Visualising your data

Once the behavpy object is created, the print function will just show your data structure. If you want to see your data and the metadata at once, use the built in method `.display()`

```
# first load your data and create a behavpy instance of it


df.display()
```

```
 ==== METADATA ====

                                    date   machine_name  region_id     species                    strain  baseline_days  strain_no         exp      time
id
2019-08-02_14-21-23_021d6b|01  2019-08-02  ETHOSCOPE_021          1       D.vir          15010-1051.87 _#9              0          1     species  14-21-23
2019-08-02_14-21-23_021d6b|02  2019-08-02  ETHOSCOPE_021          2       D.vir          15010-1051.87 _#9              0          1     species  14-21-23
2019-08-02_14-21-23_021d6b|03  2019-08-02  ETHOSCOPE_021          3       D.vir          15010-1051.87 _#9              0          1     species  14-21-23
2019-08-02_14-21-23_021d6b|04  2019-08-02  ETHOSCOPE_021          4       D.vir          15010-1051.87 _#9              0          1     species  14-21-23
2019-08-02_14-21-23_021d6b|05  2019-08-02  ETHOSCOPE_021          5       D.sec          14021-0248.25 _#3              0          1     species  14-21-23
...                               ...            ...        ...         ...                        ...            ...        ...         ...       ...
2022-02-10_18-34-55_22982f|16  2022-02-10  ETHOSCOPE_229         16       empty                      empty              0          1  wildcaught  18-34-55
2022-02-10_18-34-55_22982f|17  2022-02-10  ETHOSCOPE_229         17  wild_d.mel  Darren_obbard_wildcaught_3              0          2  wildcaught  18-34-55
2022-02-10_18-34-55_22982f|18  2022-02-10  ETHOSCOPE_229         18  wild_d.mel  Darren_obbard_wildcaught_3              0          2  wildcaught  18-34-55
2022-02-10_18-34-55_22982f|19  2022-02-10  ETHOSCOPE_229         19  wild_d.mel  Darren_obbard_wildcaught_3              0          2  wildcaught  18-34-55
2022-02-10_18-34-55_22982f|20  2022-02-10  ETHOSCOPE_229         20  wild_d.mel  Darren_obbard_wildcaught_3              0          2  wildcaught  18-34-55

[883 rows x 9 columns]
 ====== DATA ======

                                  t        x        y        w        h       phi  ...  beam_crosses  moving  micro   walk  is_interpolated  asleep
id                                                                                 ...
2019-08-02_14-21-23_021d6b|01   19380  0.623679  0.043643  0.027288  0.012393  80.312500  ...           0.0    True  False   True            False  False
2019-08-02_14-21-23_021d6b|01   19440  0.607520  0.043756  0.043559  0.021442   9.265625  ...           0.0    True   True  False            False  False
2019-08-02_14-21-23_021d6b|01   19500  0.605259  0.043394  0.049732  0.024752  25.476190  ...           0.0    True   True  False            False  False
2019-08-02_14-21-23_021d6b|01   19560  0.602718  0.044650  0.057040  0.027235  22.603175  ...           0.0    True   True  False            False  False
2019-08-02_14-21-23_021d6b|01   19620  0.601776  0.046648  0.062721  0.028235  19.476190  ...           0.0    True   True  False            False  False
...                               ...       ...       ...       ...       ...        ...  ...           ...     ...    ...    ...              ...    ...
2022-02-10_18-34-55_22982f|20  287520  0.414123  0.036036  0.050669  0.025371  72.646465  ...           0.0   False  False  False            False   True
2022-02-10_18-34-55_22982f|20  287580  0.413698  0.036036  0.050494  0.025421  55.156627  ...           0.0   False  False  False            False   True
2022-02-10_18-34-55_22982f|20  287640  0.412763  0.036036  0.050429  0.025676  38.297619  ...           0.0   False  False  False            False   True
2022-02-10_18-34-55_22982f|20  287700  0.412742  0.036036  0.050434  0.025631  47.198198  ...           0.0   False  False  False            False   True
2022-02-10_18-34-55_22982f|20  287760  0.413639  0.036036  0.050177  0.025636  91.151899  ...           0.0   False  False  False            False   True
```

You can also get quick summary statistics of your dataset with `.summary()`

```
df.summary()


# an example output of df.summary()
output:
behavpy table with:
    individuals       675
   metavariable         9
      variables        13
   measurements   3370075


# add the argument detailed = True to get information per fly
df.summary(detailed = True)
```

```
output:
                                data_points          time_range
id
2019-08-02_14-21-23_021d6b|01         5756   86400  ->  431940
2019-08-02_14-21-23_021d6b|02         5481   86400  ->  431940
```

> Be careful with the pandas method `.groupby()` as this will return a pandas object back and not a behavpy object. Most other common pandas actions will return a behavpy object.

