

```
In [1]: import biom
import pandas as pd

from birdman import NegativeBinomial

table = biom.load_table("../data/tablebiomcorrected.biom")
metadata = pd.read_csv(
    "../data/metadatacorrected.txt",
    sep="\t",
    index_col=0
)
```

```
In [2]: prevalence = table.to_dataframe().clip(upper=1).sum(axis=1)
features_to_keep = prevalence[prevalence >= 5].index.tolist()
table_filt = table.filter(features_to_keep, axis="observation")
table_filt.head()
```

Out[2]: 5 x 5 <class 'biom.table.Table'> with 20 nonzero entries (80% dense)

```
In [3]: import pandas as pd

metadata = pd.read_csv(
    "../data/metadatacorrected.txt",
    sep="\t",
    index_col=0
)
metadata.index = metadata.index.astype(str)
metadata.head()
```

```
Out[3]:
```

	Temperature	Nitrate	Treatn	Treatment	Duplicate_n	Duplicate	Aquariu
sample-id							
18-c-1a	18C	control	1	18C_control	0	one	18C_contrc
18-c-1a-rep	18C	control	1	18C_control	1	two	18C_contrc
18-c-1b	18C	control	1	18C_control	0	one	18C_contrc
18-c-1b-rep	18C	control	1	18C_control	1	two	18C_contrc
18-c-1c	18C	control	1	18C_control	0	one	18C_contrc

```
In [4]: metadata.groupby(["Temperature", "Nitrate"]).size()
```

```
Out [4]: Temperature Nitrate
18C          N100      18
           N50       18
           control  18
22C          N100      18
           N50       18
           control  18
26C          N100      18
           N50       18
           control  18
28C          N100      18
           N50       18
           control  18
Fluctuating N100      18
           N50       18
           control  18
dtype: int64
```

```
In [5]: from birdman import NegativeBinomial

nb = NegativeBinomial(
    table=table_filt,
    formula="C(Temperature, Diff, levels=['18C', '22C', '26C', '28C', 'Fluct
metadata=metadata,
num_iter=1000,
chains=4,
beta_prior=3.0,
inv_disp_sd=0.5
)
```

```
In [6]: nb.compile_model()
```

```
In [7]: %%time

import logging

cmdstanpy_logger = logging.getLogger("cmdstanpy")
cmdstanpy_logger.disabled = True

nb.fit_model()
```

```
chain 1 |          | 00:00 Status
chain 2 |          | 00:00 Status
chain 3 |          | 00:00 Status
chain 4 |          | 00:00 Status
```

```
CPU times: user 2min 4s, sys: 26.6 s, total: 2min 31s
Wall time: 20h 17min 30s
```

```
In [8]: inference = nb.to_inference()
```

```
In [9]: import birdman.diagnostics as diag

diag.loo(inference, pointwise=True)
```

```
/usr/local/lib/python3.11/site-packages/arviz/stats/stats.py:803: UserWarning: Estimated shape parameter of Pareto distribution is greater than 0.7 for one or more samples. You should consider using a more robust model, this is because importance sampling is less likely to work well if the marginal posterior and LOO posterior are very different. This is more likely to happen with a non-robust model and highly influential observations.
```

```
warnings.warn(
```

```
Out[9]: Computed from 4000 posterior samples and 194940 observations log-likelihood matrix.
```

	Estimate	SE
elpd_loo	-169592.24	821.56
p_loo	7503.98	-

There has been a warning during the calculation. Please check the results.

Pareto k diagnostic values:

		Count	Pct.
(-Inf, 0.5]	(good)	191741	98.4%
(0.5, 0.7]	(ok)	1737	0.9%
(0.7, 1]	(bad)	1138	0.6%
(1, Inf)	(very bad)	324	0.2%

```
In [10]: diag.rhat(inference).max()
```

```
Out[10]: xarray.Dataset
```

► Dimensions:

► Coordinates: (0)

▼ Data variables:

