Model diagnostics

The BI class can compute model diagnostics for a given model.

Lets concider the following model for a linear regression:

$$Y_i \sim \text{Normal}(\alpha + \beta X_i, \sigma)$$

$$\alpha \sim \text{Normal}(0, 1)$$

$$\beta \sim \text{Normal}(0, 1)$$

$$\sigma \sim \text{Uniform}(0, 50)$$

```
import os
import sys
newPath = os.path.dirname(os.path.abspath(""))
if newPath not in sys.path:
    sys.path.append(newPath)
from BI import bi
import jax.numpy as jnp
# setup platform-----------------------------------------------
m = bi(platform='cpu')

# import data --------------------------------------------
m.data('Howell1.csv', sep=';')
m.df = m.df[m.df.age > 18]
m.scale(data=['weight'])
m.data_to_model(['weight', 'height'])

 # define model ------------------------------------------------
```

```
def model(weight, height):
    a = m.dist.normal( 178, 20, name = 'a')
    b = m.dist.log_normal(  0, 1, name = 'b')
    s = m.dist.uniform( 0, 50, name = 's')
    m.dist.normal(a + b * weight , s, obs=height, shape=(weight.shape[0],))

# Run sampler ----------------------------------------------
m.fit(model, num_samples=1000,num_chains=4)
m.summary()
```

```
jax.local_device_count 32

  0%|          | 0/1500 [00:00<?, ?it/s]

  0%|          | 0/1500 [00:00<?, ?it/s]

  0%|          | 0/1500 [00:00<?, ?it/s]

  0%|          | 0/1500 [00:00<?, ?it/s]
```

	mean	sd	hdi_5.5%	hdi_94.5%
a	154.65	0.28	154.23	155.13
b	5.81	0.28	5.35	6.23
s	5.14	0.20	4.83	5.46

List of all available diagnostics

For additional documentation check the diagnostics API reference

Pareto-smoothed

```
m.diag.loo()
```

```
Computed from 4000 posterior samples and 346 observations log-likelihood matrix.

         Estimate       SE
elpd_loo -1058.44    14.67
p_loo        3.14        -
------

Pareto k diagnostic values:
                         Count   Pct.
(-Inf, 0.5]   (good)       346  100.0%
 (0.5, 0.7]   (ok)           0    0.0%
   (0.7, 1]   (bad)          0    0.0%
   (1, Inf)   (very bad)     0    0.0%
```

Widely applicable information criterion

```
m.df.head()
```

	height	weight	age	male
0	151.765	0.430669	63.0	1
1	139.700	-1.326018	63.0	0
2	136.525	-2.041868	65.0	0
3	156.845	1.238745	41.0	1
4	145.415	-0.583818	51.0	0

```
m.diag.WAIC()
```

```
Computed from 4000 posterior samples and 346 observations log-likelihood matrix.

          Estimate       SE
elpd_waic -1058.43    14.67
p_waic        3.14        -
```

