Model Diagnostic

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

Lets concider the following model for a linear regression:

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

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

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

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

```
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'])


 # 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=500,num_chains=4)
m.summary()
```

```
jax.local_device_count 32
```

```
  0%|          | 0/1000 [00:00<?, ?it/s]
```

```
  0%|          | 0/1000 [00:00<?, ?it/s]
```

```
  0%|          | 0/1000 [00:00<?, ?it/s]
```

```
  0%|          | 0/1000 [00:00<?, ?it/s]
```

	mean	sd	hdi_5.5%	hdi_94.5%	mcse_mean	mcse_sd	ess_bulk	ess_tail	r_hat
a	154.66	0.28	154.22	155.12	0.01	0.0	1773.68	1460.38	1.0
b	5.80	0.28	5.33	6.21	0.01	0.0	1835.80	1288.50	1.0
s	5.14	0.20	4.83	5.46	0.00	0.0	1867.32	1231.60	1.0

List of all available diagnostics

For additional documentation check the diagnostics API reference

Predictions from model base on specific data value

```
m.sample() # Predictions from model base on data in data_on_model
m.sample(data=dict(weight=jnp.array([0.4])), remove_obs=False)# Predictions from a given valu
```

```
{'x': Array([149.77945571], dtype=float64)}
```

Forest plot of estimated values

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

```
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```

```
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```

Density plots of the posterior distribution

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

```
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```

Posterior distribution plots

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

```
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```

Trace plots for MCMC chains

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

```
['a', 'b', 's']
```

```
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```

Pairwise plots of the posterior distribution

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

```
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```

Plot autocorrelation of the MCMC chains

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

```
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```
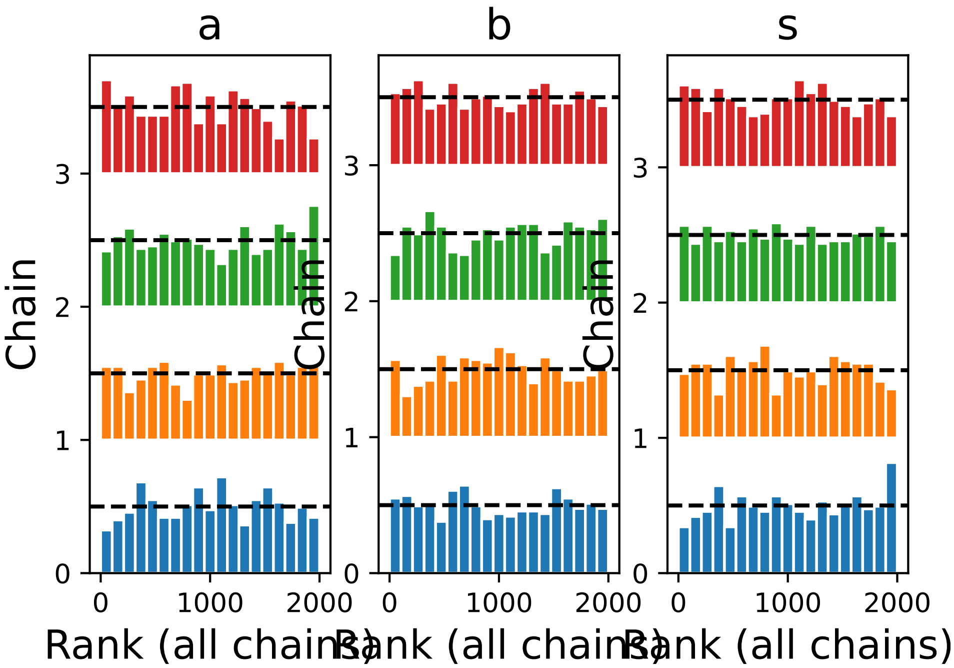

Create rank plots for MCMC chains

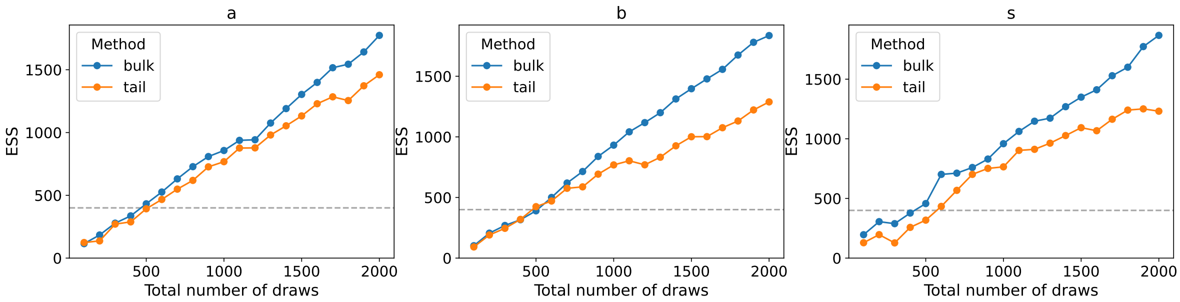
```
m.diag.rank()
```



Evolution of effective sample size across iterations

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

```
/home/sosa/.local/lib/python3.10/site-packages/xarray/core/utils.py:494: FutureWarning:

The return type of `Dataset.dims` will be changed to return a set of dimension names in futu
```



Pareto-smoothed

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

```
Computed from 2000 posterior samples and 346 observations log-likelihood matrix.

         Estimate       SE
elpd_loo -1058.46    14.68
p_loo        3.16        -
------

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.diag.WAIC()
```

```
Computed from 2000 posterior samples and 346 observations log-likelihood matrix.

          Estimate       SE
elpd_waic -1058.45    14.68
p_waic        3.15        -
```