```
"""STEP 2 2016-12-09"""
import pandas as pd
import numpy as np
import regex
import os, sys
"""Experiment name to prepend output files"""
EXPERIMENT = "sample2"
"""Directory path to input data
    (filtered; output from '1-read_fastq_id_features)
FILTERED_FILEPATH = "../output/filtered-sample2.csv"
FILTERED_FILEPATH = "../output/filtered-sample.csv"
"""Directory path to save output"""
OUTPUT_DIRECTORY = "../output"
"""Minimum number of reads as a baseline. Used to simplify data processing."""
MIN_READS = 100
"""Column names correspoinding to eponymous variables"""
SAMPLE = 'idx'
QTAG = 'qtag'
BARCODE = 'barcode'
READS = 'readsPF'
MCOUNTS = 'mcountsPF'
PERCENT_MCOUNTS = 'percent_%s'%MCOUNTS
GROUPBY = ['idx']
def check inputs():
    # modules
    assert pd
    assert np
    assert regex
    assert os
    assert sys
    # user experiment inputs
    assert EXPERIMENT
    assert FILTERED FILEPATH
    assert OUTPUT_DIRECTORY
    assert MIN_READS
    # user columns
    assert SAMPLE
    assert QTAG
    assert BARCODE
    assert READS
    assert MCOUNTS
    assert PERCENT MCOUNTS
    assert GROUPBY
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def calculate_percent_molecs(df, mcounts=MCOUNTS, percent_mcounts=PERCENT_MCOUNTS):
    """Updates percent molec counters for sample"""
   total = float(df[mcounts].values.sum()) / 100.
    df[percent mcounts] = df[mcounts].apply(lambda x: x/total)
   df = df.sort_values(by=mcounts, ascending=False)
    return df
def load_data(filtered_file, sample=SAMPLE, qtag=QTAG,
              barcode=BARCODE, mcounts=MCOUNTS, reads=READS):
    """Loads filtered lib-ID-barcode data csv to dict of samples"""
    columns = [sample, qtag, barcode, mcounts, reads]
    # loads excel file (all tabs)
   csv = pd.read_csv(filtered_file)
    # filter out null barcodes just in case (if custom user input)
   csv = csv.loc[(csv[qtag]!='None') & (csv[barcode]!='None')]
    csv = csv[columns]
    csv[sample] = csv[sample].apply(lambda x: str(x))
    # get percent molecs per sample, store as output dict entry
   groups = csv.groupby(sample)
   data = []
    for i, group in csv.groupby(sample):
        data.append((i,calculate percent molecs(group)))
    return data
def check_data(d, sample=SAMPLE, mcounts=MCOUNTS, reads=READS):
    """Check data for proper format, input values, and
    converts into list-like object if necessary
   d(list, np.array ,dict, or pd.DataFrame): input data
    Returns: data set as a list-like object, wherein
        each item is a pair containing sample name (str) and
        sample data (pd.DataFrame), in that order.
   data arr = []
    # wrangle data to list of list-like pairs, as "[idx, df]"
   if type(d) in [np.array, list] :
        data arr = d
    elif type(d) == dict:
        data arr = d.items()
    elif type(d) == pd.DataFrame :
        data arr = [(s,df) for s,df in d.groupby(sample)]
   else:
        print "Input data is not in correct format. Please provide \
        list-like, dict, or pd.DataFrame object."
   # check input has correct values
   try:
        for a in data_arr:
            assert len(a) == 2, "incorrect item length"
            s, df = a
            assert type(s) == str, 'sample name is not string type'
            assert type(df) == pd.DataFrame, "incorrect value type: must be pd.DataFrame"
            assert sample in df.columns, "%s not in dataframe"%sample
            assert mcounts in df.columns, "%s not in dataframe"%mcounts
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assert reads in df.columns, "%s not in dataframe"%reads
    # if no
    except IndexError as e:
        print "Item number of values is not 2.\n"
        print "IndexError. ",e.message
        print a
    except ValueError as e:
        print "Sample name could not be converted to float: %s\n"% type(item[i])
        print "ValueError. ",e.message
        print a
    except AssertionError as e:
        print "Assertion failed:"
        print e.message
        print a
    return data arr
def threshold(group, reps_remaining, thresh_val, thresh_i,
             percent mcounts=PERCENT MCOUNTS, mcounts=MCOUNTS):
    """Thresholds barcodes of a given sample
        group(pd.DataFrame): df containing library-ID-barcodes,
            mcountsPF and percent mcountsPF
        reps_remaining(int): reps remaining from max number
            input from user
        thresh val(float or int): initial threshold value (percent mcountPF)
            provided from previous recursion or user input
        thresh i(int): initial position of threshold value in
            percent mcountsPF list, ranging [0,len(group))
        Returns:
            None, if thresholding fails;
            passed(pd.DataFrame), if thresholding successful; or
            self, otherwise, with updated threshold values and
                group df.