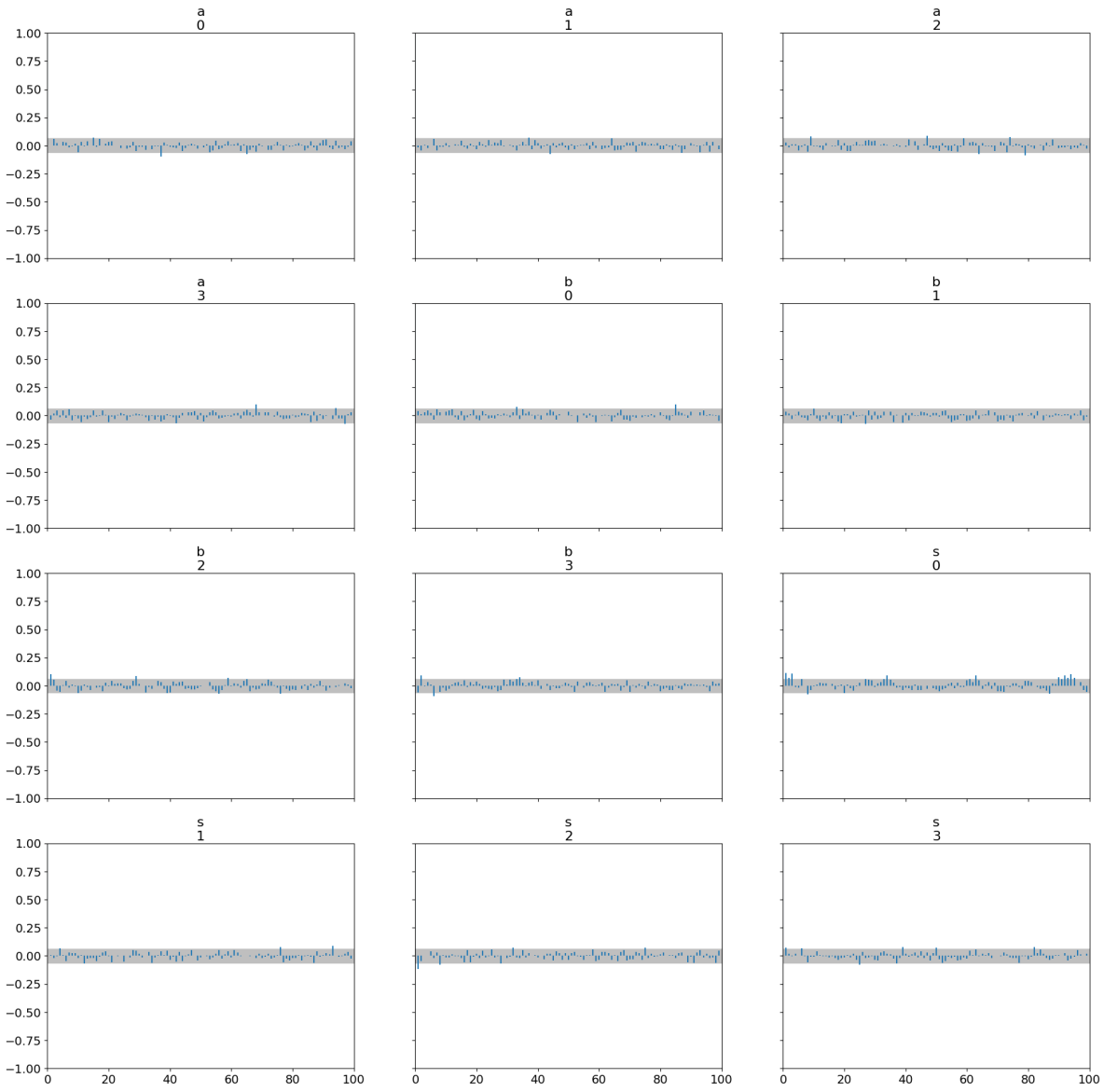
Predictions from model base on specific data value

```
m.sample()
m.sample(data=dict(weight=jnp.array([0.4])), remove_obs=False)
```

```
{'x': Array([149.77345571], dtype=float64)}
```

