Plot clustermap of Diamond output for GH7 100 sequences

Ran at fast, mid-sensitive and sensitive

Imports

```
import seaborn as sns
import pandas as pd
import numpy as np
```

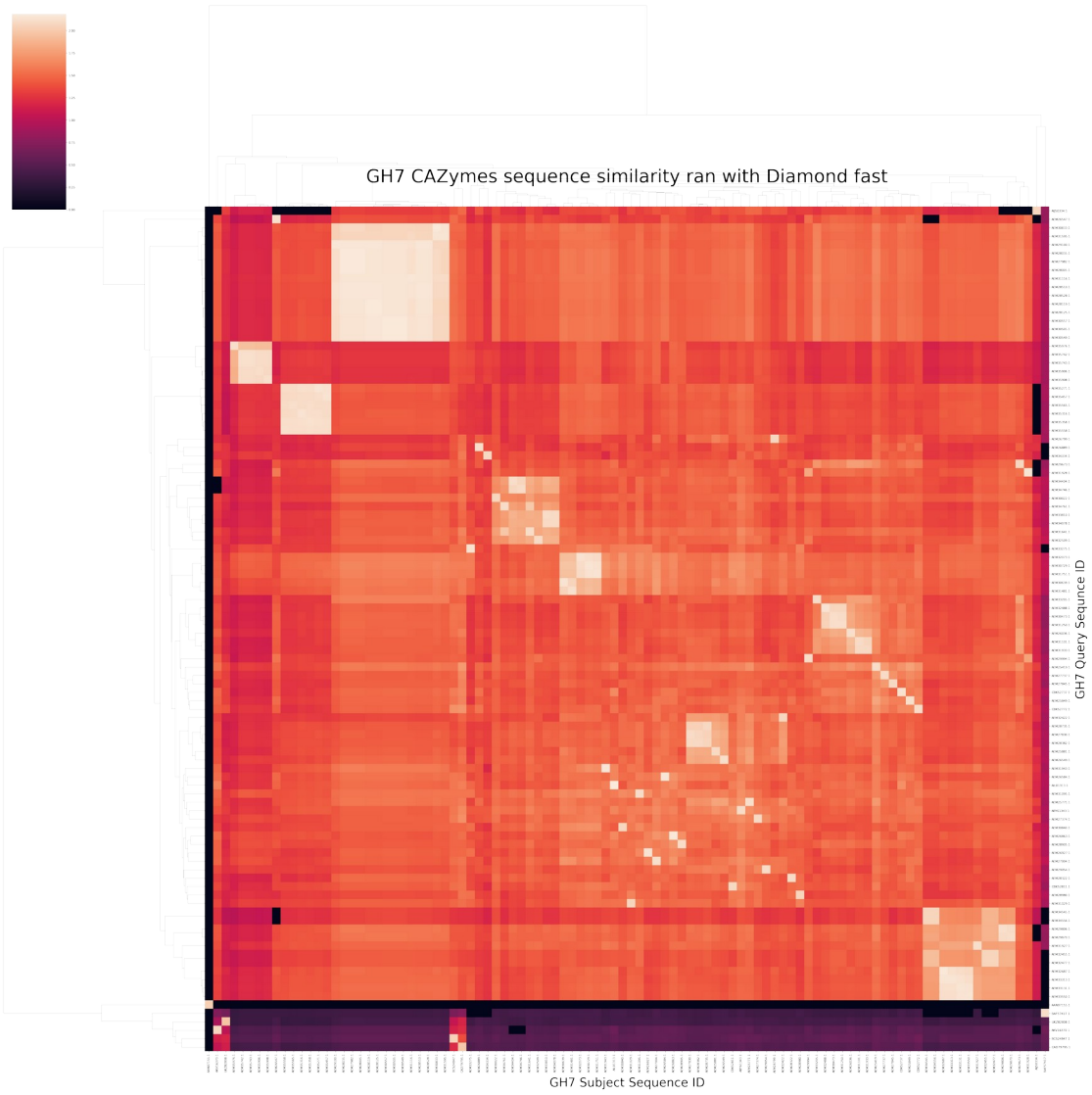
Function to create clustermap

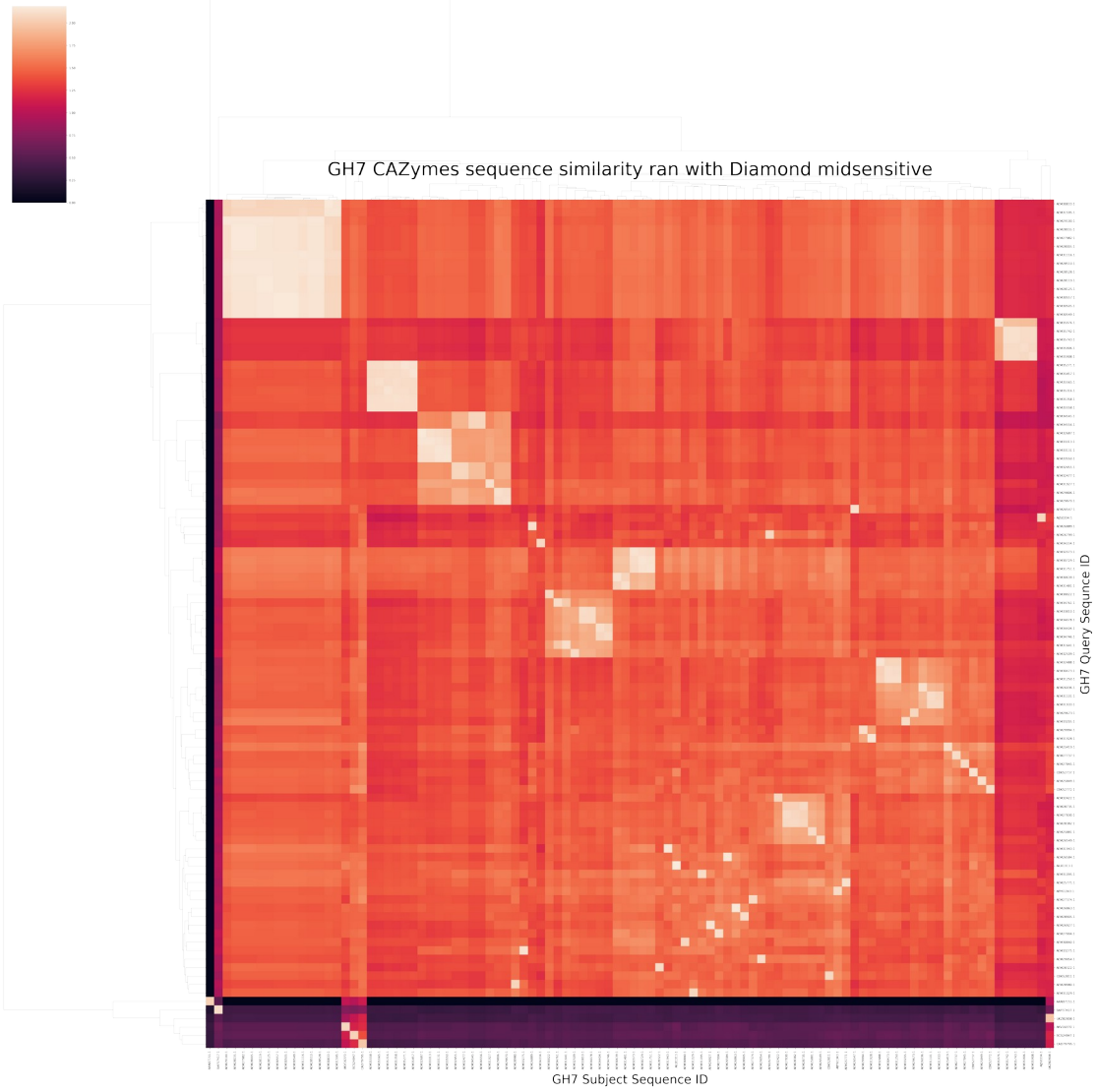
```
def plotdiamond(nseqs, speed): # Function is called plotdiamond.
    """Function takes the output matrix calculated by diamond and
plots them as a cluster map for a
    specified number of sequences (nseqs) and speed (speed). """
    infile = f"../Results/Diamond_out/{nseqs}rundiamond{speed}.tsv"
    # Set correct file with desired number of sequences and speed to
variable infile.

    df = pd.read_table(infile, header=None) # Create a dataframe.
    df.columns = ["qseqid", "sseqid", "qlen", "bitscore"] # Name the
columnes in the dataframe.
    df["normalisedbitscore"]=df["bitscore"]/df["qlen"] # Caculate the
normalised bitscore.
    df = df.drop(["qlen", "bitscore"],axis=1) # Remove uneeded
columnes.

    widedfx = pd.pivot(df, index="qseqid", columns= "sseqid",
values="normalisedbitscore")
    # Turn Long dataframe into a wide dataframe.
    widedf = widedfx.fillna(0) # Remove any values NaN and replace
with 0.

    figure=sns.clustermap(widedf, cmap="rocket", figsize=(50, 50)); #
Plot clustermap of the data frame created.
    figure.ax_heatmap.set_xlabel("GH7 Subject Sequence
ID",fontsize=40, labelpad=15)
    figure.ax_heatmap.set_ylabel("GH7 Query Sequnce ID",fontsize=40,
labelpad=15)
    figure.ax_heatmap.set_title(
        f'GH7 CAZymes sequence similarity ran with Diamond {speed}',
        fontsize=60,
        pad=80
    )

figure.savefig(f'../Results/Diamond_out/{nseqs}_diamond_{speed}.png')
# Save in results folder.
```