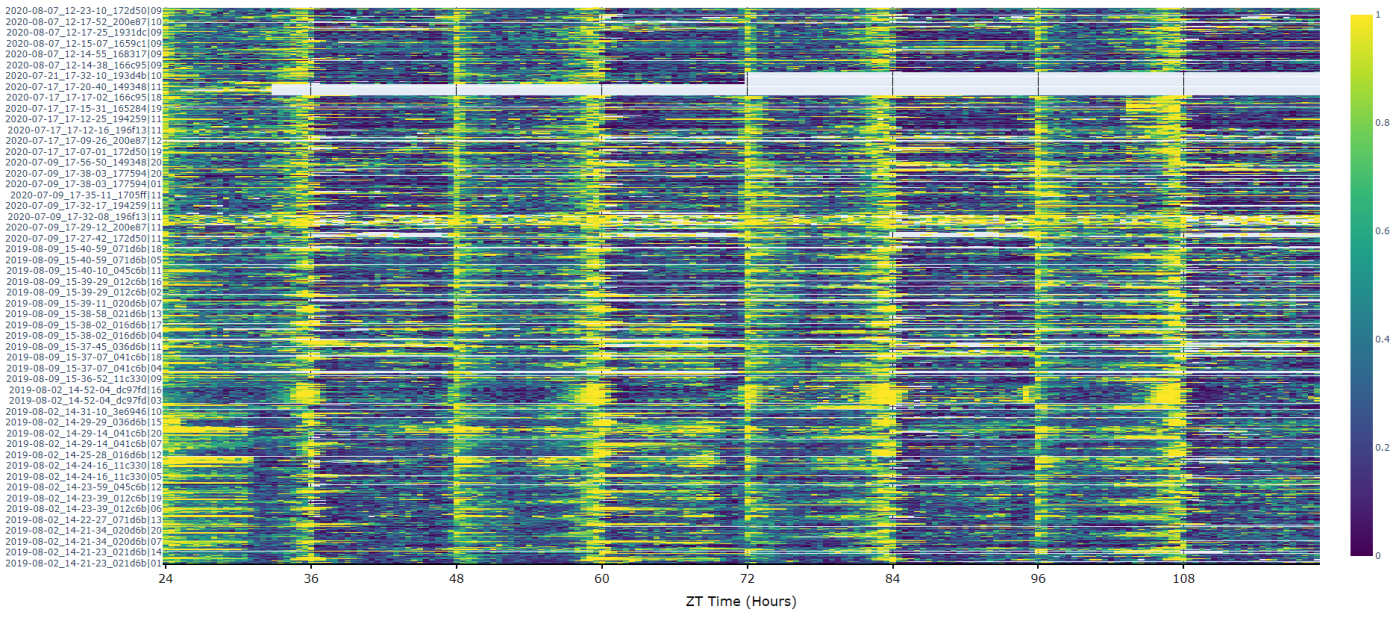
Visualising your data

Whilst summary statistics are good for a basic overview, visualising the variable of interest over time is usually a lot more informative.

Heatmaps

The first port of call when looking at time series data is to create a heatmap to see if there are any obvious irregularities in your experiments.