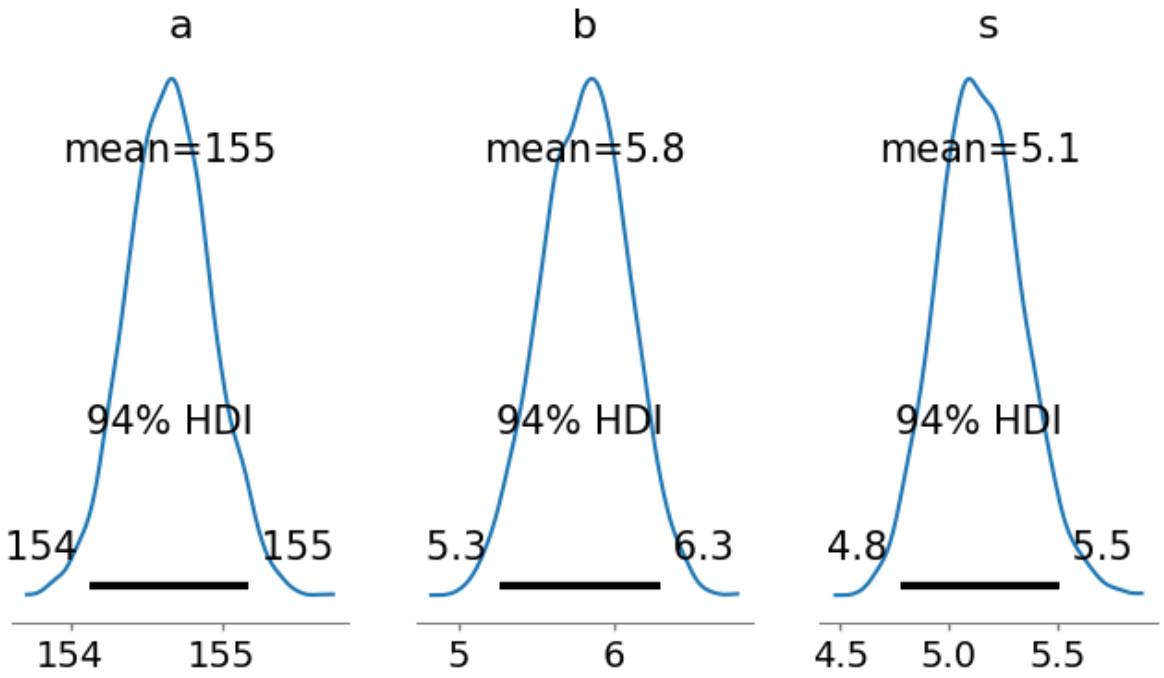
Plot autocorrelation of the MCMC chains

```
m.diag.autocor()
```



