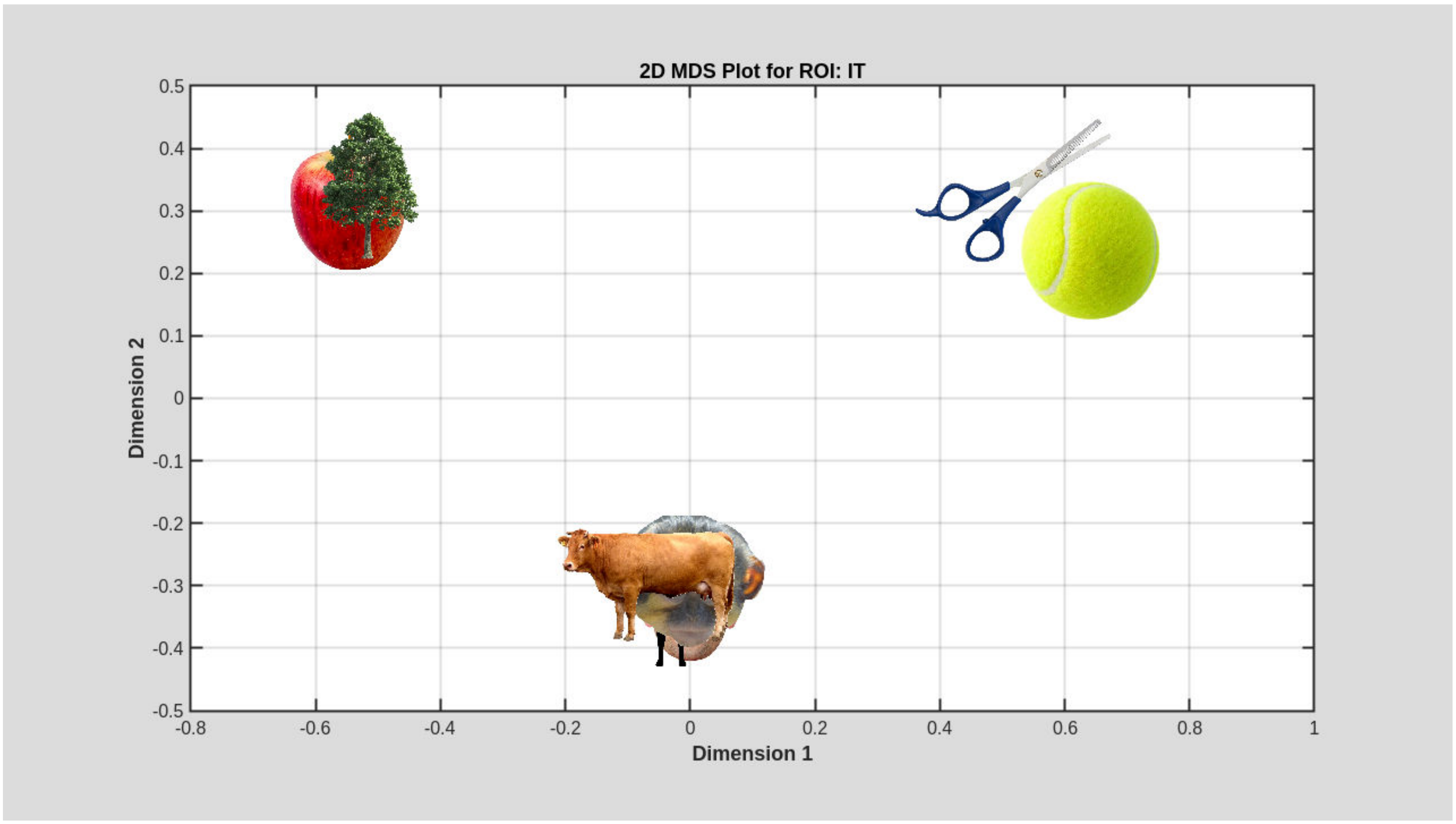
Representational Dissimilarity Matrices (RDMs)