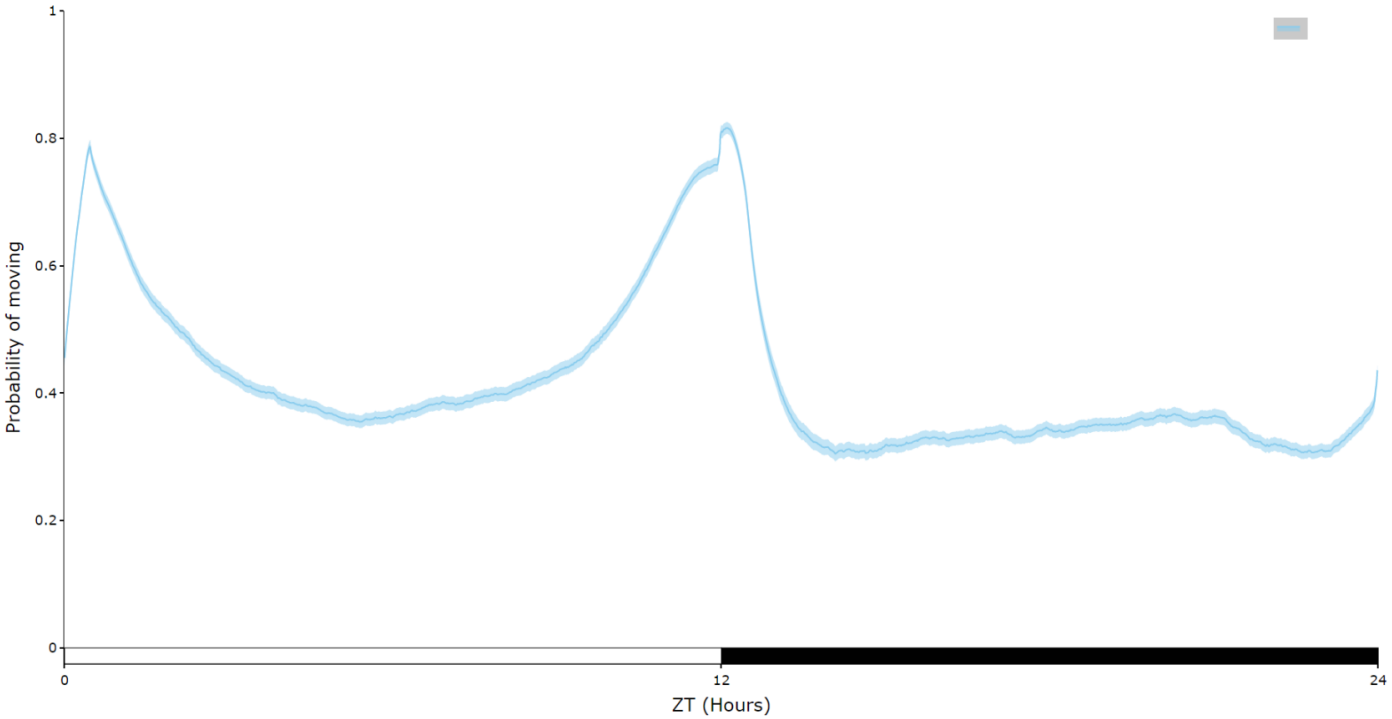
```
# To create a heatmap all you need to write is one line of code!
# All plot methods will return the figure, the usual etiquette is to save the variable as fig

fig = df.heatmap('moving') # enter as a string which ever numerical variable you want plotted
inside the brackets

# Then all you need to do is the below to generate the figure
fig.show()
```