Posterior distribution plots

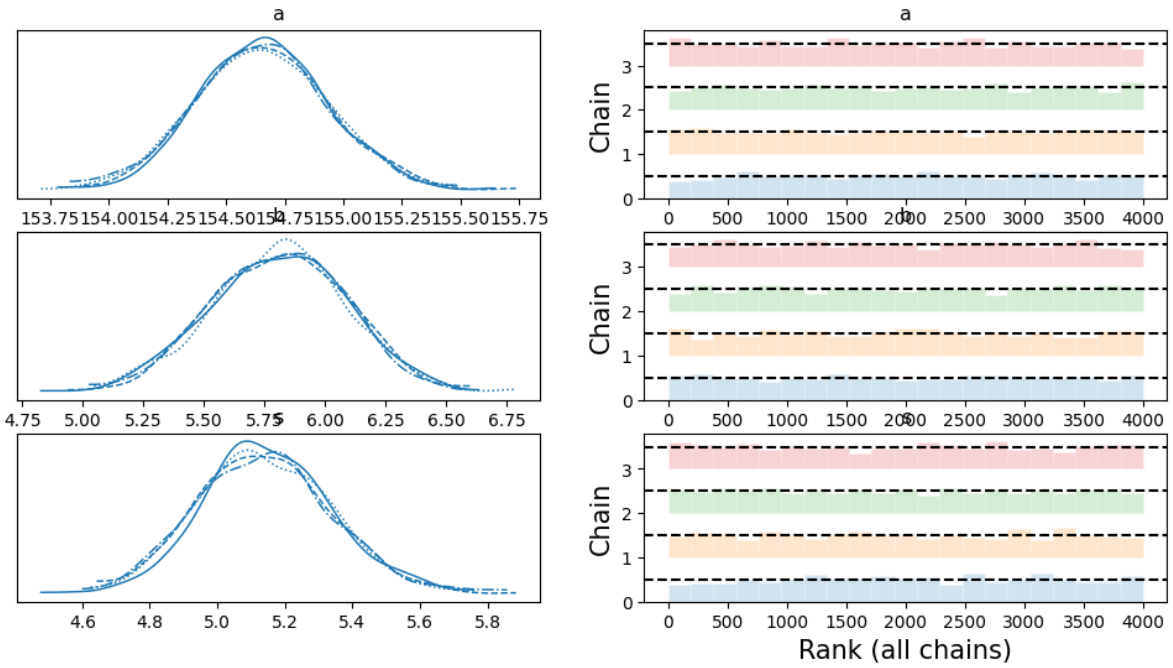
```
m.diag.posterior()
```



Trace plots for MCMC chains

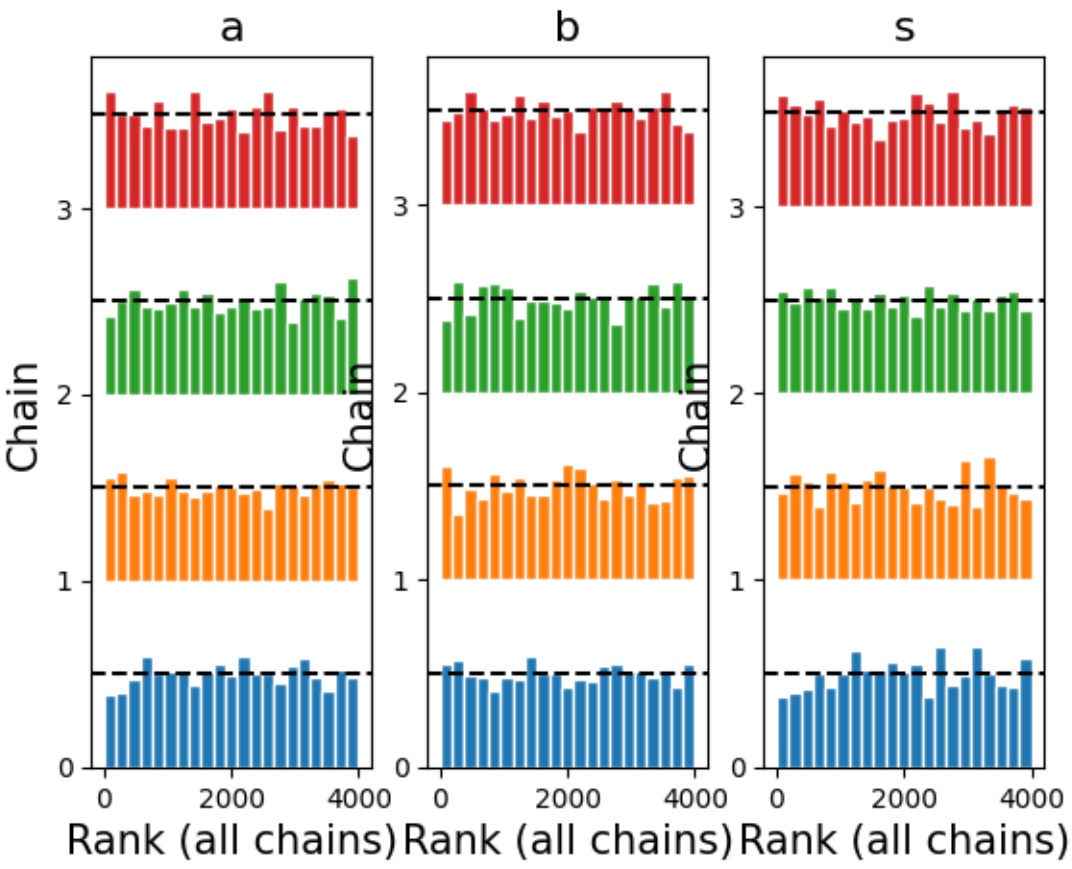
```
m.diag.plot_trace()
```

```
array([[<Axes: title={'center': 'a'}>,
        <Axes: title={'center': 'a'}, xlabel='Rank (all chains)', ylabel='Chain'>],
       [<Axes: title={'center': 'b'}>,
        <Axes: title={'center': 'b'}, xlabel='Rank (all chains)', ylabel='Chain'>],
       [<Axes: title={'center': 's'}>,
        <Axes: title={'center': 's'}, xlabel='Rank (all chains)', ylabel='Chain'>]],
      dtype=object)
```