RSA involves comparing the RDMs from brain data to RDM for our theoretical models. We do this by computing RDMs:

1. **Mean Patterns**: Average the data across runs for each category.
2. **Compute Distances**: Calculate pairwise distances (1-Correlation) between categories to form an RDM.
3. **Compare to Models**: Generate theoretical RDMs and see which best fits the data.

```
% Compute mean dataset across runs per category
dsMean = cosmo_fx(ds, @(x) mean(x, 1), 'targets');

% Visualize categories in a 2D space using MDS
plot_mds(ds, roiName, outDir);
```

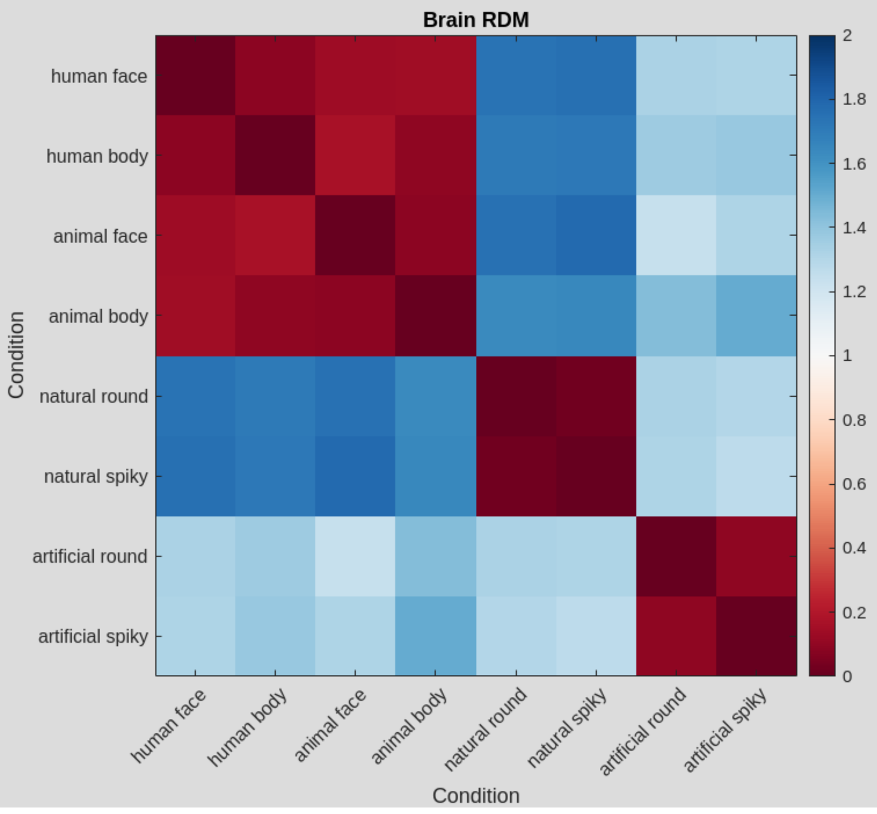


```
    "MDS plot created and saved to: "    "/home/eik-tb/OneDrive_andreaivan.costantino@kuleuven.be/GitHub/m
```