    .....
    # max out reps
    if reps remaining <= 0:</pre>
        print 'Maxed out reps. Skipping sample.'
    # no barcodes passed threshold
    elif len(group) == 0:
        print "No barcodes passed threshold. Skipping sample."
    else:
        # calculate new threshold
        # line add 2016-10-12 to pre-sort values
        group.sort values(by=mcounts, ascending=False, inplace=True)
        # existing
        group = calculate_percent_molecs(group)
        calc threshold i = calculate threshold(group[mcounts].values)
        new_thresh_i = min(calc_threshold_i, len(group)-1)
        new_thresh_val = group[percent_mcounts].values[new_thresh_i]
         print "\nTOP OF THRESHOLD "
#
         print 'group len', len(group)
#
         print 'thresh_val', thresh_val
#
          print 'thresh i', thresh i
#
          print 'calc_threshold_i', calc_threshold_i
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#
          print 'new_thresh_i', new_thresh_i
          print 'new_thresh_val', new_thresh_val, '\n'
#
        # if reached steady state
        if new thresh val == thresh val:
            # get rid of any "padding" barcodes (see eliminate_oneoffs fn)
            # line added 2016-10-12 to remove barcodes that didn't pass threshold
            passed_temp = group.loc[(group.is_padding==False) & (group[percent_mcounts]>=new_
thresh_val)]
            passed = calculate_percent_molecs(passed_temp)
            # update percent molecs
            passed.reset index(inplace=True,drop=True)
              print 'barcodes', Len(group)
#
            sys.stdout.write('Thresholded.\n')
            return passed
        # recursively clean and re-threshold
        else:
            # clean up group by eliminating one-offs
            group = calculate percent molecs(group)
            cleaned = eliminate oneoffs(group,new thresh val)
            cleaned.reset_index(inplace=True,drop=True)
            # recurse with cleaned df and new threshold values
            return threshold(cleaned, reps remaining-1, new thresh val,
                             new_thresh_i, percent_mcounts=percent_mcounts,
                             mcounts=mcounts)
    # if thresholding failed, return None
    sys.stdout.write('Skipped.\n')
    return pd.DataFrame()
# STEP 2: CALCULATE THRESHOLD via. CONCAVITY
def calculate threshold(y):
    """Calculates threshold of series with modified concavity approach
       y(np.array or list): list or list-like object of
            values as floats or ints
        Returns index of inflection point in array,
            i.e. threshold position.
    def rolling window(arr):
        """Constructs list of overlapping subarray ranges of size 2"""
        shape = arr.shape[:-1] + (arr.shape[-1]-1, 2)
        strides = arr.strides + (arr.strides[-1],)
        windows = np.lib.stride_tricks.as_strided(arr,
                              shape=shape, strides=strides)
        return windows
    def first d gen(windows):
        """Generates first derivative of windows as relative difference"""
        for w in windows:
            # amended 2016-10-12: normalize by y midpoint instead of second point to
            # better represent the count magnitude of segment
            yield float(w[1]-w[0])/(w[0]+w[1])*2
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def second d gen(windows):
        """Generates second derivative of windows"""
        for w in windows:
            yield w[1]-w[0]
   y_temp = sorted(y, reverse=True)
#
      if False in [yi==y_tempi for yi, y_tempi in zip(y, y_temp)]:
          print "DIFFERENT!"