Plots over time

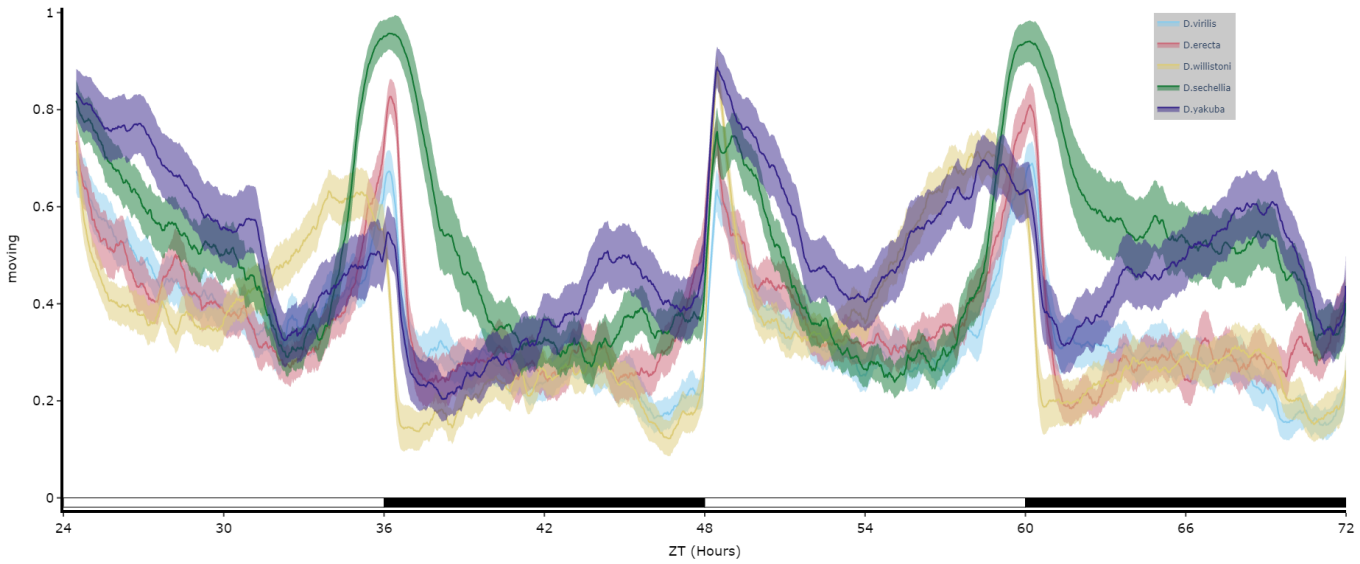
For an aggregate view of your variable of interest over time, use the .plot_overtime() method to visualise the mean variable over your given time frame or split it into sub groups using the information in your metadata.

```
# If wrapped is True each specimens data will be aggregated to one 24 day before being aggregated as a whole. If you want to view each day seperately, keep wrapped False.
# To achieve the smooth plot a moving average is applied, we found averaging over 30 minutes gave the best results
# So if you have your data in rows of 10 seconds you would want the avg_window to be 180 (the default)
# Here the data is rows of 60 seconds, so we only need 30

fig = df.plot_overtime(
variable = 'moving',
wrapped = True,
avg_window = 30
)
fig.show()
# the plots will show the mean with 95% confidence intervals in a lighter colour around the mean
```




```
# You can seperate out your plots by your specimen labels in the metadata. Specify which column you want fromn the metadata with facet_col and then specify which groups you want with facet_args
```

```
# What you enter for facet_args must be in a list and be exactly what is in that column in the metadata
# Don't like the label names in the column, rename the graphing labels with the facet_labels parameter. This can only be done if you have a same length list for facet_arg. Also make sure they are the same order

fig = df.plot_overtime(
variable = 'moving',
facet_col = 'species',
facet_arg = ['D.vir', 'D.ere', 'D.wil', 'D.sec', 'D.yak'],
facet_labels = ['D.virilis', 'D.erecta', 'D.willistoni', 'D.sechellia', 'D.yakuba']
)
fig.show()

# if you're doing circadian experiments you can specify when night begins with the parameter circadian_night to change the phase bars at the bottom. E.g. circadian_night = 18 for lights off at ZT 18.
```

