

```
classdef ResampleDatastore < matlab.io.Datastore & ...
    matlab.io.datastore.MiniBatchable & ...
    matlab.io.datastore.Shuffleable
    %RESAMPLEDATABASE Custom datastore to read in data from file structure for other DL
nets
    % To be used as a datastore to a local directory of TUEG files.
    %
    % Authors:
    %     Michael Caiola (Michael.Caiola@fda.hhs.gov)
    %     Meijun Ye (Meijun.Ye@fda.hhs.gov)
    %
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    properties
        Datastore
        Labels
        NumClasses
        SequenceDimension
        MiniBatchSize
        Augmented
        TestSet
        newHz
    end

    properties (SetAccess = protected)
        NumObservations
    end

    properties (Access = private)
        CurrentFileIndex
        %FileSet matlab.io.datastore.DsFileSet
```

end

methods

```
function ds = ResampleDatastore(folder,newHz,varargin)
% ds = ResampleDatastore(folder,newHz) creates a custom datastore
% from the data in folder with a new sampling rate newHz.
%
% Optional arguments:
%   "DataAugmentation" (default = false)
%       Augments the data in random shuffles of 90 seconds
%   "TestSet" (default = false)
%       Creates a testset of 90 second data, to be used when
%       DataAugmentation is being used

if isempty(newHz)
    ds.newHz = 250;
else
    ds.newHz = newHz;
end

inputs = ds.parseInputs(varargin{:});

if inputs.DataAugmentation
    ds.Augmented = true;
else
    ds.Augmented = false;
end

if inputs.TestSet
    ds.TestSet = true;
    ds.Augmented = false;
else
    ds.TestSet = false;
end

% Create file datastore.
fds = fileDatastore(folder, ...
    'ReadFcn',@(x) readSequence(x,ds.newHz,ds.Augmented,ds.TestSet), ...
    'IncludeSubfolders',true);
ds.Datastore = fds;

% Read labels from folder names.
numObservations = numel(fds.Files);
for i = 1:numObservations
    file = fds.Files{i};
    filepath = fileparts(file);
    [~,label] = fileparts(filepath);
    labels{i,1} = label;
end
ds.Labels = categorical(labels);
ds.NumClasses = numel(unique(labels));
```

```
% Determine sequence dimension.
X = preview(fds);
ds.SequenceDimension = size(X,1);

% Initialize datastore properties.
ds.MinibatchSize = 128;
ds.NumObservations = numObservations;
ds.CurrentFileIndex = 1;
end

function tf = hasdata(ds)
% tf = hasdata(ds) returns true if more data is available.

%tf = hasdata(ds.Datastore);
tf = ds.CurrentFileIndex + ds.MinibatchSize - 1 ...
    <= ds.NumObservations;
end

function [data,info] = read(ds)
% [data,info] = read(ds) read one mini-batch of data.

minibatchSize = ds.MinibatchSize;

for i = 1:minibatchSize
    predictors{i,1} = read(ds.Datastore);
    responses(i,1) = ds.Labels(ds.CurrentFileIndex);
    ds.CurrentFileIndex = ds.CurrentFileIndex + 1;

end

data = preprocessData(predictors,responses);
info.Size = size(data);
end

function reset(ds)
% reset(ds) resets the datastore to the start of the data.

