2.0_dcj_explore_all_profiles

July 9, 2021

0.1 Exploratory clustering attempt : applying GMM to SO-CHIC data suite

In this exploratory notebook, I'll apply PCA and GMM to the SO-CHIC data suite that has been prepared by Shenjie Zhou (BAS). The results are reasonably distinct clusters, both in PC space and in lat-lon space. The i-metric highlights boundaries between the classes.

0.1.1 Import modules

[1]:
```
#import scikit-learn
from sklearn import mixture
from sklearn import preprocessing
from sklearn.decomposition import PCA
# import matplotlib
import matplotlib.colors as colors
import matplotlib.pyplot as plt
import matplotlib.cm as cmx
import matplotlib as mpl
# pandas for just a couple things
import pandas as pd
# for label map
import cartopy
import cartopy.crs as ccrs
import cartopy.feature as cfeature
# pyxpcm, xarray, dask
import numpy as np
import xarray as xr
import datetime as dt
import random
# import dask
from dask.distributed import Client
import dask
# for 3D plotting
from mpl_toolkits.mplot3d import Axes3D
import matplotlib.cm as cm
import seaborn as sns
```

Start Dask client

```
[2]: client = Client(n_workers=2, threads_per_worker=2, memory_limit='3GB')
     client
```

```
[2]: <Client: 'tcp://127.0.0.1:60095' processes=2 threads=4, memory=6.00 GB>
```

0.1.2 Subset parameters

These values indicate which lat-lon-depth range will be used in the clustering analysis. The first parameter, called "subset", is an arbitrary selection of profiles for quick plotting purposes. That parameter does not affect how many profiles are used in the clustering.

```
[3]: # name of file for saving output
     fname = 'profiles_80W-80E_85-30S_100-900_labeled.nc'

     # save the processed output as a NetCDF file?
     saveOutput==True

     # plotting subset
     subset = range(1000,2000,1)

     lon_min = -80
     lon_max =  80
     lat_min = -85
     lat_max = -30

     # depth range
     zmin = 100.0
     zmax = 900.0
```

0.1.3 Import data

Shenjie Zhou (BAS) prepared these profiles using MITprof software, which produces a set of profiles that have been interpolated onto a specified set of depth levels. They are all in NetCDF format with standard names. I've decided to use xarray below for ease of use.

```
[4]: # load the ctds, floats, and seals
     ctds = xr.open_mfdataset('../../../so-chic-data/CTD/*.nc', concat_dim='iPROF',␣
      ↪combine='nested')
     floats = xr.open_mfdataset('../../../so-chic-data/FLOATS/*.nc',␣
      ↪concat_dim='iPROF', combine='nested')
     seals = xr.open_mfdataset('../../../so-chic-data/SEALS/*.nc',␣
      ↪concat_dim='iPROF', combine='nested')

     # combine into single xarray.Dataset object
     profiles = xr.combine_nested([ctds, floats, seals], concat_dim='iPROF')

     # assign depth coordinate
```

```
profiles.coords['iDEPTH'] = profiles.prof_depth[0,:].values

# select subset of data between 0-1000 dbar
profiles = profiles.sel(iDEPTH=slice(zmin,zmax))

# rename some of the variables
profiles = profiles.rename({'iDEPTH':'depth',
                            'iPROF':'profile',
                            'prof_lon':'lon',
                            'prof_lat':'lat'})

# drop the "prof_depth" variable, because it's redundant
profiles = profiles.drop_vars({'prof_depth'})

# change lon and lat to coordinates
profiles = profiles.set_coords({'lon','lat'})

# only keep a subset of the data variables, as we don't need them all
profiles = profiles.
 ↪get(['prof_date','prof_YYYYMMDD','prof_HHMMSS','prof_T','prof_S'])

# select lat/lon section using the subsetting parameters specified above
profiles = profiles.where(profiles.lon<=lon_max,drop=True)
profiles = profiles.where(profiles.lon>=lon_min,drop=True)
profiles = profiles.where(profiles.lat<=lat_max,drop=True)
profiles = profiles.where(profiles.lat>=lat_min,drop=True)

# drop any remaining profiles with NaN values
# the profiles with NaN values likely don't have measurements in the selected␣
 ↪depth range
profiles = profiles.dropna('profile')

# exameine Dataset
profiles
```

```
[4]: <xarray.Dataset>
Dimensions:          (depth: 15, profile: 185612)
Coordinates:
    lon              (profile) float64 dask.array<chunksize=(546,),
meta=np.ndarray>
    lat              (profile) float64 dask.array<chunksize=(546,),
meta=np.ndarray>
  * depth            (depth) float64 100.0 120.0 140.0 160.0 … 640.0 730.0 820.0
Dimensions without coordinates: profile
Data variables:
    prof_date        (profile) float64 dask.array<chunksize=(546,),
meta=np.ndarray>
```

```
    prof_YYYYMMDD  (profile) float64 dask.array<chunksize=(546,),
meta=np.ndarray>
    prof_HHMMSS    (profile) float64 dask.array<chunksize=(546,),
meta=np.ndarray>
    prof_T         (profile, depth) float64 dask.array<chunksize=(546, 15),
meta=np.ndarray>
    prof_S         (profile, depth) float64 dask.array<chunksize=(546, 15),
meta=np.ndarray>
```

0.1.4 Time and date handling (currently broken)

[5]:
```python
# select MITprof values
ntime_array_ymd = profiles.prof_YYYYMMDD.values
ntime_array_hms = profiles.prof_HHMMSS.values

# select size
nsize = ntime_array_ymd.size

# create array of zeros
time = np.zeros((nsize,), dtype='datetime64[s]')

# loop over all values, convert do datetime64[s]
for i in range(nsize):
    # extract strings for ymd and hms
    s_ymd = str(ntime_array_ymd[i]).zfill(8)
    # hms doesn't matter and has errors.
    # set to noon and ignore it
    #s_hms = str(ntime_array_hms[i]).zfill(8)
    s_hms = '120000'
    # problem with 24:00:00
    #if s_hms=='240000.0':
    #    s_hms = '235959.0'
    # format into yyyy-mm-dd hh:mm:ss
    date_str_ymd = s_ymd[0:4] + '-' + s_ymd[4:6] + '-' + s_ymd[6:8]
    date_str_hms = s_hms[0:2] + ':' + s_hms[2:4] + ':' + s_hms[4:6]
    date_str =  date_str_ymd + ' ' + date_str_hms
    # convert to datetime64 (the 's' stands for seconds)
    time[i] = np.datetime64(date_str,'s')

# convert to pandas datetime (may not may not end up using this)
time_pd = pd.to_datetime(time)

# convert time array into a DataArray
da = xr.DataArray(time, dims=['profile'])

# add DataArray as new data variable to DataSet
profiles['time'] = da
```