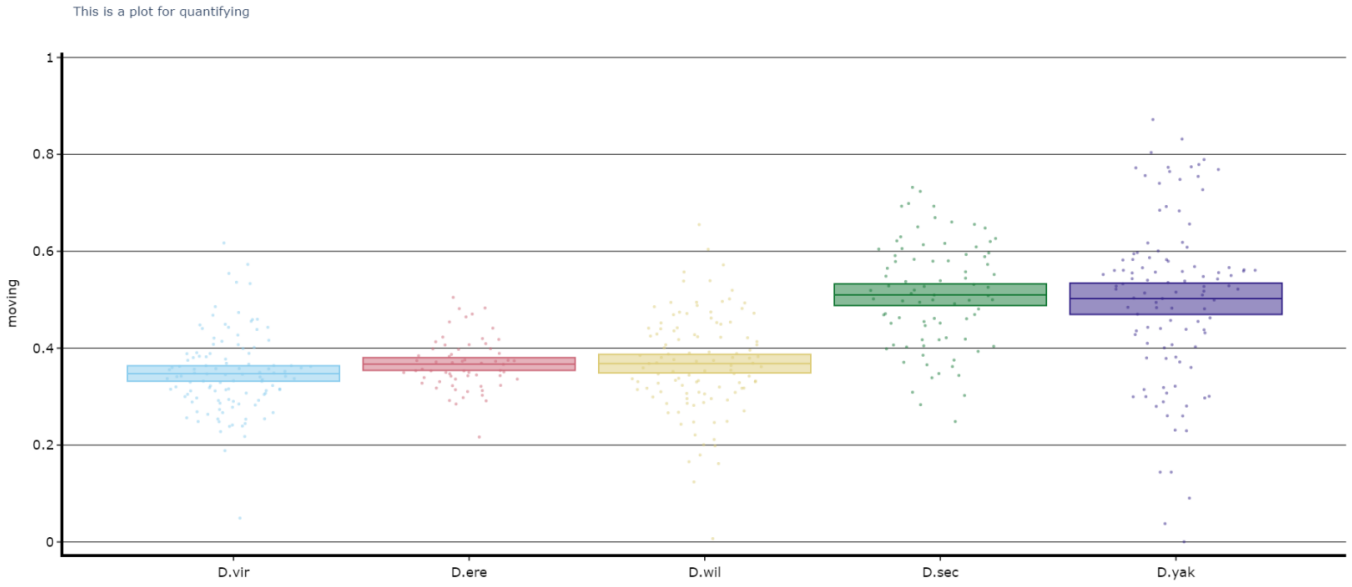


Quantifying sleep

The plots above look nice, but we often want to quantify the differences to prove what our eyes are telling us. The method `.plot_quantify()` plots the mean and 95% CI of the specimens to give a strong visual indication of group differences.

```
# Quantify parameters are near identical to .plot_overtime()
# For all plotting methods in behavpy we can add grid lines to better view the data and you can also add a title, see below for how
# All quantifying plots sill return two objects, the first will be the plotly figure as normal
```

```
and the second a pandas dataframe with
# the calculated avergages per specimen for you to perform statistics on. You can do this via
the common statistical package scipy or
# we recommend a new package DABEST, that produces non p-value related statisics and
visualtion too.
# We'll be looking to add DABEST into our ecosytem soon too!

fig, stats_df = df.plot_quantify(
variable = 'moving',
facet_col = 'species',
facet_arg = ['D.vir', 'D.ere', 'D.wil', 'D.sec', 'D.yak']
title = 'This is a plot for quantifying',
grids = True
)
fig.show()

# Tip! You can have a facet_col argument and nothing for facet_args and the method will
automatically plot all groups within that column. Careful though as the order/colour might not
be preserved in similar but different plots
```



Performing Statistical tests

If you want to perform normal statistical tests then it's best to use Scipy, a very common python package for statistics with lots of online tutorial on how and when to use it. We'll run through a demonstration of one below. Below you'll see an example table of the data from the plot above.

	D.vir	D.ere	D.wil	D.sec	D.yak
0	0.279889	0.305839	0.486261	0.484013	0.523901
1	0.294987	0.403151	0.386917	0.584337	0.627201
2	0.354461	0.383920	0.460455	0.439296	0.550845
3	0.371630	0.385240	0.565994	0.440222	0.535946
4	0.271885	0.372018	0.394810	0.491663	0.582313
...	...	...	...	...	...
107	0.263657	NaN	0.385701	NaN	0.291204
108	0.382526	NaN	0.349498	NaN	0.455093
109	0.337037	NaN	NaN	NaN	NaN
110	0.406380	NaN	NaN	NaN	NaN
111	0.268494	NaN	NaN	NaN	NaN

112 rows × 5 columns

Given we don't know the distribution type of the data and that each group is independent we'll use a non-parametric group test, the Kruskal-Wallis H-test (the non-parametric version of a one-way ANOVA).

```
# First we need to import scipy stats
from scipy import stats

# Next we need the data for each specimen in a numpy array
# Here we iterate through the columns and send each column as a numpy array into a list
stat_list = []
for col in stats_df.columns.tolist():
    stat_list.append(stats_df[col].to_numpy())

# Alternatively you can set each one as it's own variable
dv = stats_df['D.vir'].to_numpy()
de = stats_df['D.ere'].to_numpy()
... etc

# Now we call the Kruskal function, remember to always have the nan_policy set as 'omit'
otherwise the output will be a NaN

# If using the first method (the * unpacks the list)
stats.kruskal(*stat_list, nan_policy = 'omit')

# If using the second
stats.kruskal(dv, de, ..., nan_policy = 'omit')
```

