```
function output = splitfilament

% splitfilament.m
%
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%
% Last modified 7/8/2012
%
% Uses a reference plane to divide a network of vessels into two separate
% networks. Vessel networks are defined as filament coordinates, using the
% format implemented by Imaris 7.4.2 (Bitplane). Filament coordinates can
% be exported using ImarisXT.
%
% Designed to use the margin between the SEZ and the Striatum in order to
% separate the two vessel networks, allowing for separate morphometric
% analyses.
%
% Assumes the reference plane is located at a depth of 10um below the
% ependymal wall, and that the SEZ is 20um thick.
%
%    Inputs:
%    -Directory containing filament coordinates that define reference plane
%    -Directory containing vessel coordinates
%
%    Outputs (one each for the SEZ, the Striatum, and the combination):
%    -Filament coordinates for each subset of vessels (includes
%    vFilamentXYZ, vFilamentRadius, vFilamentEdges, and vFilamentTypes).
%    Each set is saved into its own subdirectory of the parent directory
%    containing the vessel filament coordinates.
%


% Define directory containing vFilamentXYZ for filaments defining reference plane
directory_name1 = uigetdir('','Select Directory Containing filaments that define the↙
reference plane (exported from Imaris)')
cd(directory_name1)
vFilamentXYZ=csvread('vFilamentXYZ.txt');
Xcolv = vFilamentXYZ(:,1);
Ycolv = vFilamentXYZ(:,2);
Zcolv = vFilamentXYZ(:,3);
Const = ones(size(Xcolv));
Coefficients = [Xcolv Ycolv Const]\Zcolv; % Find the coefficients
XCoeff = Coefficients(1); % X coefficient
YCoeff = Coefficients(2); % X coefficient
CCoeff = Coefficients(3); % constant term
clear Coefficients Const Xcolv Ycolv Zcolv

% Define directory containing vFilamentXYZ, vFilamentRadius,
% vFilamentEdges, and vFilamentTypes for filaments to be split
directory_name2 = uigetdir('','Select Directory Containing filaments to be split (exported↙
```

```
from Imaris)')
cd(directory_name2)
vFilamentXYZ=csvread('vFilamentXYZ.txt');
vFilamentRadius=csvread('vFilamentRadius.txt');
vFilamentEdges=csvread('vFilamentEdges.txt');
vFilamentTypes=csvread('vFilamentTypes.txt');

mkdir(directory_name2,'Combined')
mkdir(directory_name2,'SEZ')
mkdir(directory_name2,'Striatum')
csvwrite(strcat(directory_name2,'\Combined','\vFilamentEdges.txt'),vFilamentEdges);
csvwrite(strcat(directory_name2,'\Combined','\vFilamentTypes.txt'),vFilamentTypes);
csvwrite(strcat(directory_name2,'\Combined','\vFilamentRadius.txt'),vFilamentRadius);
csvwrite(strcat(directory_name2,'\Combined','\vFilamentXYZ.txt'),vFilamentXYZ);

% Calculate distance between each point and the reference plane. Formula
% for distance calculated by solving for the equation of a line that lies
% normal to the reference plane and intersects with the given point.
WallPtDist=((vFilamentXYZ(:,1).*XCoeff)+(vFilamentXYZ(:,2).*YCoeff)-(vFilamentXYZ(:,3))+↙
(CCoeff));
WallPtDist=(WallPtDist)./(sqrt((XCoeff^2)+(YCoeff^2)+1));
plot(WallPtDist)
mean(WallPtDist)

% Defines SEZ thickness as 20um, and determines which side of reference
% plane contains striatum

thickness=20;
halfthick=thickness/2;
if mean(WallPtDist)<0
    SEZPts=WallPtDist>(-1*halfthick);
else
    SEZPts=WallPtDist<(halfthick);
end

% Split filaments. If any points in a segment belong to the striatum, then
% the entire segment is classified as striatum.
edgetest=ismember(vFilamentEdges,find(~SEZPts));
edgetest2=edgetest(:,1)+edgetest(:,2);
StrEdges=vFilamentEdges((find(edgetest2)),:);
SEZEdges=vFilamentEdges((find(edgetest2==0)),:);
vFilamentIndex=cumsum((vFilamentXYZ(:,1).*0)+1);
SEZXYZ=vFilamentXYZ((find(ismember(vFilamentIndex,SEZEdges))),:);
SEZTypes=vFilamentTypes((find(ismember(vFilamentIndex,SEZEdges))),:);
SEZRadius=vFilamentRadius((find(ismember(vFilamentIndex,SEZEdges))),:);
StrXYZ=vFilamentXYZ((find(ismember(vFilamentIndex,StrEdges))),:);
StrTypes=vFilamentTypes((find(ismember(vFilamentIndex,StrEdges))),:);
StrRadius=vFilamentRadius((find(ismember(vFilamentIndex,StrEdges))),:);
SEZIndAdjust=vFilamentIndex-(cumsum(~ismember(vFilamentIndex,SEZEdges)));
StrIndAdjust=vFilamentIndex-(cumsum(~ismember(vFilamentIndex,StrEdges)));
testsize=size(vFilamentIndex);
indmax=testsize(1);
```

```matlab
for i=1:indmax
    SEZEdges(find(SEZEdges==i))=SEZIndAdjust(i);
end
for i=1:indmax
    StrEdges(find(StrEdges==i))=StrIndAdjust(i);
end

% Save the SEZ only filaments

csvwrite(strcat(directory_name2,'\SEZ','\vFilamentEdges.txt'),SEZEdges);
csvwrite(strcat(directory_name2,'\SEZ','\vFilamentTypes.txt'),SEZTypes);
csvwrite(strcat(directory_name2,'\SEZ','\vFilamentRadius.txt'),SEZRadius);
csvwrite(strcat(directory_name2,'\SEZ','\vFilamentXYZ.txt'),SEZXYZ);

% Save the Striatum only filaments

csvwrite(strcat(directory_name2,'\Striatum','\vFilamentEdges.txt'),StrEdges);
csvwrite(strcat(directory_name2,'\Striatum','\vFilamentTypes.txt'),StrTypes);
csvwrite(strcat(directory_name2,'\Striatum','\vFilamentRadius.txt'),StrRadius);
csvwrite(strcat(directory_name2,'\Striatum','\vFilamentXYZ.txt'),StrXYZ);

output='Finished Splitting Filaments';
```