#
    # left and right padding to cover all array vals in derivations
   yarray = np.concatenate([ [y_temp[0]], y_temp, [1] ])
    # calculates first derivative
    first_windows = rolling_window(yarray)
   first derivs = np.fromiter(first d gen(first windows), np.float
                               , count=len(first_windows))
    # calculates second derivative
    second windows = rolling window(first derivs)
    second derivs = np.fromiter(second d gen(second windows), np.float
                                , count=len(second_windows))
    # gets index or position value of inflection point (curves down ), adjust by adding 1
    # for second deriv
   thresh_i = np.argmin(second_derivs)+1
      print "\nCALCULATE THRESHOLD"
#
#
     print "2nd max", np.argmax(second_derivs), np.max(second_derivs)
     print "2nd min", np.argmin(second_derivs), np.min(second_derivs)
#
      print "\n"
#
    return thresh_i
def eliminate oneoffs(group, thresh val, pad=True,
                      qtag=QTAG, barcode=BARCODE, percent mcounts=PERCENT MCOUNTS,
                      mcounts=MCOUNTS):
    """Eliminate barcodes that are one position off from a more-abundant barcode
        group(pd.DataFrame): df containing qtag, barcode, and percent_mcounts columns
        thresh_val(float): threshold value to select high abundant barcodes
            to iterate through as 'major' ones
        pad(bool): if True, adds a right pad so last non-eliminated value
            can be analyzed in by the threshold() function. Default True.
        gtag, barcode, percent mcounts, mcounts (str): column names for the corresponding
            argument. Defaults are global vars QTAG, BARCODE, PERCENT MCOUNTS, MCOUNTS.
        Returns: table of barcodes that passed elimination
    group.loc[:,'delete'] = group[mcounts].apply(lambda _: False)
    group.loc[:,'is padding'] = group[mcounts].apply(lambda : False)
    counter = 0
    # add capability to check other parameters, i.e. qtaq
    for majorI, majorRow in group.loc[group[percent mcounts] > thresh val].iterrows():
        # if it has not yet been tested
        if majorRow.delete == False:
            subgroup = group[counter+1:].loc[(group.delete==False)]
            # for each 'minor' barcode aka. with fewer molecs, test if one-off from major
            for minorI, minorRow in subgroup.iterrows():
                query = regex.search("(%s){s<=1}" % majorRow[barcode],</pre>
                                     minorRow[barcode])
                if query:
                    group.loc[minorI,'delete'] = True
        counter+=1
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# select barcodes which pass, ie. are not eliminated
   output = group.loc[(group.delete==False) & (group[percent_mcounts] >= thresh_val)]
     print "\nEND OF ELIMINATE ONEOFFS"
#
     print len(output)
   # if requested, adds a right pad
   # line added 2016-10-12: combine two conditions: ensure that
    # no null rows get added if all barcodes are accepted
    if pad==True and len(group) != len(group.delete==False):
        deletes = group.loc[(group.delete==True) & (group[percent mcounts]<thresh val)][mcoun</pre>
ts]
          if len(deletes) > 0:
        max i = deletes.idxmax()
        output.append(group.loc[max_i,:])
        output.loc[max_i,['delete', 'is_padding']] = [False, True]
      print output.head(), "\n"
    return output
def run_threshold(d, sample=SAMPLE, qtag=QTAG, barcode=BARCODE,
                  mcounts=MCOUNTS, reads=READS, percent_mcounts=PERCENT_MCOUNTS,
                  min_reads=MIN_READS, min_mcount=50):
    """Run threshold algorithm for each sample in dataset
        d(np.array, list, dict, or pd.DataFrame): dataset for all samples
        sample, qtag, barcode, mcounts, reads, percent_mcounts(str): columns in df for
            corresponding vals. Defaults are global vars SAMPLE, QTAG, BARCODE, MCOUNTS,
            READS, PERCENT MCOUNTS.
        min reads(int): minimum number of reads for a Library-ID-barcode as an
            absolute baseline (that which any barcode below is highly likely to be
            false.) Default is global var MIN READS.
       min mcount(int): minimum number of molecs for library-ID-barcode as an
            absolute baseline. Default is 50.
        Note: min_reads and min_mcount are applied to increase performance.