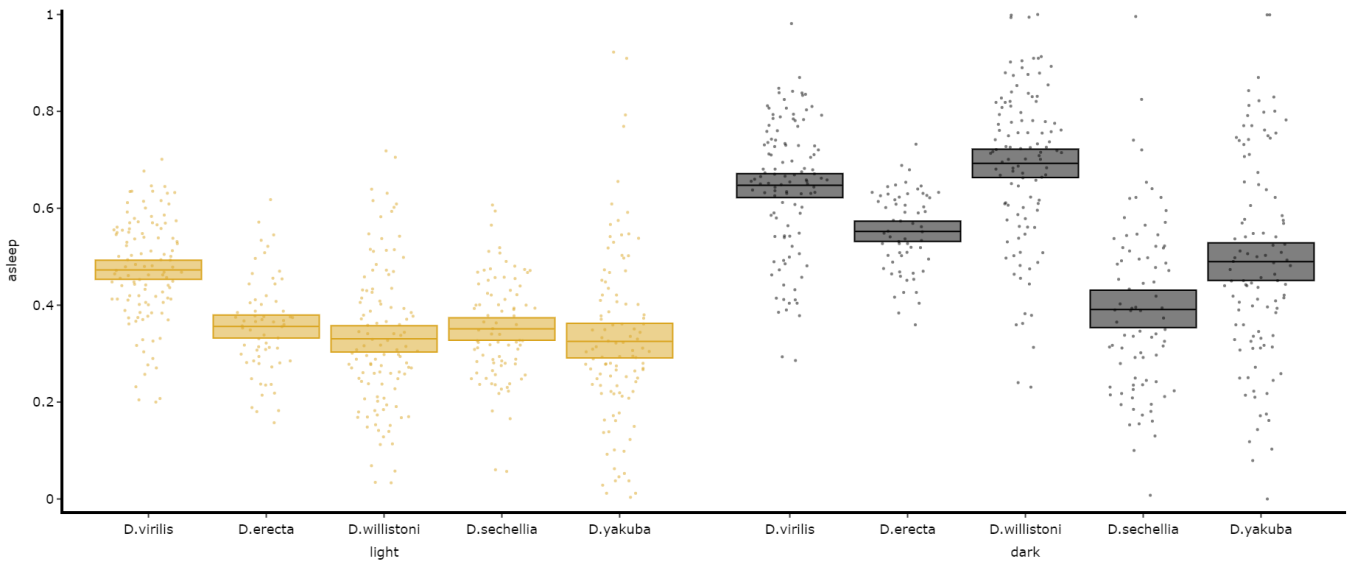
```
## output: KruskalResult(statistic=134.17956605297556, pvalue=4.970034343600611e-28)

# The pvalue ss below 0.05 so we can say that not all the groups have the same distribution

# Now we want to do some post hoc testing to find inter group significance
# For that we need another package scikit_posthocs
import scikit_posthocs as sp

p_values = sp.posthoc_dunn(stat_list, p_adjust = 'holm')
print(p_values)
## output:           1             2             3             4             5
1  1.000000e+00  2.467299e-01  0.000311  1.096731e-11  1.280937e-16
2  2.467299e-01  1.000000e+00  0.183924  1.779848e-05  7.958752e-08
3  3.106113e-04  1.839239e-01  1.000000  3.079278e-03  3.884385e-05
4  1.096731e-11  1.779848e-05  0.003079  1.000000e+00  4.063266e-01
5  1.280937e-16  7.958752e-08  0.000039  4.063266e-01  1.000000e+00

print(p_values > 0.05)
## output:        1      2      3      4      5
1   True   True  False  False  False
2   True   True   True  False  False
3  False   True   True  False  False
4  False  False  False   True   True
5  False  False  False   True   True
```