inv_disp () float64 1.006

beta_var () float64 1.009

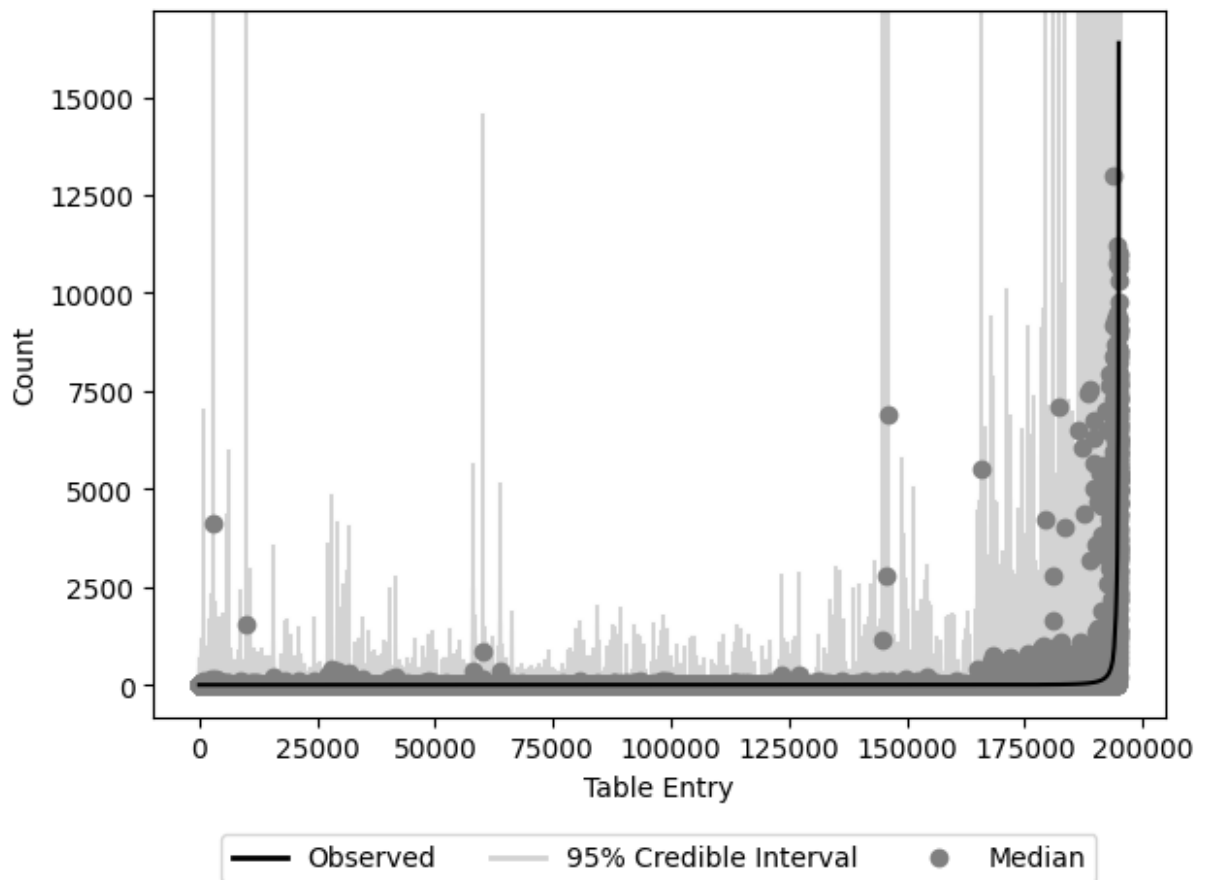


► Indexes: (0)

► Attributes: (0)

```
In [11]: import birdman.visualization as viz
import matplotlib.pyplot as plt

viz.plot_posterior_predictive_checks(inference);
```



In [12]: `%%capture`

```

from birdman import NegativeBinomial

nb_null = NegativeBinomial(
    table=table_filt,
    formula="1",
    metadata=metadata,
    num_iter=1000,
    chains=4
)
nb_null.compile_model()
nb_null.fit_model()

```

In [13]: `inference_null = nb_null.to_inference()`

In [14]: `diag.loo(inference_null, pointwise=True)`

```

/usr/local/lib/python3.11/site-packages/arviz/stats/stats.py:803: UserWarning:
Estimated shape parameter of Pareto distribution is greater than 0.7 for
one or more samples. You should consider using a more robust model, this
is because importance sampling is less likely to work well if the marginal
posterior and LOO posterior are very different. This is more likely to
happen with a non-robust model and highly influential observations.

```

```

warnings.warn(

```

Out[14]: Computed from 4000 posterior samples and 194940 observations log-likelihood matrix.

	Estimate	SE
elpd_loo	-187662.19	889.26
p_loo	1862.51	-

There has been a warning during the calculation. Please check the results.

Pareto k diagnostic values:

		Count	Pct.
(-Inf, 0.5]	(good)	194704	99.9%
(0.5, 0.7]	(ok)	146	0.1%
(0.7, 1]	(bad)	70	0.0%
(1, Inf)	(very bad)	20	0.0%

```
In [ ]: import arviz as az
```

```
az.compare({"null": inference_null, "model": inference})
```

```
In [ ]:
```