

qPCR

April 9, 2024

```
[ ]: import plotastic as plst
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
```

```
[ ]: # Set Plot Style
plst.set_style("paper")
# plst.set_palette("hls", verbose=True)
plst.set_palette(["#db5f57", "#91db57", "#57d3db"])
```

#! You chose this color palette: ['#db5f57', '#91db57', '#57d3db', '#db5f57', '#91db57', '#57d3db', '#db5f57', '#91db57']

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['#db5f57',
 '#91db57',
 '#57d3db',
 '#db5f57',
 '#91db57',
 '#57d3db',
 '#db5f57',
 '#91db57']
```

1 Example Analysis: qPCR

Raw Data: https://github.com/markur4/plotastic/tree/main/src/plotastic/example_data/data

Original Source: (unpublished)

```
[ ]: # Import Example Data
DF, _dims = plst.load_dataset("qPCR", verbose=False)
dims = dict(
    y="fc",
    x="gene",
    hue="fraction",
    # col= 'method',
    row="class",
)
DA = plst.DataAnalysis(DF, dims, subject="subject", verbose=False)
```

```
[ ]: DA.transform_y("log10", inplace=True) # Log transform
DA.check_normality() # -> Only few groups are not normal -> parametric
```

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[ ]:
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			W	pval	normal	n
class	gene	fraction				
Bone Metabolism	F1	FBN1	0.936873	0.518768	True	10
		SOST	0.880395	0.131862	True	10
		TIMP1	0.745494	0.004807	False	9
	F2	FBN1	0.954764	0.705148	True	11
		SOST	0.967810	0.863610	True	11
		TIMP1	0.914325	0.274168	True	11
	F3	FBN1	0.915247	0.281020	True	11
		SOST	0.923112	0.345415	True	11
		TIMP1	0.937230	0.488505	True	11
Chemokines	F1	LOXL2	0.930358	0.451421	True	10
		JAK2	0.897331	0.204749	True	10
	F2	LOXL2	0.874630	0.088876	True	11
		JAK2	0.960025	0.772006	True	11
	F3	LOXL2	0.943678	0.564652	True	11
		JAK2	0.878406	0.099301	True	11
Cytokines	F1	RUNX2	0.947142	0.634825	True	10
		STAT3	0.933422	0.482382	True	10
		IL6R	0.927258	0.421472	True	10
		TNFSF13	0.907481	0.264130	True	10
	F2	RUNX2	0.915611	0.283765	True	11
		STAT3	0.907354	0.226836	True	11
		IL6R	0.985709	0.989621	True	11
		TNFSF13	0.958855	0.757330	True	11
	F3	RUNX2	0.924060	0.353917	True	11
		STAT3	0.932663	0.438418	True	11
		IL6R	0.826181	0.020798	False	11
		TNFSF13	0.970421	0.890746	True	11
		IFNG	0.715267	0.001349	False	10
		FZD4	0.981633	0.973303	True	10
		PTCH1	0.911578	0.292008	True	10
ECM & Adhesion	F1	CCL5	0.969121	0.882582	True	10
		IFNG	0.899109	0.180269	True	11
		FZD4	0.979590	0.963841	True	11
		PTCH1	0.986610	0.990734	True	10
	F2	CCL5	0.925780	0.407685	True	10
		IFNG	0.905665	0.216509	True	11
		FZD4	0.923819	0.351743	True	11
		PTCH1	0.957827	0.744318	True	11
	F3	CCL5	0.940093	0.521596	True	11
		MMP7	0.955749	0.752957	True	9
		MMP9	0.675286	0.005186	False	5
		MMP7	0.926078	0.372552	True	11

Signaling	F3	MMP9	0.971128	0.901100	True	10
		MMP7	0.924886	0.361455	True	11
		MMP9	0.913554	0.268549	True	11
	F1	Vimentin	0.919696	0.354424	True	10
		TNC	0.928589	0.434161	True	10
		NOTCH1	0.922084	0.374662	True	10
		WNT5A	0.903581	0.239742	True	10
	F2	Vimentin	0.957763	0.743507	True	11
		TNC	0.959813	0.769352	True	11
		NOTCH1	0.977556	0.951045	True	11
		WNT5A	0.937156	0.487661	True	11
	F3	Vimentin	0.910924	0.250109	True	11
		TNC	0.884194	0.117578	True	11
		NOTCH1	0.779982	0.005132	False	11
		WNT5A	0.812114	0.013581	False	11

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[ ]: DA.check_sphericity()
```