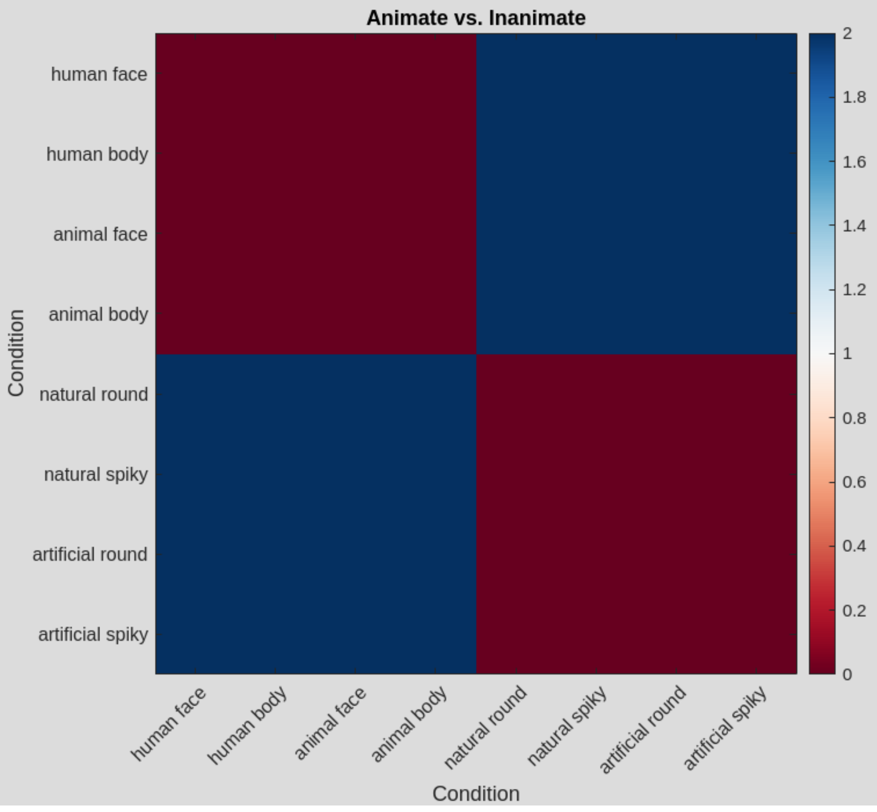
```
% Compute the data RDM
measureDsm = @cosmo_dissimilarity_matrix_measure;
argsDsm.metric = 'correlation';
argsDsm.center_data = true;

dataDsm = measureDsm(dsMean, argsDsm);
dataRdm = squareform(dataDsm.samples);

% Generate model RDMs (theoretical structures)
rdms = generate_model_rdms(numCategories);
```

And to visualize the RDMs:

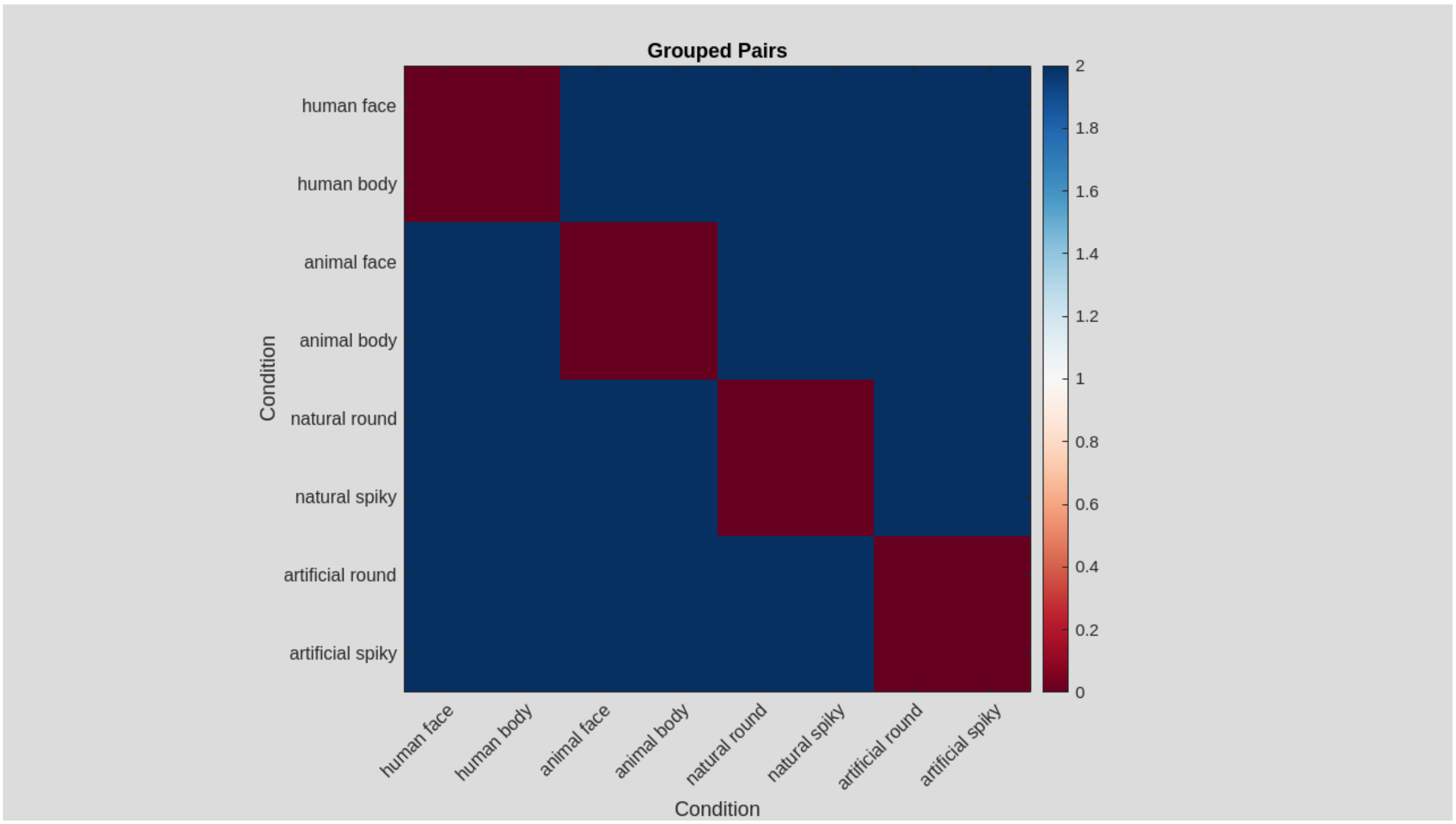
```
plot_rdm_full(dataRdm, labelNames, 'Brain RDM');
```