Create rank plots for MCMC chains

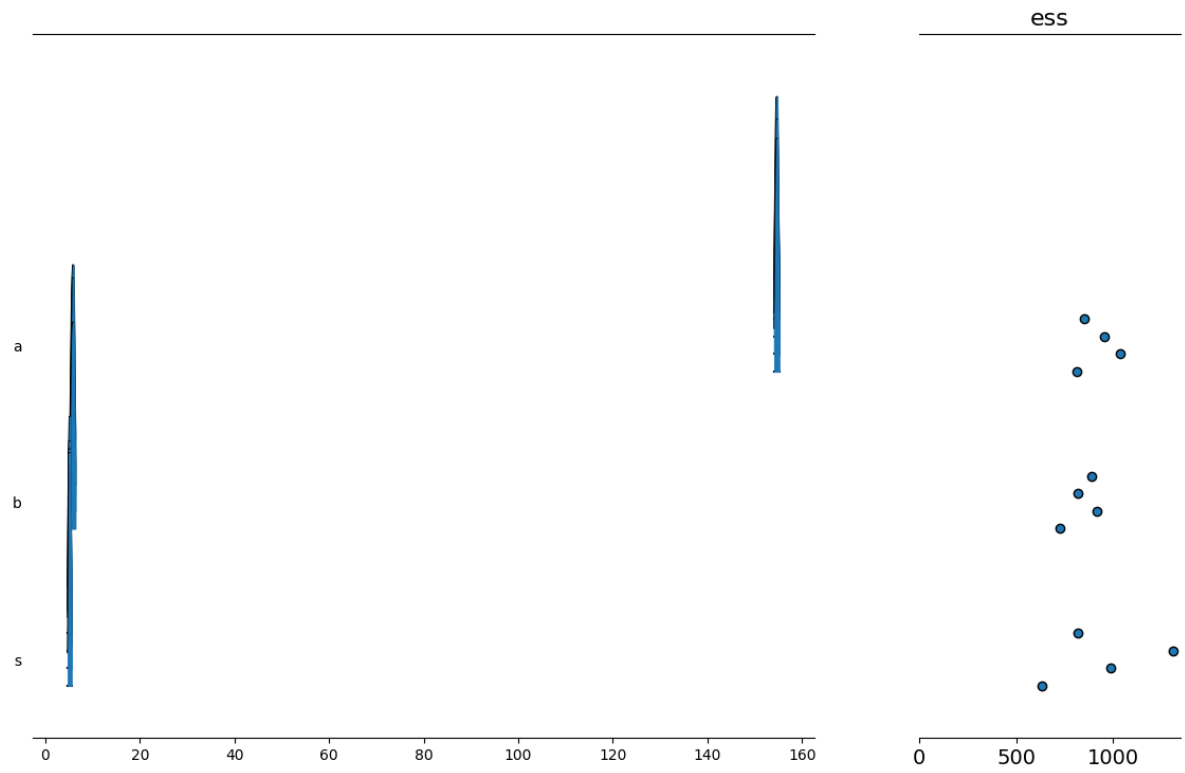
```
m.diag.rank()
```



Forest plot of estimated values

```
m.diag.forest()
```

```
array([<Axes: >, <Axes: title={'center': 'ess'}>], dtype=object)
```