Quantify day and night

Often you'll want to compare a variable between the day and night, particularly total sleep. This variation of `.plot_quantify()` will plot the mean and 96% CI of a variable for a user defined day and night.

```
# Quantify parameters are near identical to .plot_quantify() with the addtion of day_length
and lights_off which takes (in hours) how long the day is for the specimen (defaults 24) and
at what point within that day the lights turn off (night, defaults 12)

fig, stats = df.plot_day_night(
variable = 'asleep',
facet_col = 'species',
facet_arg = ['D.vir', 'D.ere', 'D.wil', 'D.sec', 'D.yak'],
facet_labels = ['D.virilis', 'D.erecta', 'D.willistoni', 'D.sechellia', 'D.yakuba'],
day_length = 24,
```

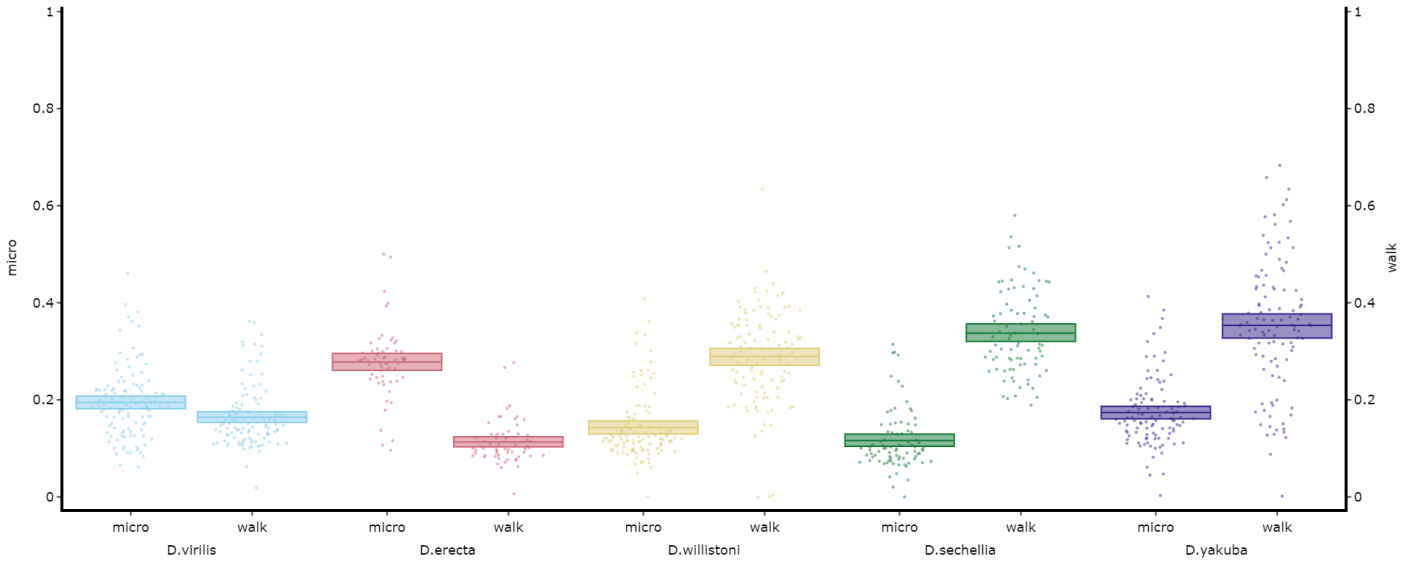
```
lights_off = 12
)
fig.show()
```



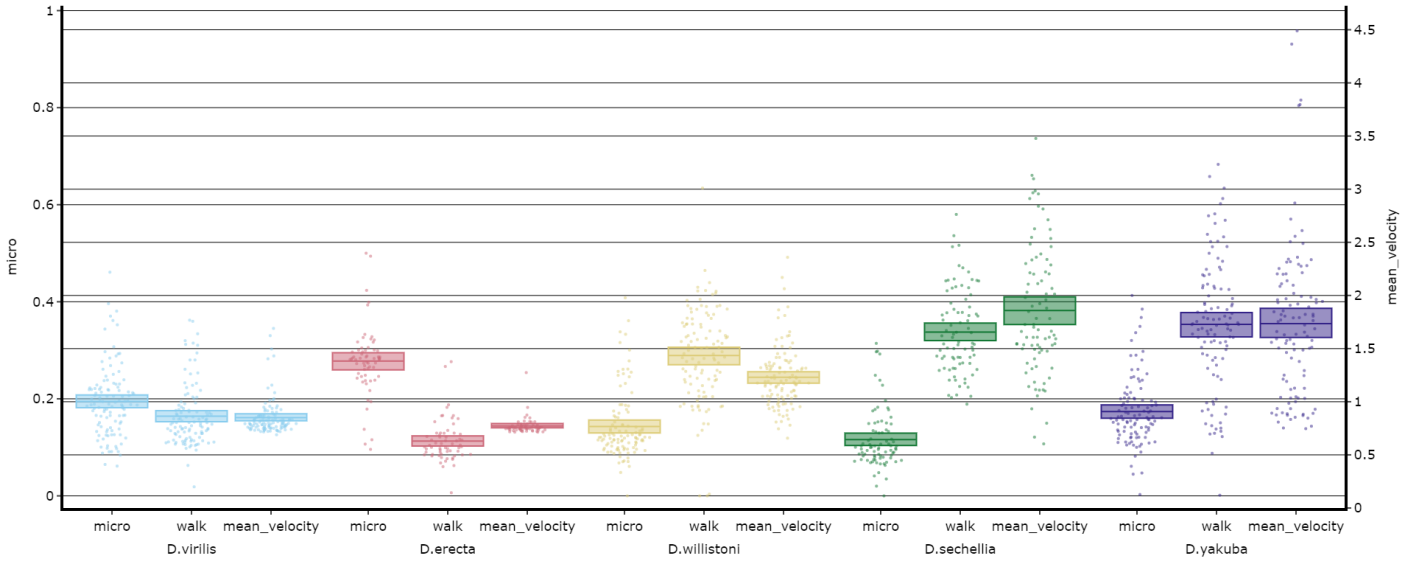
Compare variables

You may sometimes want to compare different but similar variables from your experiment, often comparing them across different experimental groups. Use `.plot_compare_variables()` to compare up to 24 different variables (we run out of colours after that...).

```
# Like the others it takes the regualar arguments. However, rather than the variable parameter it's variables, which takes a list of strings of the different columns you want to compare. The final variable in the list will have it's own y-axis on the right-hand side, so save this one for different scales.

# The most often use of this with the ethoscope data is to compare micro movements to walking movements to better understand the locomotion of the specimen, so lets look at that.

fig, stats = df.plot_compare_variables(
    variables = ['mirco', 'walk']
    facet_col = 'species',
    facet_arg = ['D.vir', 'D.ere', 'D.wil', 'D.sec', 'D.yak'],
    facet_labels = ['D.virilis', 'D.erecta', 'D.willistoni', 'D.sechellia', 'D.yakuba']
)
fig.show()
```




```
