Figure_3_A

March 7, 2024

Figure 3_A We require pandas to read and process the information in an Excel file. For generating plots, we will use seaborn, matplotlib, and from the papers citation raincloud plots which has a python package ptitprince.

We will use the color palette n_colors=1 to ensure that the figures are the same color as the paper.

- [1] Gavriilidou, A., Kautsar, S.A., Zaburannyi, N. et al. Compendium of specialized metabolite biosynthetic diversity encoded in bacterial genomes. Nat Microbiol 7, 726–735 (2022). (https://doi.org/10.1038/s41564-022-01110-2)
- [2] Allen M, Poggiali D, Whitaker K et al. Raincloud plots: a multi-platform tool for robust data visualization [version 2; peer review: 2 approved]. Wellcome Open Res 2021, 4:63 (https://doi.org/10.12688/wellcomeopenres.15191.2)

```
[1]: # ptitprince 0.2.7 requires seaborn==0.11, but you have seaborn 0.13.2 which is incompatible.

# When running this notebook seaborn version 0.11.0 required, in order to install the dependency uncomment the below command and execute

# In the end seaborn can be reset again for the global (~/requirements.txt) in requirements.

# If jupyter enviorement is utilized restarting the kernel may be required.
```

[2]: # pip install seaborn==0.11.0

```
[3]: import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import ptitprince as pt
pal = sns.color_palette(n_colors=1)
```

We selected sheet_name="Fig3 panel a" and we have all the data.

```
[4]: df = pd.read_excel("Table_3.xlsx", sheet_name="Fig3 panel a")
```

For each label (for Figure 3 A y ticks) the order and the names are like the following;

- Phyla
- Classes
- Orders
- Families
- Genera

• Species

This is why we changed the column names to the respective names and ordered them accordingly.

```
[5]: df = df.replace({"species":"Species", "genus":"Genera", "family":"Families", u o"order":"Orders", "classes", "phylum":"Phyla"})
```

This particular data point is quite complex because it determines the order in which the dots are plotted in the figure. We attempted to produce every combination by sorting by each column name, but none of the options matched the figures in the paper. Ultimately, we chose the sorting method that yielded the most similar estimate regarding Variance.

```
[6]: df = df.sort_values("Variance").reset_index(drop=True)
```

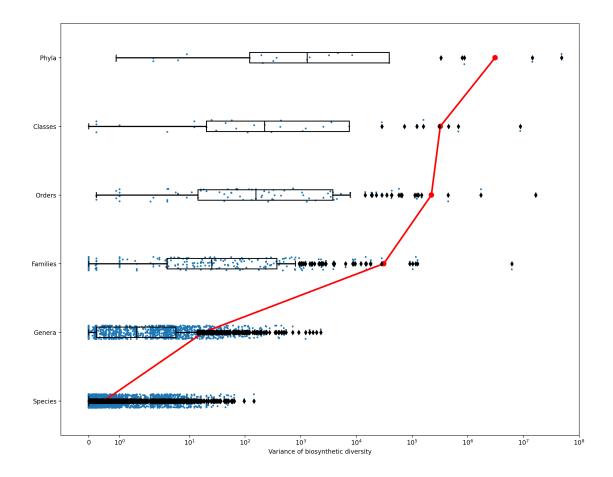
As discussed in the paper titled;

[1] Allen M, Poggiali D, Whitaker K et al. Raincloud plots: a multi-platform tool for robust data visualization [version 2; peer review: 2 approved]. Wellcome Open Res 2021, 4:63 (https://doi.org/10.12688/wellcomeopenres.15191.2)