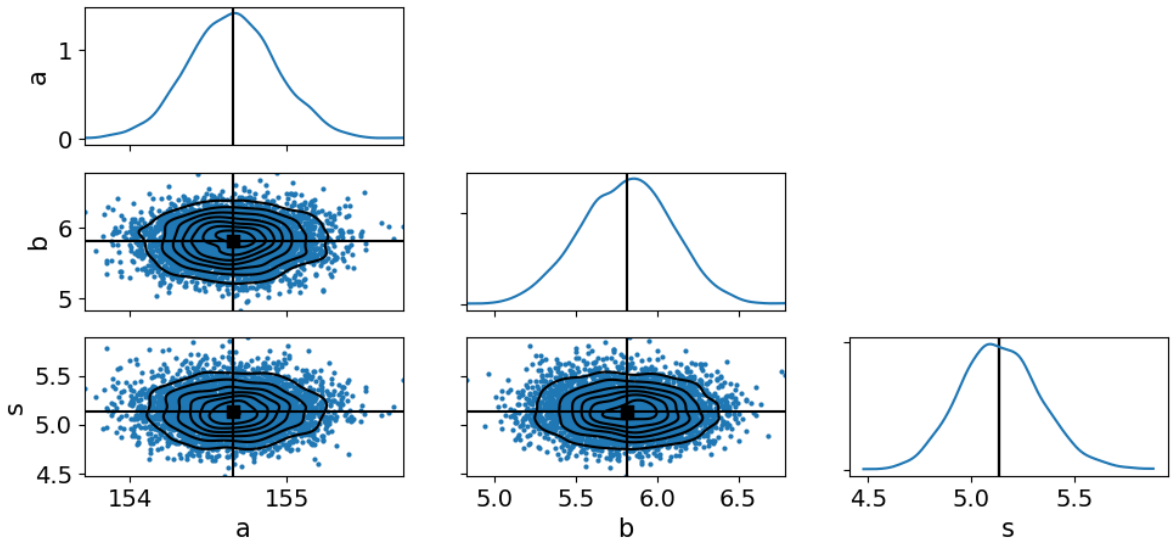


Pairwise plots of the posterior distribution

```
m.diag.pair()
```

```
/home/sosa/.local/lib/python3.10/site-packages/xarray/core/utils.py:494: FutureWarning: The i
  warnings.warn(
```

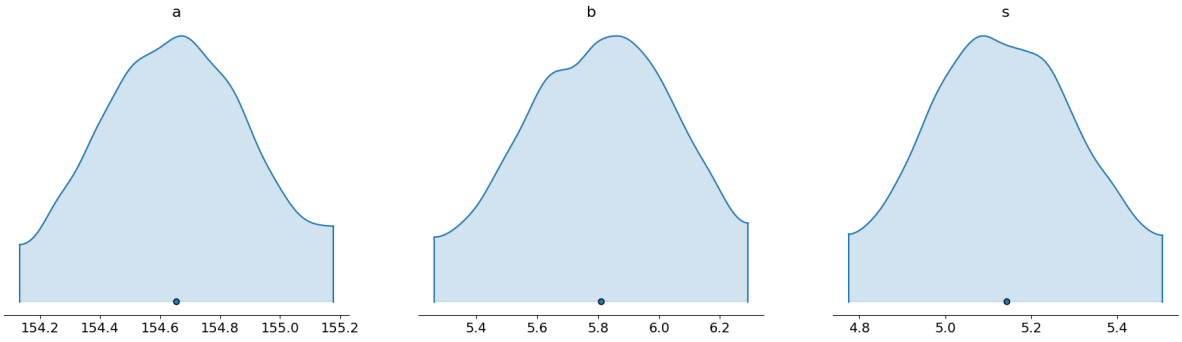
```
array([[<Axes: ylabel='a'>, <Axes: >, <Axes: >],
       [<Axes: ylabel='b'>, <Axes: >, <Axes: >],
       [<Axes: xlabel='a', ylabel='s'>, <Axes: xlabel='b'>,
        <Axes: xlabel='s'>]], dtype=object)
```



Density plots of the posterior distribution

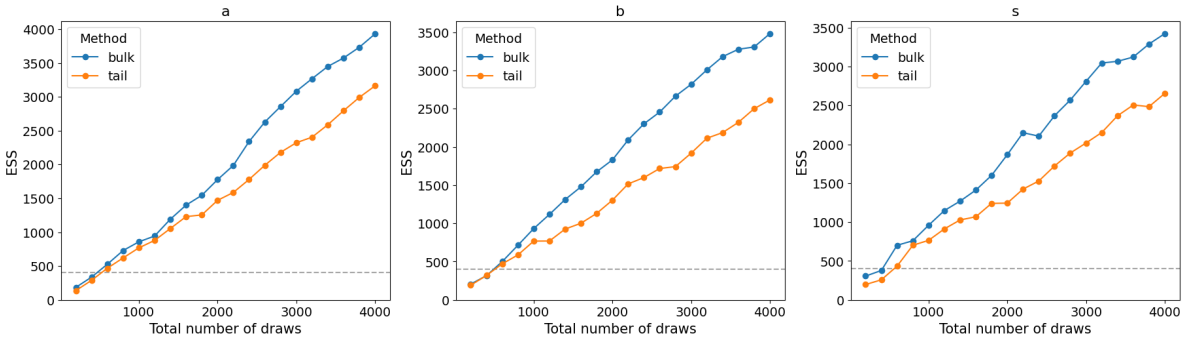
```
m.diag.density()
```

```
array([[<Axes: title={'center': 'a'}>, <Axes: title={'center': 'b'}>,
        <Axes: title={'center': 's'}>]], dtype=object)
```



Evolution of effective sample size across iterations

```
m.diag.plot_ess()
```


a
b
s
Method
bulk
tail
ESS
Total number of draws