

```
classdef CohortFiles
    %COHORTFILES Files for Normal, TBI, and Stroke Cohorts
    % List of functions to better use cohort files and read medical
    % records
    %
    % Some functions require the Text Analytics Toolbox
    %
    % Authors:
    %     Michael Caiola (Michael.Caiola@fda.hhs.gov)
    %     Meijun Ye (Meijun.Ye@fda.hhs.gov)
    %
    % Disclaimer: This software and documentation (the "Software") were
    % developed at the Food and Drug Administration (FDA) by employees of
    % the Federal Government in the course of their official duties.
    % Pursuant to Title 17, Section 105 of the United States Code,
    % this work is not subject to copyright protection and is in the
    % public domain. Permission is hereby granted, free of charge, to any
    % person obtaining a copy of the Software, to deal in the Software
    % without restriction, including without limitation the rights to
    % use, copy, modify, merge, publish, distribute, sublicense, or sell
    % copies of the Software or derivatives, and to permit persons to
    % whom the Software is furnished to do so. FDA assumes no
    % responsibility whatsoever for use by other parties of the Software,
    % its source code, documentation or compiled executables, and makes
    % no guarantees, expressed or implied, about its quality,
    % reliability, or any other characteristic. Further, use of this code
    % in no way implies endorsement by the FDA or confers any advantage
    % in regulatory decisions. Although this software can be
    % redistributed and/or modified freely, we ask that any derivative
    % works bear some notice that they are derived from it, and any
    % modified versions bear some notice that they have been modified.

    properties
        AllFiles
        NormalFiles
        Normal_idx
        NormalRecord
        TBIFiles
        TBI_idx
        TBIRecord
        StrokeFiles
        Stroke_idx
        StrokeRecord
        UnknownFiles
        Unknown_idx
        UnknownRecord
    end

    methods
        function obj = CohortFiles(A)
```

```

%COHORTFILES Construct an instance of this class
% Detailed explanation goes here
if isstring(A)
    if endsWith(A, ".xlsx")
        A = ConvertToTable(A);
    else

    end
end

obj.A = A;
obj.AllFiles = A.Filename;
obj.Normal_idx = or(A.Category=="Normal", A.Category=="HEA");
obj.NormalFiles = A.Filename(obj.Normal_idx);
obj.NormalRecord = A.("Full Note");
obj.TBI_idx = A.Category=="TBI";
obj.TBIFiles = A.Filename(obj.TBI_idx);
obj.TBIRecord = A.("Full Note");
obj.Stroke_idx = or(A.Category=="Stroke", A.Category=="STR");
obj.StrokeFiles = A.Filename(obj.Stroke_idx);
obj.StrokeRecord = A.("Full Note");
obj.Unknown_idx = A.Category=="Unknown";
obj.UnknownFiles = A.Filename(obj.Unknown_idx);
obj.UnknownRecord = A.("Full Note");
end

function y = NumFiles(obj)
    y = [sum(obj.A.Category == "Normal") sum(obj.A.Category == "TBI") sum(obj.A.
Category == "Stroke")];
    disp("Number of Total files: " + height(obj.A));
    disp("Number of Normal files: " + y(1));
    disp("Number of TBI files: " + y(2));
    disp("Number of Stroke files: " + y(3));
end

function y = NumSubjects(obj)
    y = [numel(unique(obj.A.Subject(obj.A.Category == "Normal"))), ...
        numel(unique(obj.A.Subject(obj.A.Category == "TBI"))), ...
        numel(unique(obj.A.Subject(obj.A.Category == "Stroke")))]];
    disp("Number of Total subjects: " + numel(unique(obj.A.Subject)));
    disp("Number of Normal subjects: " + y(1));
    disp("Number of TBI subjects: " + y(2));
    disp("Number of Stroke subjects: " + y(3));
end

function outputArg = method1(obj, inputArg)
    %METHOD1 Summary of this method goes here
    % Detailed explanation goes here
    outputArg = obj.Property1 + inputArg;
end