reset(ds.Datastore);
ds.CurrentFileIndex = 1;
end

function dsNew = subset(ds,in)
dsNew = copy(ds);
dsNew.Datastore=subset(ds.Datastore,in);
dsNew.NumObservations = numel(dsNew.Datastore.Files);
for i = 1:dsNew.NumObservations
    file = dsNew.Datastore.Files{i};
    filepath = fileparts(file);
    [~,label] = fileparts(filepath);
    labels{i,1} = label;
end
```

```
end
dsNew.Labels = categorical(labels);
dsNew.NumClasses = numel(unique(labels));

end

function varargout = grabEachLabel(ds,N,varargin)
    % pulls a certain number of each individual label
    opt_random=0;
    numvarargin=length(varargin);
    k=1;
    while k<=numvarargin
        switch varargin{k}
            case "random"
                opt_random=1;
        end
        k=k+1;
    end
    for i=1:length(N)
        in{i}=[];
    end
    labels=unique(ds.Labels);
    for i=1:ds.NumClasses
        labs=ds.Labels==labels(i);
        numLabs=sum(labs);
        x=find(labs);
        if opt_random
            x=x(randperm(length(x)));
        end
        if sum(N)>numLabs
            n=floor(numLabs.*N/sum(N));
            warning("Not enough " + string(labels(i))+" Labels")
        else
            n=N;
        end
        in{1}=[in{1}; x(1:n(1))];
        for j=2:length(n)
            in{j}=[in{j};x(n(j-1)+1:n(j-1)+n(j))];
        end
    end
    for i=1:length(in)
        varargout{i} = subset(ds,in{i});
    end
end

function dsNew = shuffle(ds)
    % dsNew = shuffle(ds) shuffles the files and the corresponding
    % labels in the datastore.

    % Create copy of datastore.
    dsNew = copy(ds);
```

```
        dsNew.Datastore = copy(ds.Datastore);
        fds = dsNew.Datastore;

        % Shuffle files and corresponding labels.
        numObservations = dsNew.NumObservations;
        idx = randperm(numObservations);
        fds.Files = fds.Files(idx);
        dsNew.Labels = dsNew.Labels(idx);
    end

end

methods (Hidden = true)
    function frac = progress(ds)
        % frac = progress(ds) returns the percentage of observations
        % read in the datastore.

        frac = (ds.CurrentFileIndex - 1) / ds.NumObservations;
    end
end

methods (Access = 'private')
    function inputStruct = parseInputs(ds,varargin)
        p = inputParser();

        p.addParameter('DataAugmentation',false,@augmentationValidator);
        p.addParameter('TestSet',false,@augmentationValidator);
        p.parse(varargin{:});
        inputStruct = p.Results;
    end
end

end

function data = preprocessData(Predictors,Response)
% data = preprocessData(predictors,responses) preprocesses
% the data in predictors and responses and returns the table
% data

miniBatchSize = size(Predictors,1);

% Pad data to length of longest sequence.
sequenceLengths = cellfun(@(X) size(X,2),Predictors);
maxSequenceLength = max(sequenceLengths);
for i = 1:miniBatchSize
    X = Predictors{i};

    % Pad sequence with zeros.
    if size(X,2) < maxSequenceLength
        X(:,maxSequenceLength) = 0;
    end
end
```

```
Predictors{i} = X;
end

% Return data as a table.
data = table(Predictors,Response);
end

function data = readSequence(filename,newHz,aug,ts)
    % data = readSequence(filename) reads the sequence y from the MAT file
    % filename
    oldHz = 250;
    try
        S = load(filename);
    catch
        if startsWith(filename,"D","IgnoreCase",true)
            filename = replace(filename,'D:','C:');
        else
            filename = replace(filename,'C:','D:');
        end
        S = load(filename);
    end
    if newHz == oldHz
        data = S.y;
    else
        data = single(resample(double(S.y),newHz,oldHz,'Dimension',2)); % ↙
resampled
    end

    downsample = 90; %sec
    if aug
        r = randi(downsample*newHz-2)+1;
        data = data(:,r:r+(downsample*newHz-1));
    end
    if ts
        data = data(:,1:1+(downsample*newHz-1));
    end
end

function p=spect(x)
p=zeros(1024,521,19);
for i=1:19
    %[p(:,:,i),~,~]=wvd(x(i,:),250,'smoothedPseudo','NumTimePoints',22502);
    [p(:,:,i),~,~]=pspectrum(x(i,:),250,'spectrogram','FrequencyLimits',[0 50]);
end
p=log(p);
end

function TF = augmentationValidator(valIn)
```

```
% if ischar(valIn) || isstring(valIn)
%     TF = string('none').contains(lower(valIn)); %#ok<STRQUOT>
% elseif isa(valIn,'imageDataAugmenter') && isscalar(valIn)
%     TF = true;
if islogical(valIn)
    TF = true;
else
    TF = false;
end

end
```