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[ ]:
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			spher	W	chi2	dof	pval	\
class	fraction							
Bone Metabolism	F1	0	True	0.592922	3.658847	2	0.160506	
	F2	0	True	0.703252	3.168356	2	0.205116	
	F3	0	True	0.832864	1.645964	2	0.439120	
Chemokines	F1	0	True	NaN	NaN	1	1.000000	
	F2	0	True	NaN	NaN	1	1.000000	
	F3	0	True	NaN	NaN	1	1.000000	
Cytokines	F1	0	True	0.629185	3.577934	5	0.614197	
	F2	0	False	0.262747	11.657816	5	0.040987	
	F3	0	False	0.210032	13.610980	5	0.019012	
ECM & Adhesion	F1	0	True	0.486690	5.560987	5	0.354712	
	F2	0	True	0.295164	8.202615	5	0.149255	
	F3	0	True	0.297080	10.586623	5	0.061736	
MMPs	F1	0	True	NaN	NaN	1	1.000000	
	F2	0	True	NaN	NaN	1	1.000000	
	F3	0	True	NaN	NaN	1	1.000000	
Signaling	F1	0	True	0.536227	4.812474	5	0.442437	
	F2	0	True	0.554009	5.151113	5	0.400336	
	F3	0	False	0.117602	18.669462	5	0.002375	

			group count	n per group
class	fraction			
Bone Metabolism	F1	0	3	[10, 10, 9]
	F2	0	3	[11, 11, 11]
	F3	0	3	[11, 11, 11]
Chemokines	F1	0	2	[10, 10]
	F2	0	2	[11, 11]
	F3	0	2	[11, 11]