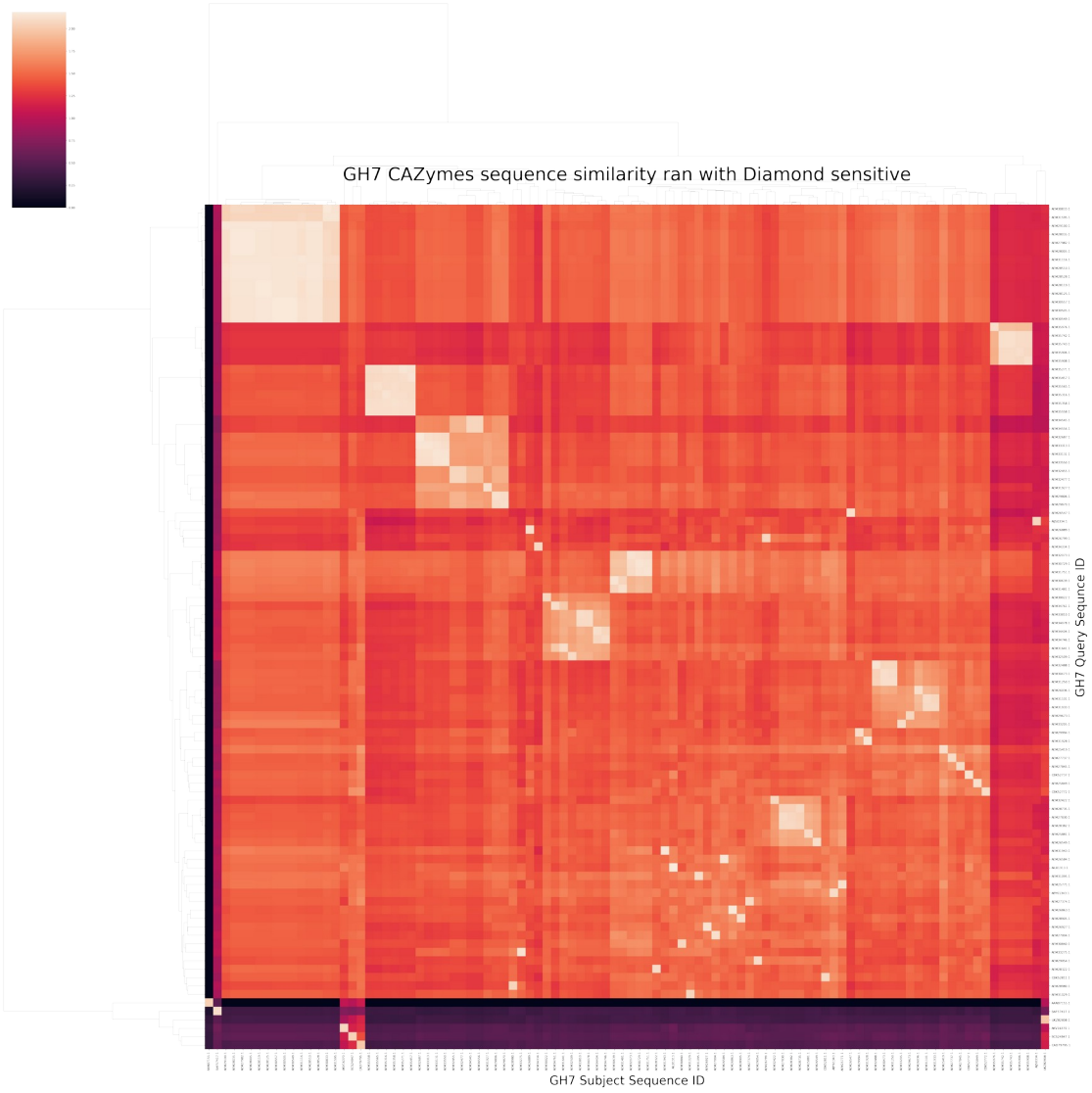
```
plot = plotdiamond(100, 'fast') # Run function for 100 sequences at
fast
plot = plotdiamond(100, 'midsensitive')
plot = plotdiamond(100, 'sensitive')

help(plotdiamond) # Call functions doc string to explain what the
function does.
```

```
/home/cjohns/.local/lib/python3.6/site-packages/seaborn/matrix.py:654:
UserWarning: Clustering large matrix with scipy. Installing
`fastcluster` may give better performance.
  warnings.warn(msg)
```

```
Help on function plotdiamond in module __main__:

plotdiamond(nseqs, speed)
    Function takes the output matrix calculated by diamond and plots
them as a cluster map for a
    specified number of sequences (nseqs) and speed (speed).
```


GH7 CAZymes sequence similarity ran with Diamond fast
GH7 Query Sequnce ID
GH7 Subject Sequence ID


GH7 CAZymes sequence similarity ran with Diamond midsensitive
GH7 Query Sequnce ID
GH7 Subject Sequence ID


GH7 CAZymes sequence similarity ran with Diamond sensitive
GH7 Query Sequnce ID
GH7 Subject Sequence ID