```

```

function [inT,inA] = Index(obj,T)
    T = [T.Subject,T.Session];
    B = [obj.A.Subject,obj.A.Session];
    [inT,inA] = ismember(T,B,'rows');
end

function files = Compare(obj,T,varargin)
    files = {zeros(height(T),length(varargin)),zeros(height(T),length(varargin)),↵
zeros(height(T),length(varargin))};
    C = T.Category;
    T = [T.Subject,T.Session];
    B = [obj.A.Subject,obj.A.Session];
    for k = 1:length(varargin)
        files{1}(:,k) = and(ismember(T,B(obj.Normal_idx,:), 'rows'), C == varargin↵
{k});
        files{2}(:,k) = and(ismember(T,B(obj.TBI_idx,:), 'rows'), C == varargin↵
{k});
        files{3}(:,k) = and(ismember(T,B(obj.Stroke_idx,:), 'rows'), C == varargin↵
{k});
        %files{1}(:,k) = all([ismember(T.Subject,obj.A.Subject(obj.Normal_idx)) ,↵
ismember(T.Session,obj.A.Session(obj.Normal_idx)) , T.Category == varargin{k}],2);
        %files{2}(:,k) = all([ismember(T.Subject,obj.A.Subject(obj.TBI_idx)) ,↵
ismember(T.Session,obj.A.Session(obj.TBI_idx)) , T.Category == varargin{k}],2);
        %files{3}(:,k) = all([ismember(T.Subject,obj.A.Subject(obj.Stroke_idx)) ,↵
ismember(T.Session,obj.A.Session(obj.Stroke_idx)) , T.Category == varargin{k}],2);
    end
    tit = ["Normal", "TBI", "Stroke"];
    for i = 1:3
        figure;
        X = categorical(string(varargin));
        X = reordercats(X,string(varargin));
        b = bar(X,sum(files{i}));
        %b.FaceColor = "flat";
        %b.CData(i,:) = [.5 0 .5];
        title("Number of files from " + inputname(2) + " Table in " + tit(i) + " "↵
+ inputname(1))
        xlabel("Comparison Table")
    end
end

function files = Compare1(obj,T,varargin)
    for i = length(varargin):-1:1
        files{i} = zeros(height(obj.A),length(varargin));
    end
    C = T.Category;
    T = [T.Subject,T.Session];
    B = [obj.A.Subject,obj.A.Session];
    for k = 1:length(varargin)
        files{k}(:,1) = and(ismember(B,T(C == varargin{k},:), 'rows'), obj.A.↵
Category == "Normal");
        files{k}(:,2) = and(ismember(B,T(C == varargin{k},:), 'rows'), obj.A.↵

```

```

Category == "TBI");
    files{k}(:,3) = and(ismember(B,T(C == varargin{k},:),'rows'), obj.A.✓
Category == "Stroke");
end
tit = ["Normal", "TBI", "Stroke"];
for i = 1:length(varargin)
    figure;
    X = categorical(string(tit));
    X = reordercats(X,string(tit));
    b = bar(X,sum(files{i}));
    %b.FaceColor = "flat";
    %b.CData(i,:) = [.5 0 .5];
    title("Number of files from " + inputname(1) + " Table in " + varargin{i}✓
+ " " + inputname(2))
    xlabel("Comparison Table")
end
end
function PlotWordClouds(obj,thresh)
    if nargin <2
        thresh = 50;
    end
    pat = regexpPattern('[A-Z\s]*[A-Z]+:');
    wc = wordCloudCounts(obj.A.("Full Note"));
    wc = wc(1:thresh,1);

    x = erase(obj.A.("Full Note")(obj.A.Category=="Normal"),pat); % Remove✓
capital headings
    x = erase(x,wc);
    x = erase(x," ic ");
    x = erase(x,"BPM");
    x = erase(x,"Digital");
    x = erase(x,"Hz");
    x = erase(x,"epileptiform");
    x = replace(x,regexpPattern('\s[a-z][\s*\)\.\,]'),' ');
    x = replace(x," ", " ");

    y = erase(obj.A.("Full Note")(obj.A.Category=="TBI"),pat);
    y = erase(y,wc);
    y = erase(y," ic ");
    y = erase(y,"BPM");
    y = erase(y,"Digital");
    y = erase(y,"Hz");
    y = erase(y,"epileptiform");
    y = replace(y,regexpPattern('\s[a-z][\s*\)\.\,]'),' ');
    y = replace(y," ", " ");

    z = erase(obj.A.("Full Note")(obj.A.Category=="Stroke"),pat);
    z = erase(z,wc);
    z = erase(z," ic ");
    z = erase(z,"BPM");
    z = erase(z,"Digital");

```

```
z = erase(z, "Hz");
z = erase(z, "epileptiform");
z = replace(z, regexpPattern('\s[a-z][\s*\s)\.\. ,]'), " ");
z = replace(z, " ", " ");
```

```
figure;
wordcloud(x)
title("Normal")
figure;
wordcloud(y)
title("TBI")
figure;
wordcloud(z)
title("Stroke")
```

```
end
```

```
end
```

```
end
```

```
function T = ConvertToTable(txt)
T = readtable(txt);
filename = "";
session = [];
categ = "";
for i = 1:height(T)
    s = split(string(T.Location(i)), '\');
    %s = split(s(end), "_");
    filename(i) = s(end);
    session(i) = str2double(T.Session{i}(end-2:end));
    categ(i) = categorical(missing);
```

```
end
```

```
T.Filename = filename';
T.Session = session';
T.Category = categ';
T = renamevars(T, "Notes", "Full Note");
end
```