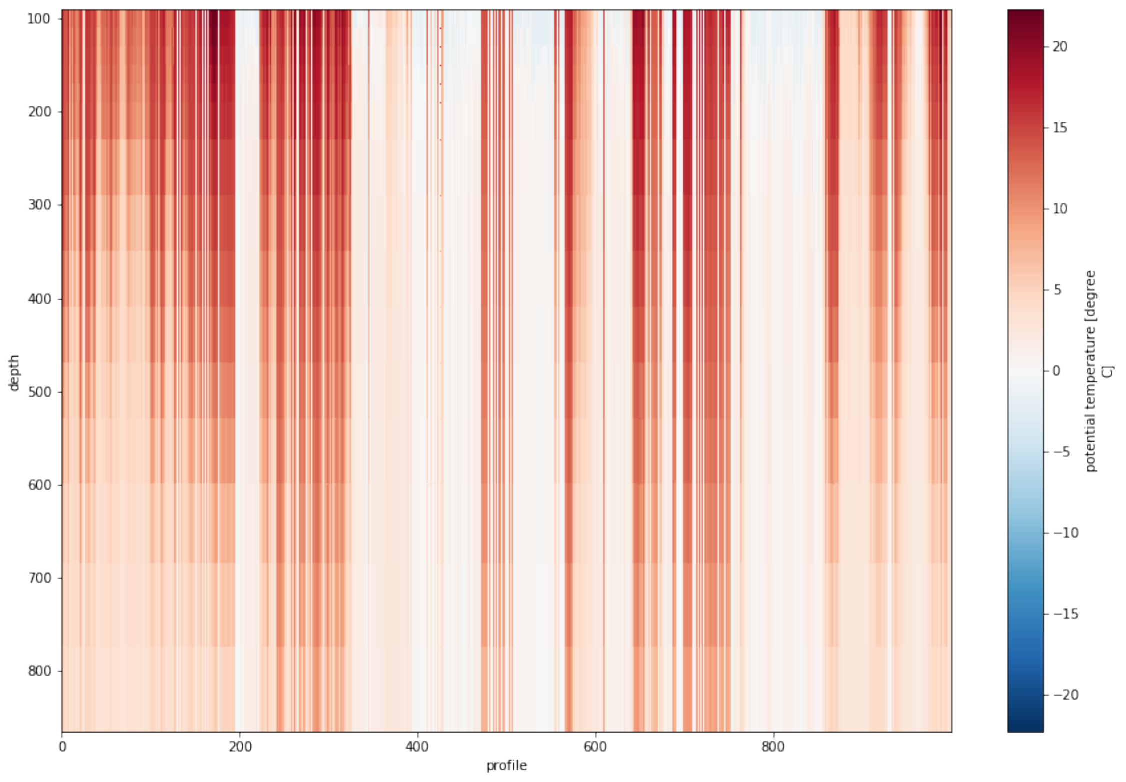
```
# set time as a coordinate
profiles = profiles.set_coords('time')

# examine Dataset again
#profiles
```

0.1.5 Plot subset of temperature profiles

This is an arbitrary subset of the profiles, just for data visualization purposes.

```
[6]: fig, ax = plt.subplots(figsize=(15,10))
     profiles.prof_T[subset].plot(y='depth', yincrease=False)
```

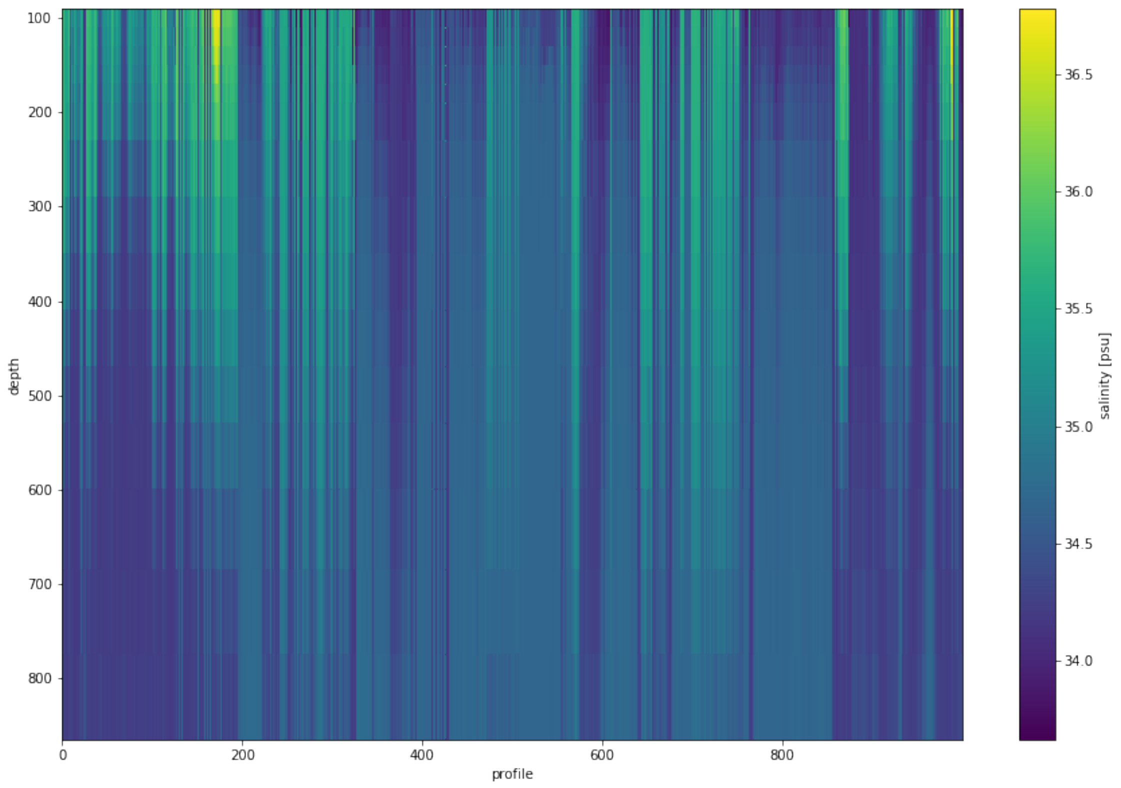
```
[6]: <matplotlib.collections.QuadMesh at 0x7fbc245b38d0>
```



0.1.6 Plot subset of salinity profiles

```
[7]: fig, ax = plt.subplots(figsize=(15,10))
     profiles.prof_S[subset].plot(y='depth', yincrease=False)
```

```
[7]: <matplotlib.collections.QuadMesh at 0x7fbc23f7c1d0>
```

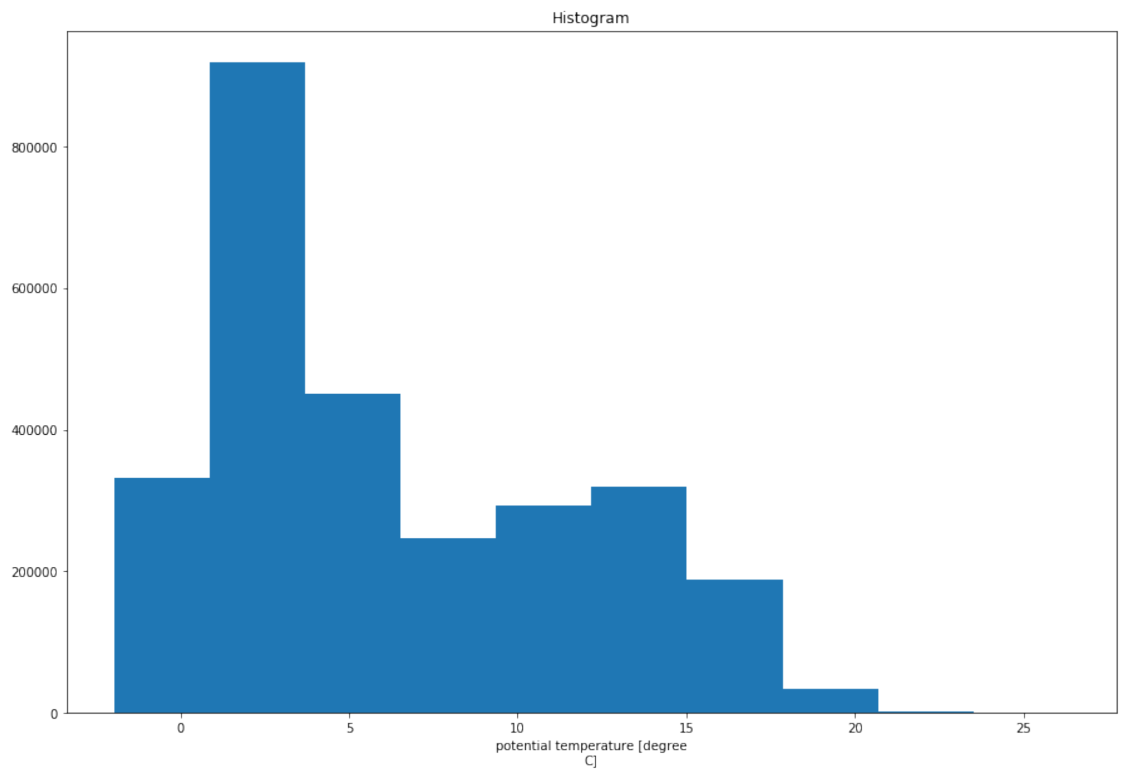


0.1.7 Plot histograms to get a sense of the data distribution

First, plot the potential temperature histogram

```
[8]: xr.plot.hist(profiles.prof_T,figsize=(15,10))
```