They utilized the seaborn library to generate stripplot, half_violinplot, and boxplot graphs, with the pointplot option.

```
[7]: f, ax = plt.subplots(figsize=(15, 12), dpi=200)
     dy="Rank"
     dx="Variance"
     ort="h"
     kwpoint = dict(capsize = 0., errwidth = 0., zorder = 20)
     order_fig = ["Species", "Genera", "Families", "Orders", "Classes", "Phyla"]
     ax=sns.stripplot(x = dx,
                      y = dy,
                      data = df,
                      palette = pal,
                      edgecolor = "white",
                      size = 3,
                      jitter = 1,
                      zorder = 0,
                      orient = ort,
                      dodge = False,
                      order=order_fig[::-1])
     ax=sns.boxplot(x = dx,
                    y = dy,
                    data = df,
                    color = "black",
```

```
width = .15,
               zorder = 10,\
               showcaps = True,
               boxprops = {'facecolor':'none', "zorder":10},\
               showfliers=True,
               whiskerprops = {'linewidth':2, "zorder":10},\
               saturation = 1,
               orient = ort,
               dodge = False,
               order=order_fig[::-1])
ax = sns.pointplot(x=dx, y=dy, data=df, color='red', ax=ax, dodge = False,__
⇔orient = ort, **kwpoint, order=order_fig[::-1])
ax.set_xscale("symlog")
# 'linear', 'log', 'symlog', 'asinh', 'logit', 'function', 'functionlog'
ax.set_xlim([-0.9, 1e+8])
ax.set_ylabel(None)
ax.set_xlabel("Variance of biosynthetic diversity");
# plt.title("Figure_3_A_Reproduced_Topic_10");
```



After using the seaborn library, we can utilize the ptitprince library and incorporate its .RainCloud() functionality to create a one-line code. If we don't want to draw a cloud plot, we can avoid it.

```
# Draw cloud/half-violin
```

The half_violinplot function from the module was commented out to avoid drawing the half-violin plot. Therefore, lines 743-748 of the module were altered.

```
# Draw cloud/half-violin
# half_violinplot(x = x, y = y, hue = hue, data = data,

# order = order, hue_order = hue_order,

# orient = orient, width = width_viol,

# inner = None, palette = palette, bw = bw, linewidth = linewidth,
```

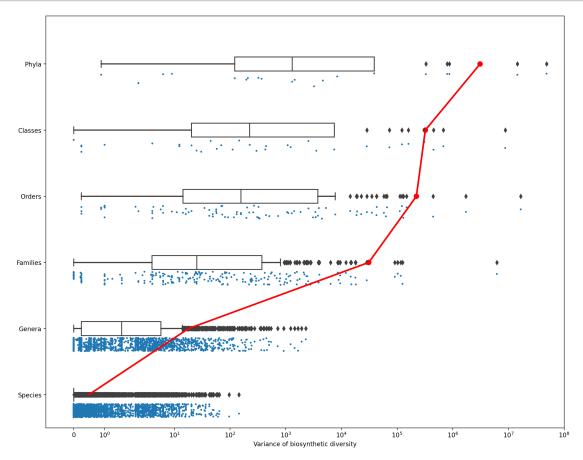
```
cut = cut, scale = scale, split = split, offset = offset, ax = ax, **kwcloud
```

For our purpose, we need a log transformation which the paper states they made the X axis in logarithmic scale. First the log option utilized then the correct option symlog utilized and the expected and desired result is produced.

```
The code to open the file is below and for commenting out the code it should be done manually,
    for non unix-based operating systems please use prefered procedure to open the file.
[8]: import os
     path = os.path.abspath(pt.__file__)
     modified_path = "/".join(path.split("/")[:-1])
     print(f"Go to the following path:\n{modified_path}\n\nUse the commands;")
     print(f"cd {modified_path}")
     print("open PtitPrince.py")
     print("You may need to restart your kernel")
    Go to the following path:
    /Users/sinaberkgolech/.pyenv/versions/3.9.18/lib/python3.9/site-
    packages/ptitprince
    Use the commands:
    cd /Users/sinaberkgolech/.pyenv/versions/3.9.18/lib/python3.9/site-
    packages/ptitprince
    open PtitPrince.py
    You may need to restart your kernel
[9]: f, ax = plt.subplots(figsize=(15, 12),dpi=200)
     ax=pt.RainCloud(x = dy,
                     y = dx,
                      data = df,
                     palette = pal,
                     width_box = .21,
                     ax = ax,
                     orient = ort,
                     pointplot = True,
                     move=0.24,
                      order=order_fig[::-1])
     ax.set_xscale("symlog")
     ax.set xlim([-0.9, 1e+8])
     ax.set_ylabel(None)
     ax.set_xlabel("Variance of biosynthetic diversity");
     # plt.title("Figure_3_A_Reproduced_Topic_10");
```

```
# Save the figure option.
# plt.savefig("Figures_3_Original_Format/output_figure_3_A_Topic_10.png",

dpi=300)
```



