

# Build in models

## PCA

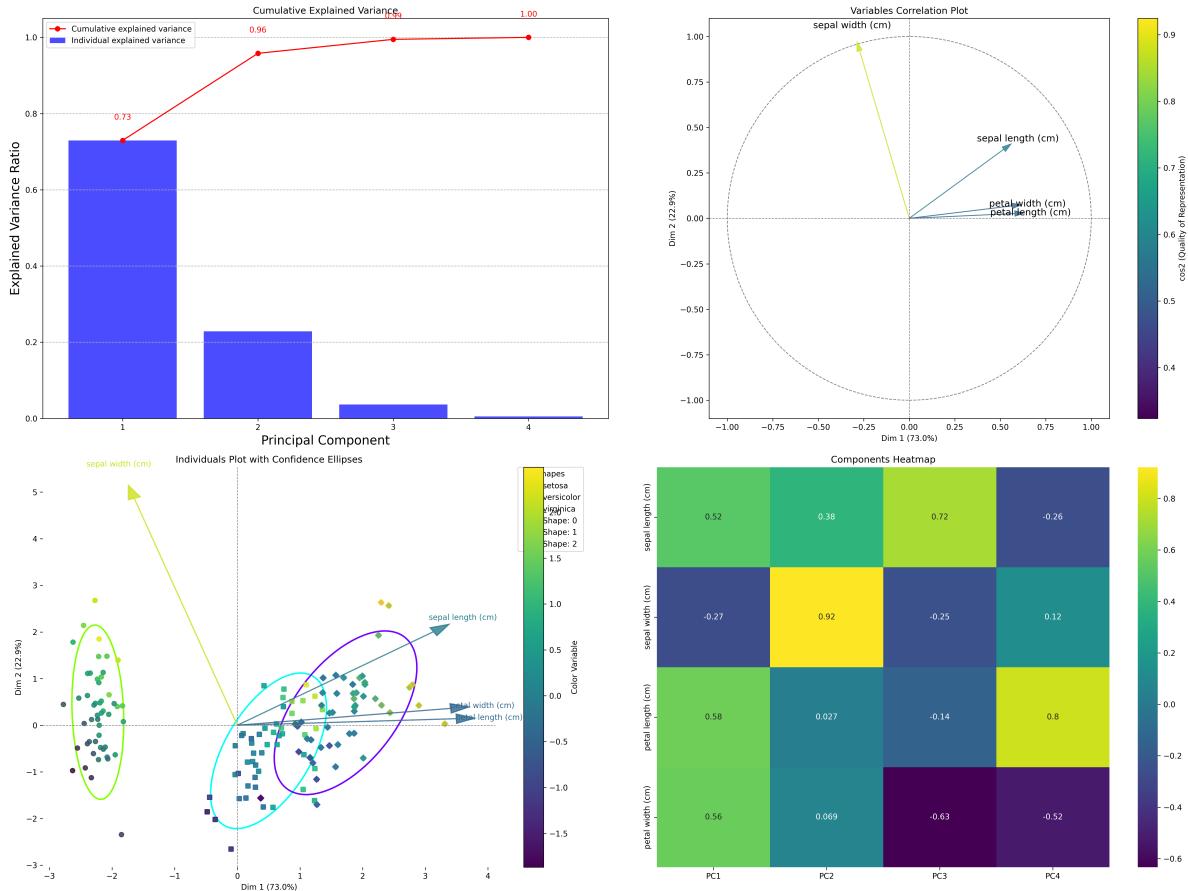
```
from BI import bi, jnp

m=bi()
m.data('iris.csv', sep=',') # Data is already scaled
m.data_on_model = dict(
    X=jnp.array(m.df.iloc[:,0:-2].values)
)
m.fit(m.models.pca(type="classic"), progress_bar=False) # or robust, sparse, classic, sparse

m.models.pca.plot(
    X=m.df.iloc[:,0:-2].values,
    y=m.df.iloc[:, -2].values,
    feature_names=m.df.columns[0:-2],
    target_names=m.df.iloc[:, -1].unique(),
    color_var=m.df.iloc[:, 0].values,
    shape_var=m.df.iloc[:, -2].values
)

jax.local_device_count 16
```

## PCA Analysis Dashboard



## Survival analysis

```
from BI import bi, jnp

m = bi()
m.data('mastectomy.csv', sep=',').head()
m.df.metastasized = (m.df.metastasized.values == "yes").astype(jnp.int64)

# Import time-steps and events
m.models.survival.import_time_event(
    m.df.time.values,
    m.df.event.values, interval_length=3
```

```

)
# To import time-fixed covariates
m.models.survival.import_covF(
    m.df.metastasized.values, ['metastasized']
)

# To import time-varying covariates Experimental feature
# m.models.survival.import_covV

m.fit(m.models.survival.model, num_samples=500)

m.summary()

m.models.survival.plot_surv( beta = 'Hazard_rate_metastasized')

```

jax.local\_device\_count 16

---

Survival concern 44 individuals in 76 intervals.  
18.0 individuals experienced the event.