Cytokines	F1	0	4	[10, 10, 10, 10]
	F2	0	4	[11, 11, 11, 11]
	F3	0	4	[11, 11, 11, 11]
ECM & Adhesion	F1	0	4	[10, 10, 10, 10]
	F2	0	4	[10, 11, 11, 10]
	F3	0	4	[11, 11, 11, 11]
MMPs	F1	0	2	[9, 5]
	F2	0	2	[11, 10]
	F3	0	2	[11, 11]
Signaling	F1	0	4	[10, 10, 10, 10]
	F2	0	4	[11, 11, 11, 11]
	F3	0	4	[11, 11, 11, 11]

```
[ ]: # Default is (paired) t-test, and since DA has subject: paired=True
DA.test_pairwise()
```

```
[ ]:
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			gene	A	B	mean(A)	\
class		fraction Contrast					
ECM & Adhesion	-	gene	-	CCL5	FZD4	0.591713	
		gene	-	CCL5	IFNG	0.591713	
		gene	-	CCL5	PTCH1	0.591713	
		gene	-	FZD4	IFNG	0.622994	
		gene	-	FZD4	PTCH1	0.622994	
...				
MMPs	NaN	gene * fraction	MMP9	F1	F3	0.256111	
		gene * fraction	MMP9	F2	F3	0.677357	
	F1	fraction * gene	NaN	MMP7	MMP9	0.032549	
	F2	fraction * gene	NaN	MMP7	MMP9	0.185211	
	F3	fraction * gene	NaN	MMP7	MMP9	0.742060	
class		fraction Contrast		std(A)	mean(B)	std(B)	Paired \
ECM & Adhesion	-	gene		0.253752	0.622994	0.266747	True
		gene		0.253752	-0.026656	0.149430	True
		gene		0.253752	0.469495	0.330886	True
		gene		0.266747	-0.026656	0.149430	True
		gene		0.266747	0.469495	0.330886	True
...				
MMPs	NaN	gene * fraction		0.802159	1.845550	0.600687	True
		gene * fraction		0.546148	1.845550	0.600687	True
	F1	fraction * gene		0.228544	0.256111	0.802159	True
	F2	fraction * gene		0.361750	0.677357	0.546148	True
	F3	fraction * gene		0.567249	1.845550	0.600687	True
class		fraction Contrast		Parametric	T	dof	\
ECM & Adhesion	-	gene		True	-0.327586	10.0	

		gene	True	7.882620	10.0
		gene	True	1.320783	10.0
		gene	True	7.532512	10.0
		gene	True	2.105924	10.0
...		
MMPs	NaN	gene * fraction	True	-3.513968	4.0
		gene * fraction	True	-5.680475	9.0
	F1	fraction * gene	True	-0.543884	4.0
	F2	fraction * gene	True	-3.811156	9.0
	F3	fraction * gene	True	-15.767066	10.0

class		fraction Contrast	alternative	p-unc	BF10 \
ECM & Adhesion	-	gene	two-sided	7.499799e-01	0.312
		gene	two-sided	1.339935e-05	1643.947
		gene	two-sided	2.160003e-01	0.598
		gene	two-sided	1.987311e-05	1165.781
		gene	two-sided	6.146203e-02	1.461
...		
MMPs	NaN	gene * fraction	two-sided	2.458360e-02	3.686
		gene * fraction	two-sided	3.016844e-04	111.751
	F1	fraction * gene	two-sided	6.154168e-01	0.448
	F2	fraction * gene	two-sided	4.145762e-03	12.636
	F3	fraction * gene	two-sided	2.163081e-08	4.845e+05

class		fraction Contrast	hedges	**p-unc	Sign. \
ECM & Adhesion	-	gene	-0.115597	ns	False
		gene	2.856874	****	signif.
		gene	0.398765	ns	False
		gene	2.890772	****	signif.
		gene	0.491362	0.061	toler.
...		
MMPs	NaN	gene * fraction	-2.179426	*	signif.
		gene * fraction	-2.024511	***	signif.
	F1	fraction * gene	-0.255634	ns	False
	F2	fraction * gene	-0.939861	**	signif.
	F3	fraction * gene	-1.817138	****	signif.

class		fraction Contrast	pairs cross
ECM & Adhesion	-	gene	(CCL5, FZD4) x
		gene	(CCL5, IFNG) x
		gene	(CCL5, PTCH1) x
		gene	(FZD4, IFNG) x
		gene	(FZD4, PTCH1) x
...			...

MMPs	NaN	gene * fraction	((MMP9, F3), (MMP9, F1))	hue
		gene * fraction	((MMP9, F3), (MMP9, F2))	hue
	F1	fraction * gene	((MMP9, F1), (MMP7, F1))	x
	F2	fraction * gene	((MMP9, F2), (MMP7, F2))	x
	F3	fraction * gene	((MMP9, F3), (MMP7, F3))	x

[167 rows x 19 columns]

```
[ ]: # Plot
(
    DA.switch("row", "col", verbose=False)
    .set(y="fc", inplace=False) # set y back to to fc to display non-log values
    .plot_box_strip(
        subplot_kws=dict(
            figsize=(10, 2.5),
            width_ratios=[4, 5, 3, 2, 5, 2],
        ),
        strip_kws=dict(alpha=0.8),
    )
    .edit_grid()
    .edit_y_scale_log(10)
    .edit_xy_axis_labels(y_leftmost_col="Fold Change", x="Gene")
    .annotate_pairwise(include="__HUE")
)

plt.savefig("qpcr1.png", dpi=300, bbox_inches="tight")
```