        Returns:
            pd.DataFrame, if successful, of 'true' (passed) library-ID-barcodes
                for all samples
            None, if no samples had passing library-ID-barcodes.
   passed = []
    counter = 1
    # checks and formats data (d) to list-like obj of pairs
   data arr = check data(d, sample=sample, mcounts=mcounts, reads=reads)
    # run for each (sample, df) in dataset
    for s, group in data_arr:
#
          print '\n\n>>>> NEW INDEX'
        sys.stdout.write("Sample %d of %d (%s): "%(counter,len(data arr),s))
        # select valid data meeting absolute baseline
        group = group.loc[(group[qtag] != 'None') & (group[barcode] != 'None')
                          & (group[mcounts] > min_mcount)
                          & (group[reads] > min_reads)]
        result = threshold(group, 20, -1, len(group)+2)
        passed.append(result)
        sys.stdout.flush()
        counter += 1
    # if we do have data (i.e. some barcodes that passed in the samples)
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if len(passed) > 0:
        # concat all df together
        passeddf = pd.concat(passed)
        # formatting
        passeddf.sort_values(by=[sample,percent_mcounts]
                             ,ascending=[True, False]
                             ,inplace=True)
        passeddf.drop(['delete','is_padding'], axis=1, inplace=True)
        passeddf.reset_index(inplace=True,drop=True)
        return passeddf
    else:
        print "No samples were successfully thresholded."
   return
def save_data(filtered,passed, output_directory=OUTPUT_DIRECTORY, experiment=EXPERIMENT):
    # Save passed dataframe
    passed.to_csv('%s/threshold-%s-passed.csv'%(output_directory,experiment), index=False)
    # count and save results
    counts = count_sample_barcodes(passed)
    counts.to_csv('%s/threshold-%s-counts.csv'%(output_directory,experiment), index=False)
    # merge passed and filtered data and save
    fc temp = pd.concat([d[1] for d in filtered])
    filtered_concat = apply_passed_data(fc_temp, passed)
    filtered_concat.to_csv('%s/threshold-%s-merged.csv'%(output_directory,experiment),
index=False)
def count sample barcodes(df, groupby=SAMPLE, barcode=BARCODE, sample=SAMPLE, qtag=QTAG
                      , percent_mcounts=PERCENT MCOUNTS):
    """Counts passed barcodes per sample and saves as csv
        df(pd.DataFrame): input dataframe containing passed
            barcodes of all samples
       groupby(str or list-like): columns to group samples by
    agg = df.groupby(groupby).agg(len)
    counts = agg[agg.columns[0]]
    counts.name = 'count'
    counts = pd.DataFrame(counts)
    counts.reset_index(inplace=True)
    return counts
def apply passed data(filtered, passed, sample=SAMPLE, qtag=QTAG
                      , barcode=BARCODE, percent_mcounts=PERCENT_MCOUNTS):
    """Cross reference passed barcodes with raw filtered data
        filtered(pd.DataFrame): raw filtered data as dataframe for all samples
        passed(pd.DataFrame): data passed threshold (output of run threshold)
        sample, qtag, barcode, percent_mcounts(str): names corresponding to df columns.
            Defaults are SAMPLE, QTAG, BARCODE, PERCENT_MCOUNTS.
        Returns:
            filtered(pd.DataFrame) updated with 'passed threshold' and
            percent mcounts columns
    .. .. ..
    def cross_ref_passed(row):
        key = (row[sample],row[qtag],row[barcode])
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if key in passed indexed.index:
            row[percent_mcounts+'_thresholded'] = passed_indexed.loc[key,percent_mcounts]
            row['passed_threshold'] = True
        return row
   passed_indexed = passed.set_index([sample,qtag,barcode])
   filtered.rename(columns={percent_mcounts:percent_mcounts+'_filtered'})
   filtered['passed_threshold'] = False
   filtered[percent_mcounts+'_thresholded'] = 0
   filtered = filtered.apply(cross ref passed, axis=1)
   return filtered
if __name__=='__main__':
    # Check all inputs exist and are valid
   check_inputs()
   # Runs data Loading in script
   filtered = load data(FILTERED FILEPATH)
   # Run thresholding of all samples in dataset
   passed = run threshold(filtered)
    save_data(filtered, passed, output_directory=OUTPUT_DIRECTORY, experiment=EXPERIMENT)
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