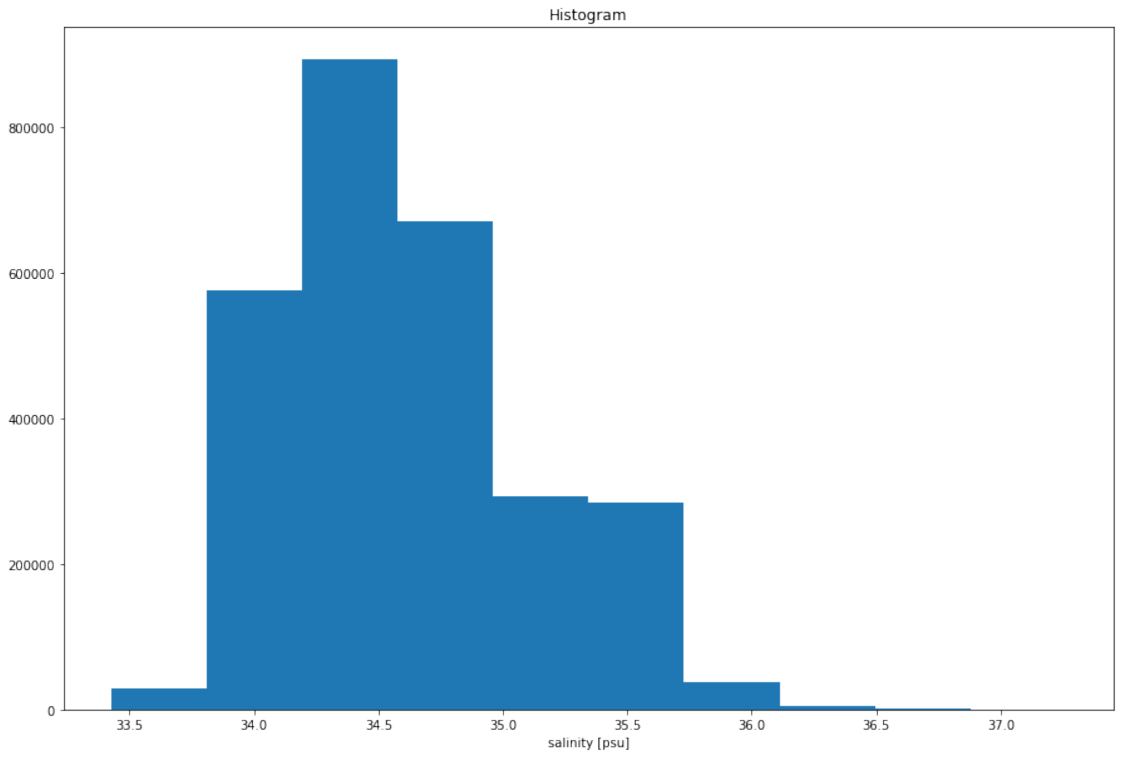
```
[8]: (array([3.31094e+05, 9.17855e+05, 4.50864e+05, 2.47243e+05, 2.92072e+05,
             3.19577e+05, 1.88427e+05, 3.49050e+04, 2.08100e+03, 6.20000e+01]),
      array([-1.9605945 ,  0.8698903 ,  3.70037509,  6.53085988,  9.36134467,
             12.19182947, 15.02231426, 17.85279905, 20.68328384, 23.51376864,
             26.34425343]),
      <a list of 10 Patch objects>)
```



Next, plot the salinity histogram

```
[9]: xr.plot.hist(profiles.prof_S,figsize=(15,10))
```

```
[9]: (array([2.84180e+04, 5.75468e+05, 8.92284e+05, 6.69577e+05, 2.91880e+05,
             2.83763e+05, 3.70670e+04, 4.70700e+03, 8.87000e+02, 1.29000e+02]),
      array([33.42644781, 33.80997736, 34.19350691, 34.57703646, 34.96056601,
             35.34409556, 35.7276251 , 36.11115465, 36.4946842 , 36.87821375,
             37.2617433 ]),
      <a list of 10 Patch objects>)
```



0.2 Clustering with GMM

Preprocessing/scaling and dimensionality reduction via PCA

[10]:
```
# scale salinity
X = profiles.prof_S
scaled_S = preprocessing.scale(X)
scaled_S.shape

# scale temperature
X = profiles.prof_T
scaled_T = preprocessing.scale(X)
scaled_T.shape

# concatenate
Xscaled = np.concatenate((scaled_T,scaled_S),axis=1)

# create PCA object
pca = PCA(n_components=3)

# fit PCA model
pca.fit(Xscaled)

# transform input data into PCA representation
```

```
Xpca = pca.transform(Xscaled)

# add PCA values to the profiles Dataset
PCA1 = xr.DataArray(Xpca[:,0],dims='profile')
PCA2 = xr.DataArray(Xpca[:,1],dims='profile')
PCA3 = xr.DataArray(Xpca[:,2],dims='profile')

# calculated total variance explained
total_variance_explained_ = np.sum(pca.explained_variance_ratio_)
total_variance_explained_
```

[10]:
```
0.9858584618007592
```

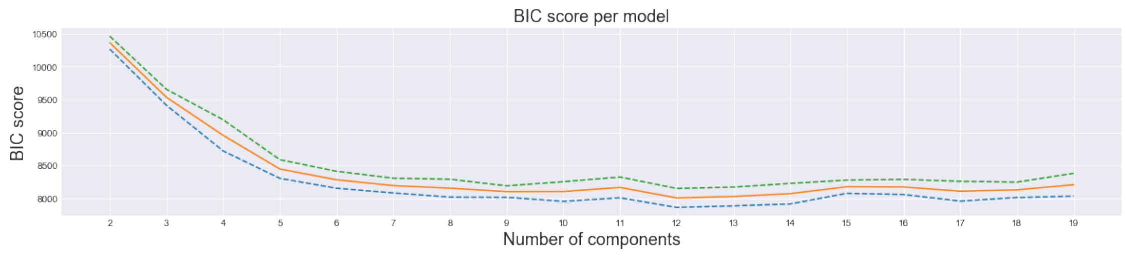
0.2.1 Calculate BIC to inform selection of the number of clusters