# Lets add the velocity of the specimen to see how it looks with different scales.

fig, stats = df.plot_compare_variables(
    variables = ['mirco', 'walk', 'mean_velocity']
    facet_col = 'species',
    facet_arg = ['D.vir', 'D.ere', 'D.wil', 'D.sec', 'D.yak', 'D.sims'],
    facet_labels = ['D.virilis', 'D.erecta', 'D.willistoni', 'D.sechellia', 'D.yakuba',
'D.Simulans'],
    # Add grids to the plot so we can better see how the plots align
    grids = True
)
fig.show()
```



> Head to the Overview Tutorial for interactive examples of some of these plots. It also shows you how to edit the fig object after it's been generated if you wish to change things like axis titles and axis range.

Saving plots

As seen above all plot methods will produce a figure structure that you use .show() to generate the plot. To save these plots all we need to do is place the fig object inside a behavpy function called etho.save_figure()

You can save your plots as PDFs, SVGs, JPEGs or PNGS. It's recommended you save it as either a pdf or svg for the best quality and then the ability to alter then later.

You can also save the plot as a html file. Html files retain the interactive nature of the plotly plots. This comes in most useful when using jupyter notebooks and you want to see your plot full screen, rather than just plotted under the cell.

```
# simply have you returned fig as the argument alongside its save path and name to save


# remember to change the file type at the end of path as you want it
# you can set the width and height of the saved image with the parameters width and height
(this has no effect for .html files)
etho.save_figure(fig, './tutorial_fig.pdf', width = 1500, height = 1000)


# or to get a better view of it and keep the interactability save it as a html file
etho.save_figure(fig, './tutorial_fig.html')  # you can't change the height and width wehn
saved as a html
```

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