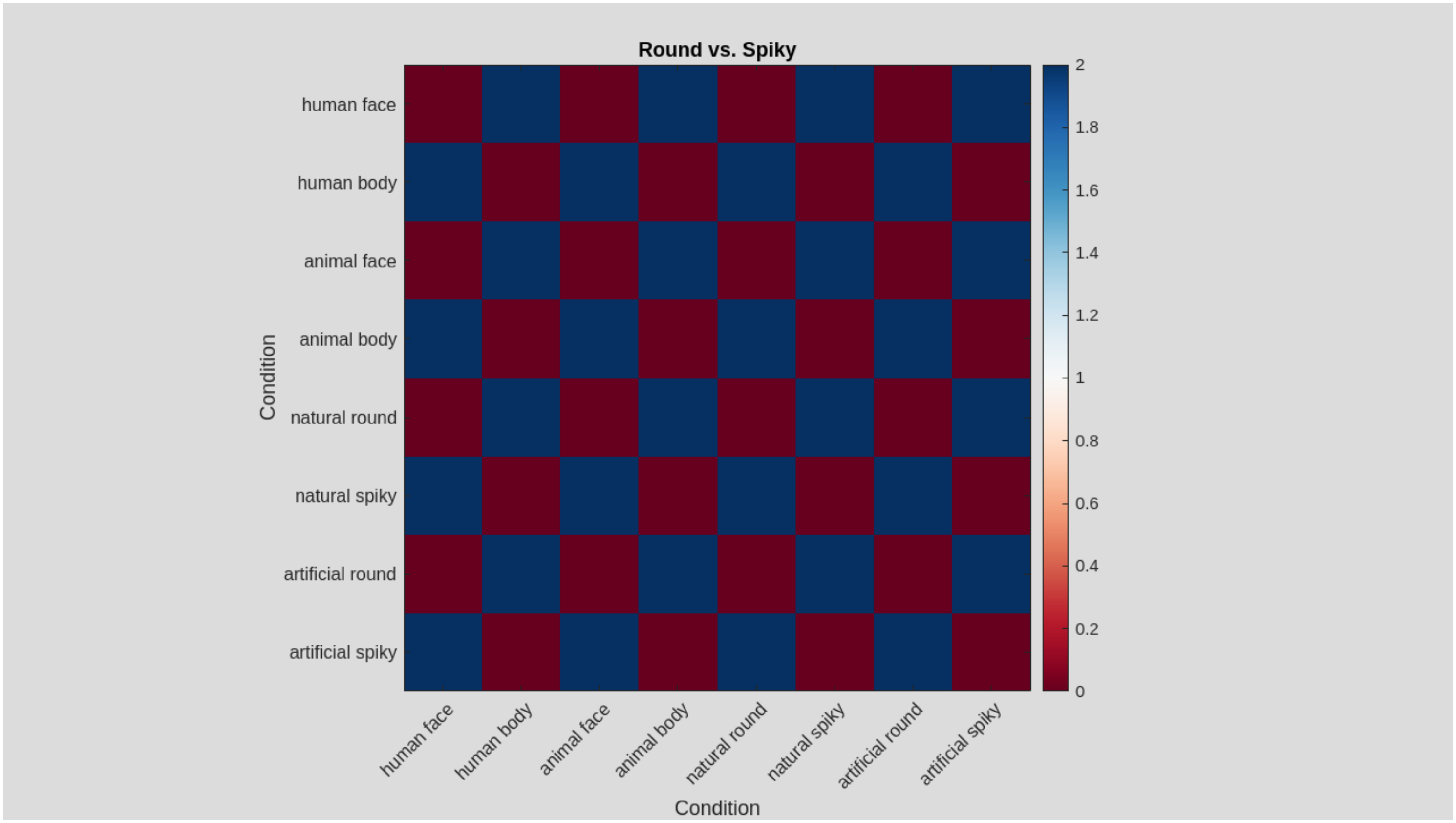
```
plot_rdm_full(rdms(1).dsm, labelNames, rdms(1).description);
```



```
plot_rdm_full(rdms(2).dsm, labelNames, rdms(2).description);
```



```
plot_rdm_full(rdms(3).dsm, labelNames, rdms(3).description);
```