[11]:
```
# select parameters
max_N = 20      # the maximum number of classes to try
max_bic_iter = 20  # the maximum number of iterations for BIC

# for the BIC step, try using a subset of the profiles
# you can change this 1000 value for different subsets
#Xpca_for_BIC = Xpca[::1000]

# initialise, declare variables
lowest_bic = np.infty
bic_scores = np.zeros((2,max_bic_iter))

# loop through the maximum number of classes, estimate BIC
n_components_range = range(2, max_N)
bic_iter_range = range(0,max_bic_iter)
# iterate through all the covariance types (just 'full' for now)
cv_types = ['full']
for cv_type in cv_types:
    # iterate over all the possible numbers of components
    for n_components in n_components_range:
        bic_one = []
        # repeat the BIC step for better statistics
        for bic_iter in bic_iter_range:
            # select a new random subset
            rows_id = random.sample(range(0,Xpca.shape[0]-1), 1000)
            Xpca_for_BIC = Xpca[rows_id,:]
            # fit a Gaussian mixture model
            gmm = mixture.GaussianMixture(n_components=n_components,
                                          covariance_type=cv_type,
                                          random_state=42)

            # uncomment for 'rapid' BIC fitting
            gmm.fit(Xpca_for_BIC)
            # uncomment for 'full' BIC fitting
            #gmm.fit(Xpca)

            # append this BIC score to the list
            bic_one.append(gmm.bic(Xpca_for_BIC))
            Xpca_for_BIC = []

        # stack the bic scores into a single 2D structure
        bic_scores = np.vstack((bic_scores, np.asarray(bic_one)))

# the first two rows are not needed; they were only placeholders
bic_scores = bic_scores[2:,:]

# mean values for BIC
bic_mean = np.mean(bic_scores, axis=1)

# standard deviation for BIC
bic_std = np.std(bic_scores, axis=1)

# examine the mean bic values
#bic_mean
```

0.2.2 Plot the BIC scores

[12]:
```
# plot the BIC scores
plt.figure(figsize=(20, 8))
plt.style.use('seaborn-darkgrid')
spl = plt.subplot(2, 1, 1)
plt.plot(n_components_range, bic_mean-bic_std, '--')
plt.plot(n_components_range, bic_mean, '-')
plt.plot(n_components_range, bic_mean+bic_std, '--')
plt.xticks(n_components_range)
#plt.ylim([bic.min() * 1.01 - .01 * bic.max(), bic.max()])
plt.title('BIC score per model', fontsize=18)
spl.set_xlabel('Number of components',fontsize=18)
spl.set_ylabel('BIC score',fontsize=18)
#plt.show()
```

[12]:
```
Text(0, 0.5, 'BIC score')
```



As with many other oceanographic applications, there is not a clear minimum. Instead, the BIC curve flattens. We can opt for a smaller number of classes for ease of interpretation. Choosing a value of 5 is not quite the minimum, but after 5 the decrease in BIC is much more gradual, so it's still a reasonable choice.

0.2.3 Select the actual GMM to be used in the analysis

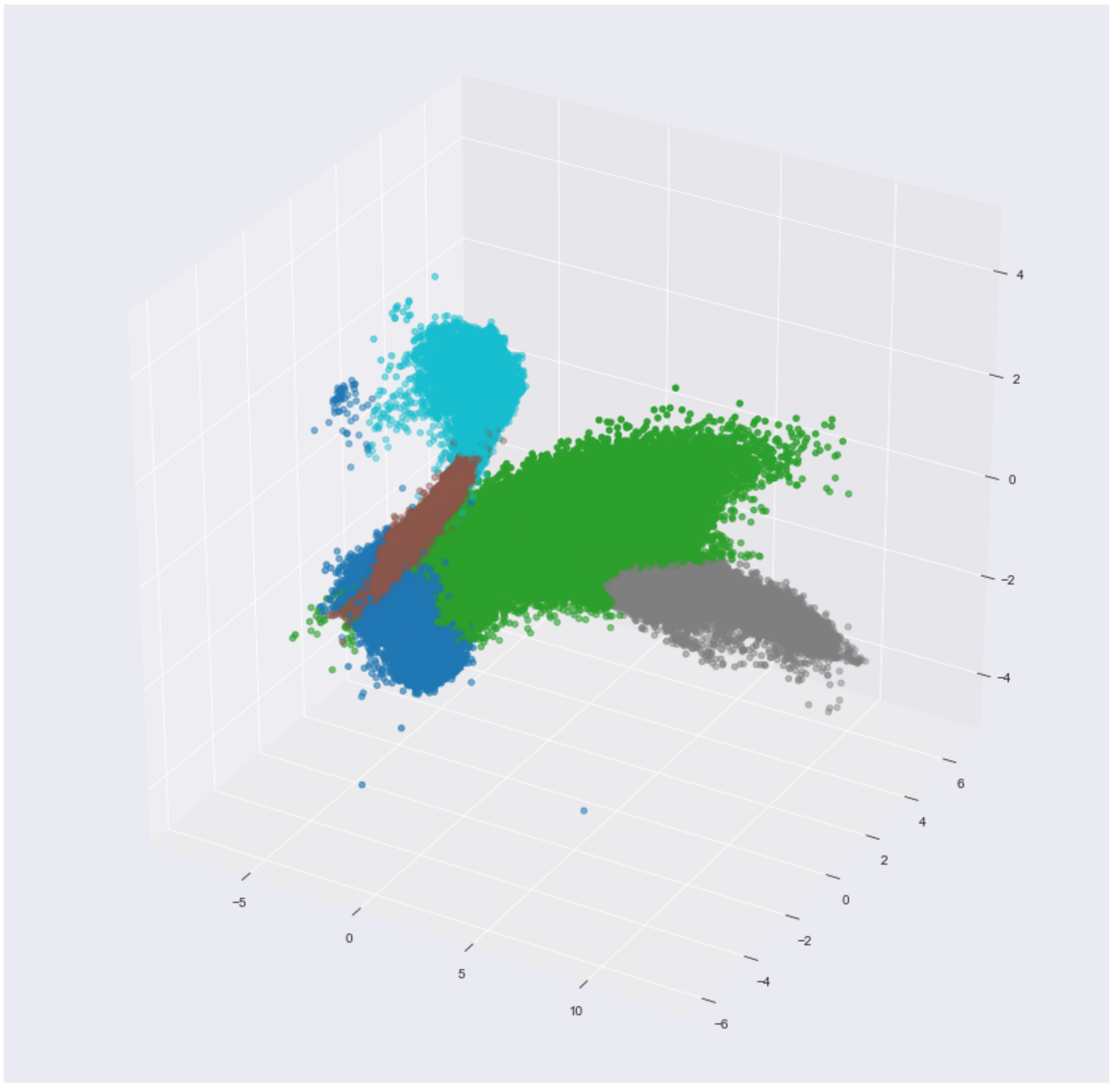
[13]:
```
# set variables
n_components_selected = 5

# establish gmm
best_gmm = mixture.GaussianMixture(n_components=n_components_selected,
                                   covariance_type='full',
                                   random_state=42)

# fit this GMM
best_gmm.fit(Xpca)

# check to make sure that n_comp is as expected
n_comp = gmm.n_components

# select colormap
colormap = plt.get_cmap('tab10', n_comp)

# assign class labels ("predict" the class using the selected GMM)
labels = best_gmm.predict(Xpca)

# find posterior probabilities (the probabilities of belonging to each class)
posterior_probs = best_gmm.predict_proba(Xpca)

# maximum posterior probability (the class is assigned based on this value)
max_posterior_probs = np.max(posterior_probs,axis=1)

# put the labels and maximum posterior probabilities back in original dataframe
#df.insert(3,'label',labels,True)
#df.insert(4,'max posterior prob',max_posterior_probs,True)
```

```
# print out best_gmm parameters
#posterior_probs.shape

# convert labels into xarray format
xlabels = xr.DataArray(labels, coords=[profiles.profile], dims='profile')

# convert posterior probabilities into xarray format
gmm_classes = [b for b in range(0,n_components_selected,1)]
xprobs = xr.DataArray(posterior_probs,
                      coords=[profiles.profile, gmm_classes],
                      dims=['profile', 'CLASS'])

# add label DataArray to Dataset
profiles = profiles.assign({'label':xlabels})
profiles = profiles.assign({'posteriors':xprobs})
```