END OF REPRODUCING FIGURE 3 A. Here are the efforts and attempted steps that are necessary but not included in reproducing Figure 3A. It is always better to comment rather than delete code.

```
#
                          size=2,
      #
                          orient=ort, \
      #
                          x=dx.
      #
                          y=dy,
                          jitter=1,
                          zorder=0)
      #
      # ax=sns.boxplot(data=df,
                        color="black",
      #
                        orient=ort,
      #
                        width=.15.
                        x=dx,
      #
                        y=dy,
                        zorder=10, \
      #
      #
                       showcaps=True,
                        boxprops={'facecolor':'none', "zorder":10},\
      #
      #
                        showfliers=True,
      #
                        whiskerprops={'linewidth':2, "zorder":10},
      #
                        saturation=1)
      # #ax = sns.pointplot(x=dx, y=dy, data=ddf,color='red')
      # # Finalize the figure
      # #ax.set(ylim=(3.5, -.7))
      # sns.despine(left=True)
[12]: # #adding a red line connecting the groups' mean value (useful for longitudinal
       \hookrightarrow data
      \# sigma = .2
      # f, ax = plt.subplots(figsize=(7, 5))
      \# ax=pt.RainCloud(x = dx, y = dy, data = df, palette = pal, bw = sigma,
      #
                          width\_viol = .6, ax = ax, orient = ort,
                        pointplot = True)
[13]: \# f, ax = plt.subplots(figsize=(15, 9))
      # pal = sns.color_palette(n_colors=1)
      \# dx = "Rank"
      # dy = "Variance"
      # ort = "h"
      \# ax = pt.RainCloud(x = df[dx],
      #
                           y = df[dy],
      #
                           palette = pal,
      #
                           width\_viol = .1,
```

```
#
                           width_box = 0.15,
      #
                           ax = ax,
      #
                           orient = ort.
      #
                           move = .18,
                           pointplot = True,
      #
                           dodge=True,
                           offset=1000)
      # ax.set_xlabel("Variance of biosynthetic diversity")
      # ax.set ylabel(None)
      # ax.set xscale('log')
      # plt.show()
[14]: \# f, ax = plt.subplots(fiqsize=(15, 15), dpi=200)
      \# ax = sns.boxplot(y = df["Rank"], x = df["Variance"], data = df, orient='h')
      # ax.set_xscale('log')
[15]: \# f, ax = plt.subplots(figsize=(15, 9))
      \# ax=sns.boxplot(x = dx, y = dy, data = df, color = "black", width = .15, <math>\sqcup
       \Rightarrow zorder = 10, \
                     showcaps = True, boxprops = {'facecolor':'none', "zorder":10},\
                     showfliers=True, whiskerprops = {'linewidth':2, "zorder":10},\
      #
                        saturation = 1, orient = ort)
      \# ax=sns.stripplot( x = dx, y = dy, data = df, palette = sns.
       ⇔color_palette(n_colors=1), edgecolor = "white",
                          size = 3, jitter = 0, zorder = 0, orient = ort)
      #
      # ax.set_xscale('log')
[16]: \# f, ax = plt.subplots(fiqsize=(15, 9))
      # pal = sns.color_palette(n_colors=1)
      \# ax=sns.stripplot(x = dx, y = dy, data = df, palette = pal, edgecolor = \Box
       →"white".
      #
                          size = 3, jitter = 1, zorder = 0, orient = ort, ax = ax)
      # ax=sns.boxplot(x = dx, y = dy, data = df, color = "black", width = .15, \( \square
       \Rightarrowzorder = 10,\
                     showcaps = True, boxprops = {'facecolor':'none', "zorder":10},\
```

```
# showfliers=True, whiskerprops = {'linewidth':2, "zorder":10},\
# saturation = 1, orient = ort,move = .2)
#
# ax.set_xscale('log')

[17]: # help(pt.RainCloud)

[18]: # df2["Variance"] = np.log(df2["Variance"])

[19]: # df2 = df2[df2["Variance"] != df2["Variance"].iloc[-1]]

[20]: # df2 = df2[df2.Variance != float('-inf')]

[21]: # df["Variance"].iloc[-1]

[22]: # help(pd.DataFrame.replace)
```