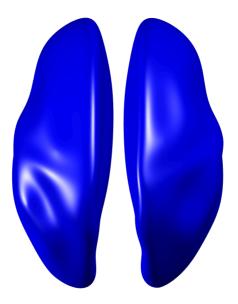
```
clc, clear, close all;
% Clear command window, clear workspace variables, and close all figures
% Load GIFTI toolbox to read GII format (surface-based data)
% Import surface data of Freesurfer template
% Vertices: Locations of individual points (x, y, z) or nodes that make up a surface mesh
% Faces: Polygons formed by connecting the vertices of a surface mesh model
% Faces are defined by indices that specify which vertices are connected to form each face.
% These indices are usually stored in groups of three, representing the three vertices that for
init;
g_mesh = struct with fields:
     faces: [655360×3 int32]
       mat: [4×4 double]
   vertices: [327684×3 single]
g_lh = struct with fields:
     faces: [327680×3 int32]
       mat: [4×4 double]
   vertices: [163842×3 single]
g_rh = struct with fields:
     faces: [327680×3 int32]
       mat: [4×4 double]
   vertices: [163842×3 single]
% Initialize the GIFTI toolbox for further operations
% Total vertices are 327,684; each hemisphere of the brain has 163,842 vertices
% (We can use a template with a smaller number of vertices)
n_vertices = size(g_mesh.vertices, 1);
figure;
% Plot brain surface without weight
```

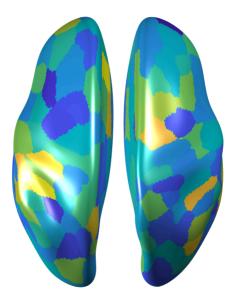
plot(g\_mesh)



```
% Plot the brain surface without applying any weight
% Plot brain surface with weight from atlas
% Note that the Schaefer atlas is not symmetric, so we have to read annotations for both the le
% Read annotation: 101 regions in the left brain (100 regions + medial wall of the brain)
[~, gg_lh1_cdata, lh_mapping_table] = read_annotation('brainspace/lh.Schaefer2018_200Parcels_7)
% Store the annotation data and mapping table of the left hemisphere
lh_mapping_table
lh_mapping_table = struct with fields:
     numEntries: 101
      orig tab: 'Schaefer2018 200Parcels 7Networks'
   struct_names: {101×1 cell}
         table: [101×5 double]
% Display the mapping table for the left hemisphere
% Read annotation: 101 regions in the right brain (100 regions + medial wall of the brain)
[~, gg_rh1_cdata, rh_mapping_table] = read_annotation('brainspace/rh.Schaefer2018_200Parcels_7N
% Store the annotation data and mapping table of the right hemisphere
rh_mapping_table
```

```
rh_mapping_table = struct with fields:
    numEntries: 101
    orig_tab: 'Schaefer2018_200Parcels_7Networks'
    struct_names: {101×1 cell}
        table: [101×5 double]
```

```
% Display the mapping table for the right hemisphere
% Each region has a specific ID
lh_atlas_id = lh_mapping_table.table(:, 5);
rh atlas id = rh mapping table.table(:, 5);
% Store the specific ID for each region in the left and right hemisphere
% read weight from csv
table = readtable('data/mean.layer.0.csv');
corticalThicknesses = double(table2array(table(:, 2)));
% Read the cortical thickness data from a CSV file
% Convert weight of 200 regions to weight on the brain surface
w_left_cdata = zeros(n_vertices / 2, 1);
w_right_cdata = zeros(n_vertices / 2, 1);
for j = 1:size(corticalThicknesses, 1) / 2
  % Vlookup mapping table
  w_left_cdata(find(gg_lh1_cdata == lh_atlas_id(j))) = corticalThicknesses(2*j-1);
  w_right_cdata(find(gg_rh1_cdata == rh_atlas_id(j))) = corticalThicknesses(2*j);
end
% Convert the weight of 200 regions to weight on the brain surface
% by mapping the cortical thickness values to the corresponding vertices
final_cdata = [w_left_cdata; w_right_cdata];
gg_mesh.cdata = final_cdata;
% Assign the final weight data to the GIFTI mesh
figure;
plot(g_mesh, gg_mesh)
```



```
% Plot the brain surface with the weight data
```

% Convert MATLAB Live Script to PDF matlab.internal.liveeditor.openAndConvert('tutorial\_livescript.mlx', 'tutorial.pdf', 'HideCode'