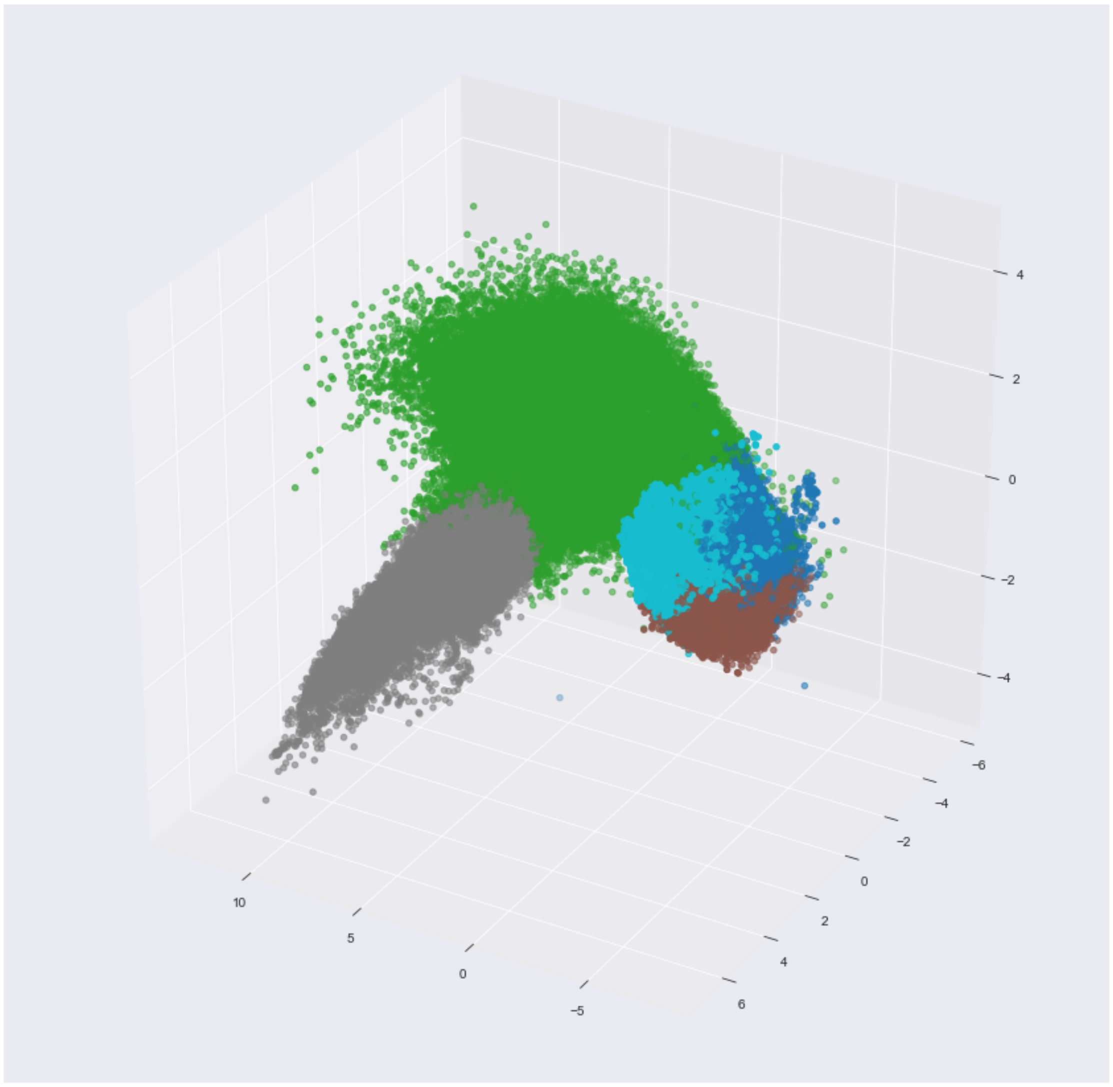
0.2.4 Visualise clustering in PC space

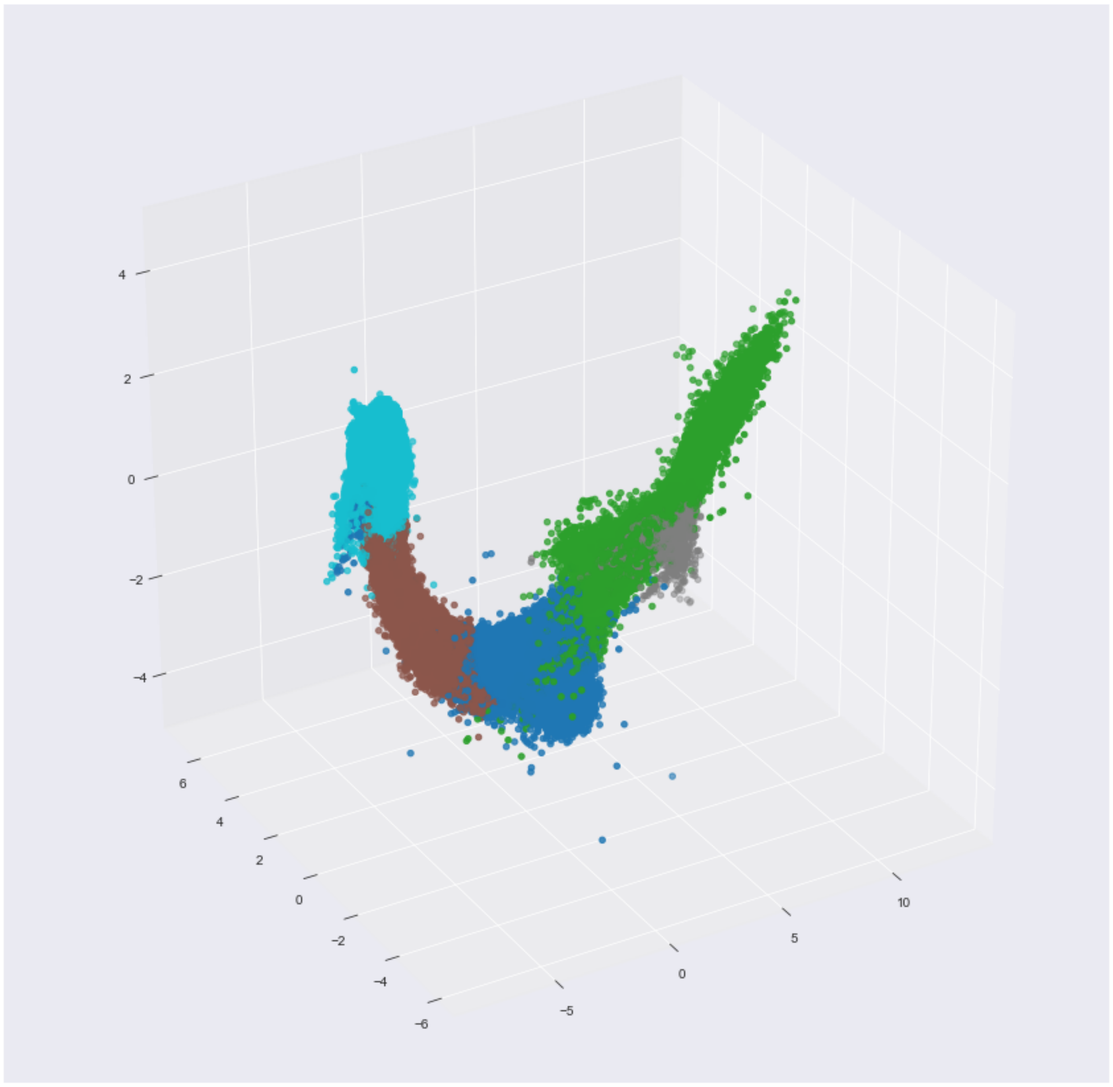
[14]:
```
# initial view
fig = plt.figure(figsize=(15,15))
ax = fig.add_subplot(projection='3d')
ax.scatter(PCA1.values, PCA2.values, PCA3.values, c=labels, cmap=cm.tab10)

# new view
fig = plt.figure(figsize=(15,15))
ax = fig.add_subplot(projection='3d')
ax.view_init(30, 120)
ax.scatter(PCA1.values, PCA2.values, PCA3.values, c=labels, cmap=cm.tab10)

# new view
fig = plt.figure(figsize=(15,15))
ax = fig.add_subplot(projection='3d')
ax.view_init(30, 240)
ax.scatter(PCA1.values, PCA2.values, PCA3.values, c=labels, cmap=cm.tab10)
```