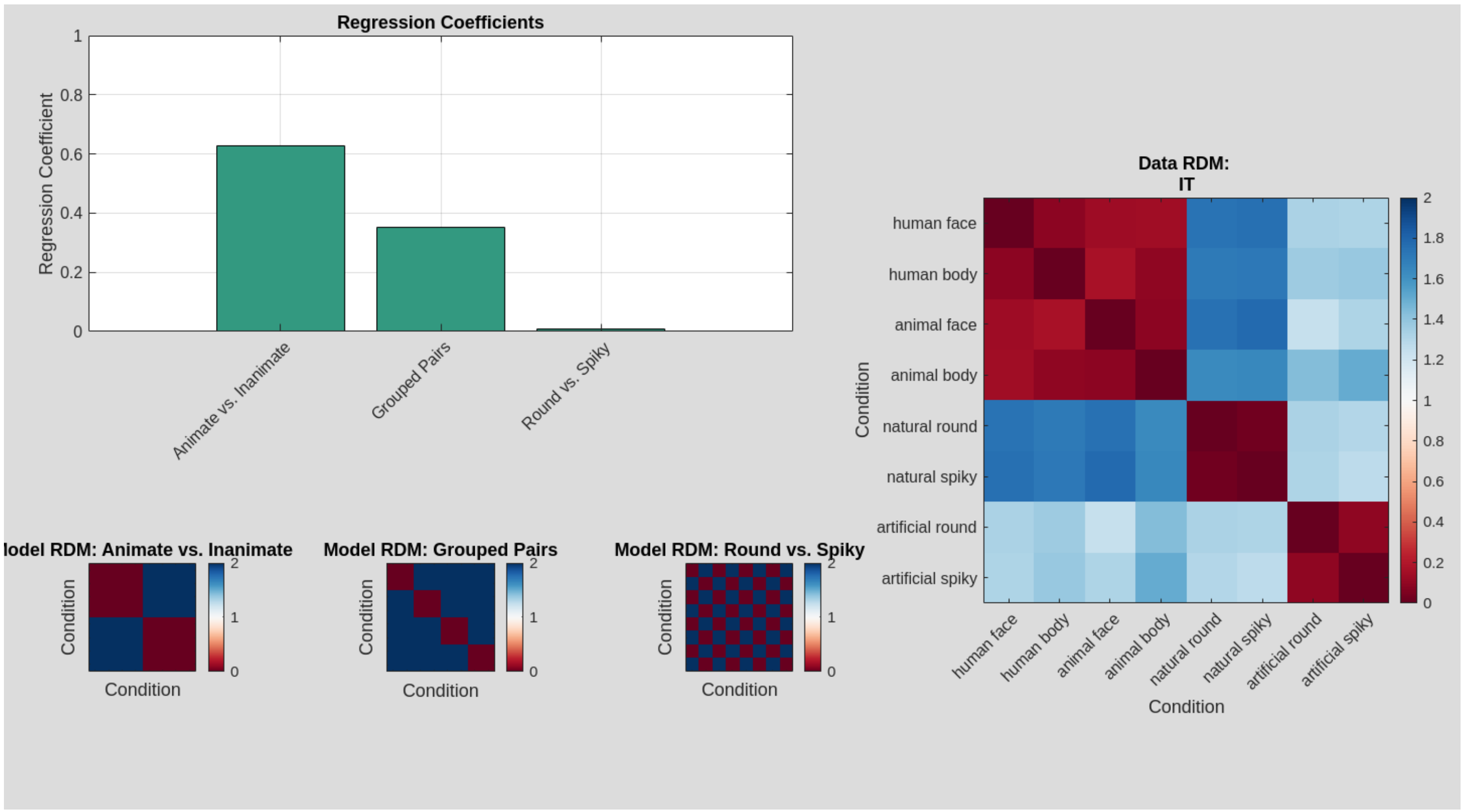


RSA Regression

We now fit a linear model that predicts the data RDM from these model RDMs.

The regression coefficients indicate how strongly each model explains the observed data’s representational geometry.

```
% Set up RSA regression
measure = @cosmo_target_dsm_corr_measure;
measureArgs = struct();
measureArgs.center_data = true;

% Prepare model RDM regressors
regressorRDMs = cellfun(@(x) squareform(x)', {rdms.dsm}, 'UniformOutput',
false);
measureArgs.glm_dsm = regressorRDMs;

% Run RSA regression
result = measure(dsMean, measureArgs);

% Extract category labels
labels = dsMean.sa.labels;

% Plot results: observed RDM, model RDMs, and regression coefficients
plot_rdms_and_coefficients(dataRdm, rdms, labels, result.samples, roiName,
outDir);
```



```
    "RDM and regression plot saved to: "    "/home/eik-tb/OneDrive_andreaivan.costantino@kuleuven.be/GitHu
```

Interpreting these results allows you to see if IT or V1 better matches certain theoretical frameworks (e.g., categorization by animacy vs. perceptual features).

Conclusion

What we learned:

- How to **structure and preprocess fMRI data** (BIDS, fMRIPrep, SPM) for MVPA and RSA.
- How to decode category information using **MVPA**.
- How to apply **RSA** to compare observed brain patterns to theoretical representational models.