[14]:
```
<mpl_toolkits.mplot3d.art3d.Path3DCollection at 0x7fbc12e5edd0>
```



−5
0
5
10
−6
−4
−2
0
2
4
6
−4
−2
0
2
4


4
2
0
−2
−4
−6
−4
−2
0
2
4
6
10
5
0
−5



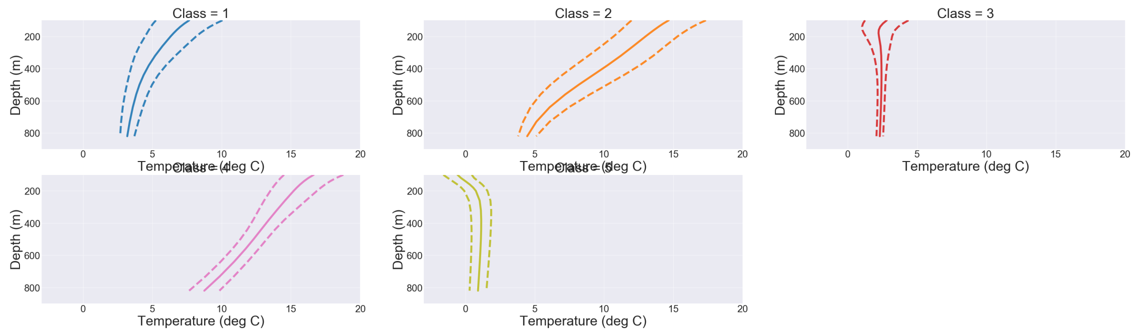
The classes look reasonably distinct in PCA space. There are some subtle oddities that might be better captured by a different clustering method; we'll explore later.

0.2.5 Calculate class means and standard deviations

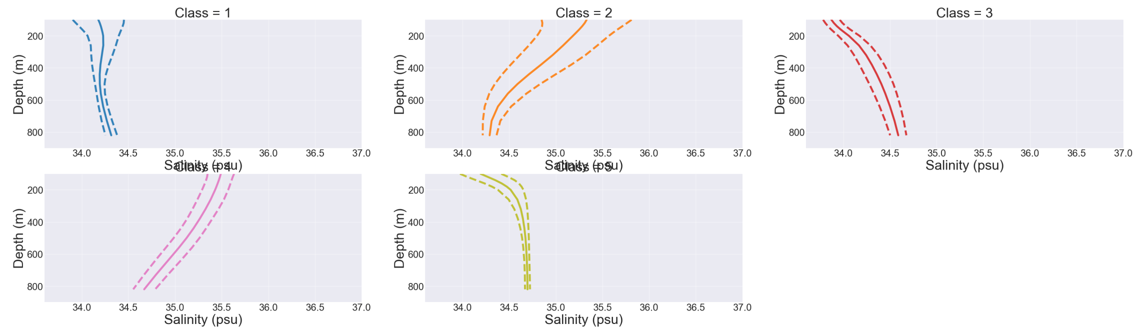
[15]:
```
# create grouped object using the labels
grouped = profiles.groupby("label")

# class means and standard deviations
class_means = grouped.mean()
class_stds = grouped.std()

# visualize grouped dataset
#class_means
```

0.2.6 Plot vertical T and S structure of the classes

[16]:
```
cNorm = colors.Normalize(vmin=0, vmax=n_components_selected)
scalarMap = cmx.ScalarMappable(norm=cNorm, cmap=colormap)

# initialize the figure
plt.figure(figsize=(60, 60))
plt.style.use('seaborn-darkgrid')
#palette = cmx.Paired(np.linspace(0,1,n_comp))

# vertical coordinate
z = profiles.depth.values

# iterate over groups
num = 0
for nrow in range(0,n_components_selected):
    num += 1
    colorVal = scalarMap.to_rgba(nrow)

    # extract means
    mean_T = class_means.prof_T[nrow,:].values

    # extract stdevs
    std_T = class_stds.prof_T[nrow,:].values

    # select subplot
    ax = plt.subplot(np.ceil(n_comp/3),3,num)
    plt.plot(mean_T, z, marker='', linestyle='solid', color=colorVal,␣
↪linewidth=6.0, alpha=0.9)
    plt.plot(mean_T+std_T, z, marker='', linestyle='dashed', color=colorVal,␣
↪linewidth=6.0, alpha=0.9)
    plt.plot(mean_T-std_T, z, marker='', linestyle='dashed', color=colorVal,␣
↪linewidth=6.0, alpha=0.9)

    # custom grid and axes
    plt.ylim([zmin,zmax])
    plt.xlim([-3, 20])

   #text box
    fs = 42 # font size
    plt.xlabel('Temperature (deg C)', fontsize=fs)
    plt.ylabel('Depth (m)', fontsize=fs)
    plt.title('Class = ' + str(num), fontsize=fs)

    # font and axis stuff
    plt.gca().invert_yaxis()
    ax.tick_params(axis='x', labelsize=30)
    ax.tick_params(axis='y', labelsize=30)
```



[17]:
```
cNorm = colors.Normalize(vmin=0, vmax=n_components_selected)
scalarMap = cmx.ScalarMappable(norm=cNorm, cmap=colormap)

# initialize the figure
plt.figure(figsize=(60, 60))
plt.style.use('seaborn-darkgrid')
#palette = cmx.Paired(np.linspace(0,1,n_comp))

# vertical coordinate
z = profiles.depth.values

# iterate over groups
num = 0
for nrow in range(0,n_components_selected):
    num += 1
    colorVal = scalarMap.to_rgba(nrow)

    # extract means
    mean_S = class_means.prof_S[nrow,:].values

    # extract stdevs
    std_S = class_stds.prof_S[nrow,:].values

    # select subplot
    ax = plt.subplot(np.ceil(n_comp/3),3,num)
    plt.plot(mean_S, z, marker='', linestyle='solid', color=colorVal,␣
↪linewidth=6.0, alpha=0.9)
    plt.plot(mean_S+std_S, z, marker='', linestyle='dashed', color=colorVal,␣
↪linewidth=6.0, alpha=0.9)
    plt.plot(mean_S-std_S, z, marker='', linestyle='dashed', color=colorVal,␣
↪linewidth=6.0, alpha=0.9)

    # custom grid and axes
    plt.ylim([zmin, zmax])
    plt.xlim([33.6, 37.0])

   #text box
    fs = 42 # font size
    plt.xlabel('Salinity (psu)', fontsize=fs)
    plt.ylabel('Depth (m)', fontsize=fs)
    plt.title('Class = ' + str(num), fontsize=fs)

    # font and axis stuff
    plt.gca().invert_yaxis()
    ax.tick_params(axis='x', labelsize=30)
    ax.tick_params(axis='y', labelsize=30)
```

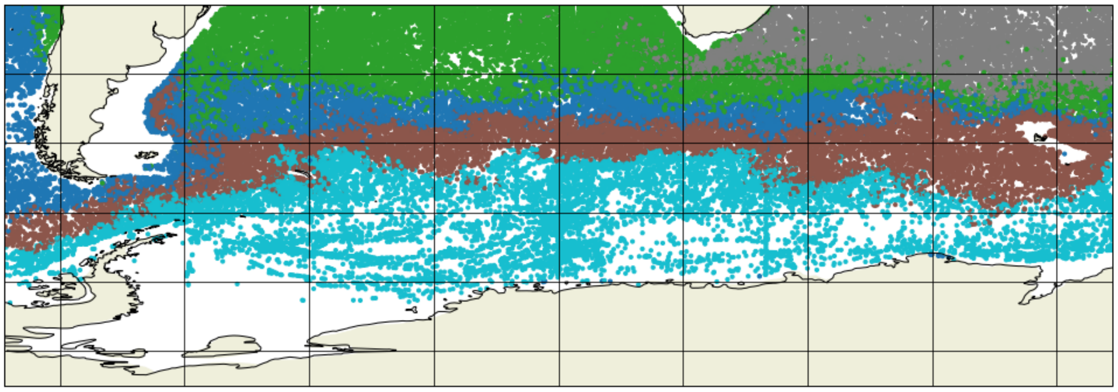


0.2.7 Label map of the classes

[18]:
```
# extract values as new DataArrays
df1D = profiles.isel(depth=0)
da_lon = df1D.lon
da_lat = df1D.lat
da_label = df1D.label

# extract values
lons = da_lon.values
lats = da_lat.values
clabels = da_label.values

# size of random sample
random_sample_size = int(np.ceil(0.30*df1D.profile.size))

# random sample for plotting
rows_id = random.sample(range(0,clabels.size-1), random_sample_size)
lons_random_sample = lons[rows_id]
lats_random_sample = lats[rows_id]
```

```
clabels_random_sample = clabels[rows_id]

#colormap with Historical data
plt.figure(figsize=(17, 13))
ax = plt.axes(projection=ccrs.PlateCarree())
ax.set_extent([lon_min, lon_max, lat_min, lat_max], ccrs.PlateCarree())
CS = plt.scatter(lons_random_sample-360,
                 lats_random_sample,
                 c=clabels_random_sample,
                 marker='o',
                 cmap= colormap,
                 s=10.0,
                 transform=ccrs.Geodetic(),
                 )
ax.coastlines(resolution='50m')
ax.gridlines(color='black')
ax.add_feature(cartopy.feature.LAND)
```

[18]:
```
<cartopy.mpl.feature_artist.FeatureArtist at 0x7fbc283dd190>
```



Note the emergence of the near-Antarctic class. One idea would be to take only those profiles and re-apply a clustering algorithm to them in order to capture finer-scale structure.

0.2.8 Calculate the i-metric

https://os.copernicus.org/preprints/os-2021-40/

[19]:
```
# function to calculate the i_metric, label, and runner-up label
def get_i_metric(posterior_prob_list):
    sorted_posterior_list = sorted(posterior_prob_list)
    ic_metric = 1 - (sorted_posterior_list[-1] - sorted_posterior_list[-2])
    runner_up_label = posterior_prob_list.index(sorted_posterior_list[-2])
    label = posterior_prob_list.index(sorted_posterior_list[-1])
    return ic_metric, np.array([label, runner_up_label]) # np.sort()
```

Loop through profiles (this may take a few minutes)

```
[20]: # declare variables
i_metric = np.zeros(df1D.profile.size)
a_b = np.zeros((df1D.profile.size,2))

# loop through the profiles, calculate the i_metric for each one
for i in range(df1D.profile.size):
      i_metric[i], a_b[i,:] = get_i_metric(df1D.posteriors[i, :].values.
 ↪tolist())
```

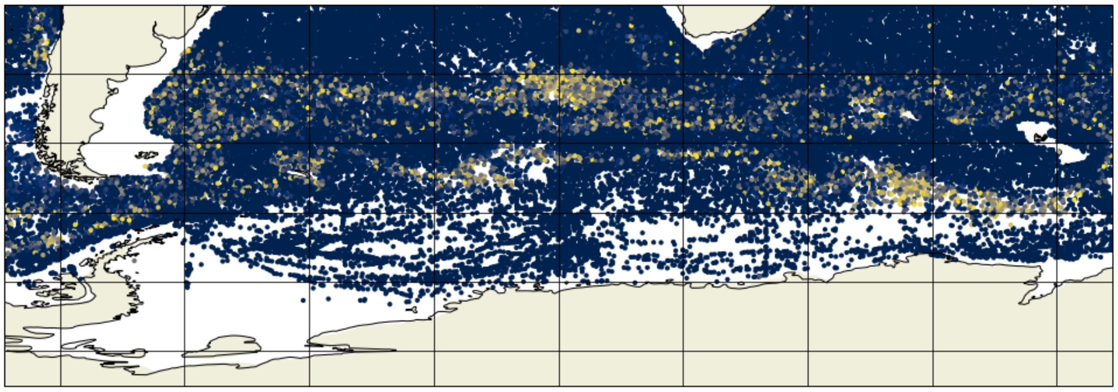
```
distributed.comm.tcp - WARNING - Closing dangling stream in <TCP
local=tcp://127.0.0.1:60178 remote=tcp://127.0.0.1:60095>
distributed.comm.tcp - WARNING - Closing dangling stream in <TCP
local=tcp://127.0.0.1:60181 remote=tcp://127.0.0.1:60095>
distributed.comm.tcp - WARNING - Closing dangling stream in <TCP
local=tcp://127.0.0.1:60246 remote=tcp://127.0.0.1:60095>
```

```
[21]: # convert i_metric numpy array to xarray DataArray
i_metric = xr.DataArray(i_metric, coords=[profiles.profile], dims='profile')

# add i_metric DataArray to Dataset
df1D = df1D.assign({'i_metric':i_metric})
```

0.2.9 Plot i-metric map

```
[22]: # extract values as new DataArrays
da_lon = df1D.lon
da_lat = df1D.lat
da_i_metric = df1D.i_metric

# extract values
lons = da_lon.values
lats = da_lat.values
c = da_i_metric.values

# random sample for plotting
rows_id = random.sample(range(0,c.size-1), random_sample_size)
lons_random_sample = lons[rows_id]
lats_random_sample = lats[rows_id]
clabels_random_sample = c[rows_id]

#colormap with Historical data
plt.figure(figsize=(17, 13))
ax = plt.axes(projection=ccrs.PlateCarree())
ax.set_extent([lon_min, lon_max, lat_min, lat_max], ccrs.PlateCarree())
CS = plt.scatter(lons_random_sample-360,
                 lats_random_sample,
                 c=clabels_random_sample,
                 marker='o',
                 cmap= plt.get_cmap('cividis'),
                 s=10.0,
                 transform=ccrs.Geodetic(),
                 )
ax.coastlines(resolution='50m')
ax.gridlines(color='black')
ax.add_feature(cartopy.feature.LAND)
```

```
[22]: <cartopy.mpl.feature_artist.FeatureArtist at 0x7fbc28ba7ad0>
```

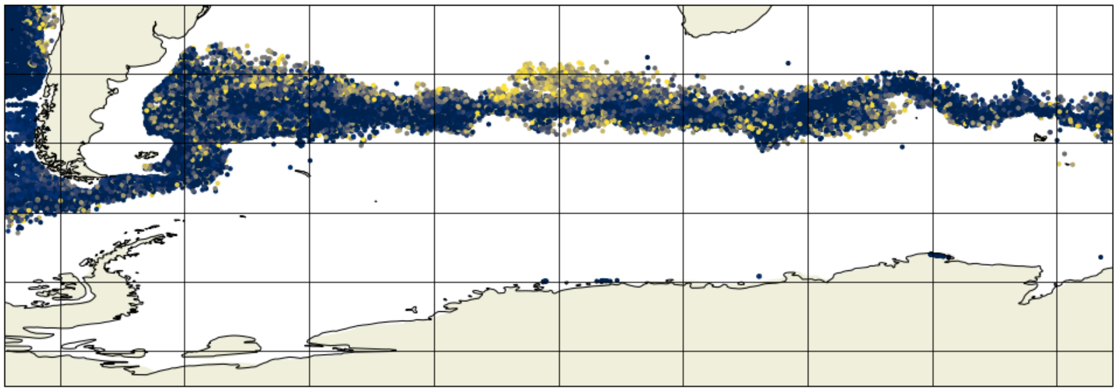


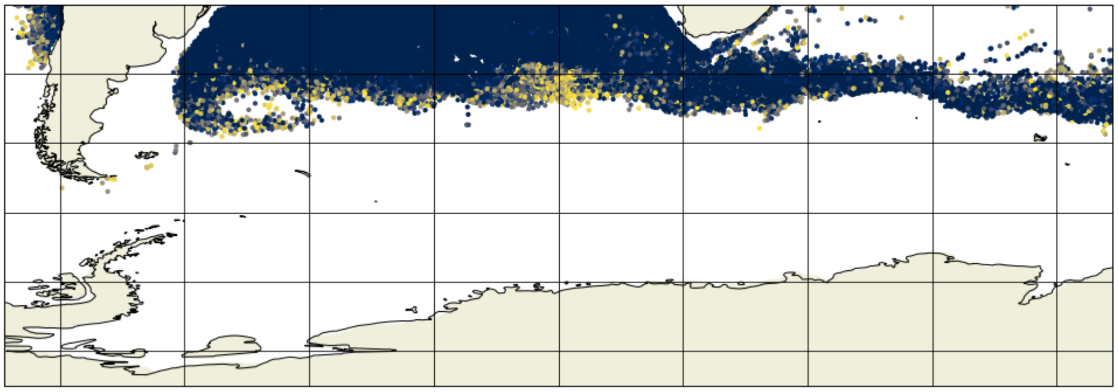
Darker shading indicates that the profile is *less* likely to be near a boundary between classes. Ligher shading indicates that the profile is *more* likely to be near a boundary between classes.

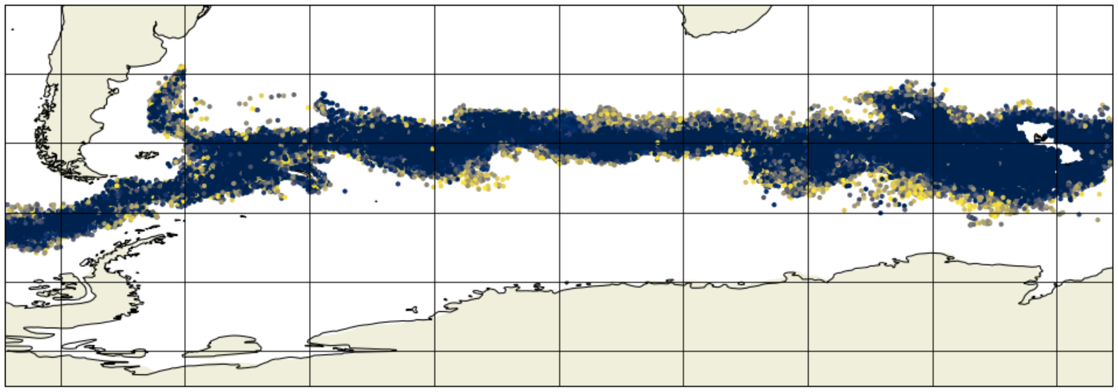
0.2.10 Plot i-metric by class

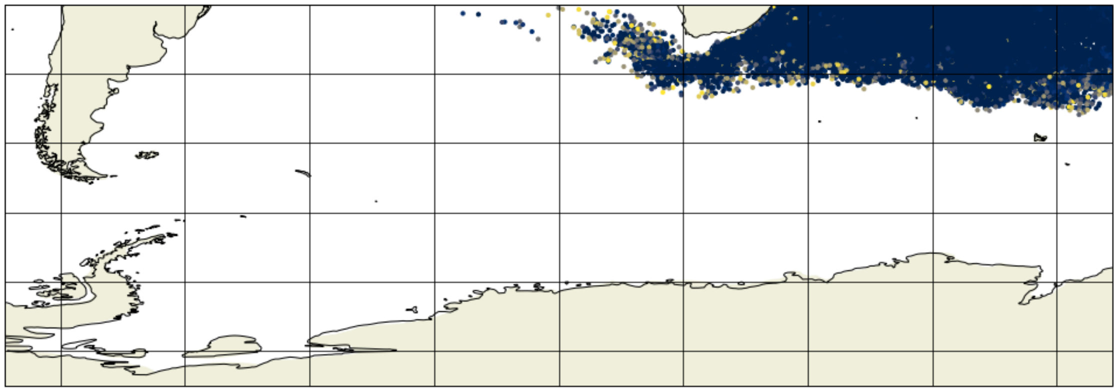
```
[23]: # extract values as new DataArrays
da_lon = df1D.lon
da_lat = df1D.lat
da_i_metric = df1D.i_metric

# extract values
lons = da_lon.values
lats = da_lat.values
c = da_i_metric.values

for iclass in range(n_components_selected):

    # random sample for plotting
    lons_random_sample = lons[labels==iclass]
    lats_random_sample = lats[labels==iclass]
    clabels_random_sample = c[labels==iclass]
```

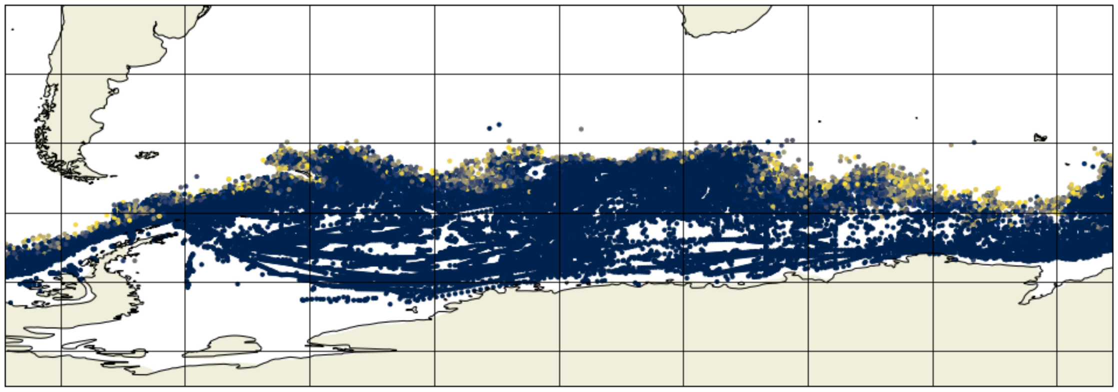
```
#colormap with Historical data
plt.figure(figsize=(17, 13))
ax = plt.axes(projection=ccrs.PlateCarree())
ax.set_extent([-80, 80, -85, -30], ccrs.PlateCarree())
CS = plt.scatter(lons_random_sample-360,
                 lats_random_sample,
                 c=clabels_random_sample,
                 marker='o',
                 cmap= plt.get_cmap('cividis'),
                 s=10.0,
                 transform=ccrs.Geodetic(),
                 )
ax.coastlines(resolution='50m')
ax.gridlines(color='black')
ax.add_feature(cartopy.feature.LAND)
```











This view makes it easier to see that the classes are reasonably spatially distinct, with “fuzzy” boundaries in the expected locations.

Save this dataset for further processing

[30]:
```
if saveOutput==True:
    profiles.chunk().compute().to_netcdf(path='processed_data/' + fname,␣
 ↪engine='netcdf4')
```