---

Covariates imported: ['metastasized']  
Surv object now has 1 covariates: ['metastasized']  
This function is still in development. Use it with caution.  
This function is still in development. Use it with caution.

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

This function is still in development. Use it with caution.

warmup: 0% | 1/1000 [00:02<46:26, 2.79s/it, 1 steps of size 2.34e+00. acc. prob-

This function is still in development. Use it with caution.  
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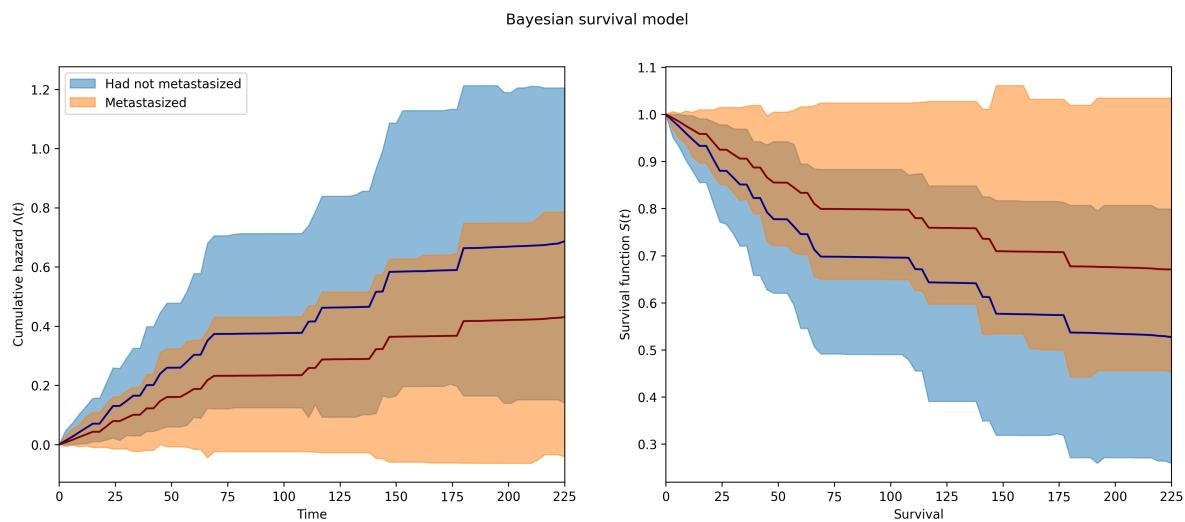
arviz - WARNING - Shape validation failed: input\_shape: (1, 500), minimum\_shape: (chains=2, c  
/home/sosa/work/.venv/lib/python3.12/site-packages/arviz/plots/hdiplot.py:166: FutureWarning

hdi currently interprets 2d data as (draw, shape) but this will change in a future release to

```

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```



## Gaussian Mixture Models

```

from BI import bi
from sklearn.datasets import make_blobs
m = bi()

# Generate synthetic data
data, true_labels = make_blobs(
    n_samples=500, centers=8, cluster_std=0.8,
    center_box=(-10,10), random_state=101
)

```

```
m.data_on_model = {"data": data, "K": 8 }
m.fit(m.models.gmm) # Optimize model parameters through MCMC sampling
m.plot(X=data,sampler=m.sampler) # Experimental feature
```

```
jax.local_device_count 16
```

```
0%|          | 0/1000 [00:00<?, ?it/s] warmup: 0%|          | 1/1000 [00:02<43:32, 2.61s]
```

## Dirichlet Process Mixture Models

### Python

```
from BI import bi
from sklearn.datasets import make_blobs
m = bi()

# Generate synthetic data
data, true_labels = make_blobs(
    n_samples=500, centers=8, cluster_std=0.8,
    center_box=(-10,10), random_state=101
)
m.data_on_model = dict(data=data,T=10)
m.fit(m.models.dpmm)
m.plot(data,m.sampler) # Experimental feature
```

```
jax.local_device_count 16
```

```
0%|          | 0/1000 [00:00<?, ?it/s] warmup: 0%|          | 1/1000 [00:02<46:26, 2.79s]
```

## Network Models

### Python

```

# Setup device-----
from BI import bi, jnp

# Setup device-----
m = bi(platform='cpu')
# Simulate data -----
N = 50
individual_predictor = m.dist.normal(0,1, shape = (N,1), sample = True)

kinship = m.dist.bernoulli(0.3, shape = (N,N), sample = True)
kinship = kinship.at[jnp.diag_indices(N)].set(0)

def sim_network(kinship, individual_predictor):
    # Intercept
    alpha = m.dist.normal(0,1, sample = True)

    # SR
    sr = m.net.sender_receiver(individual_predictor, individual_predictor, s_mu = 0.4, r_mu = 0.4)

    # D
    DR = m.net.dyadic_effect(kinship, d_sd=2.5, sample = True)

    return m.dist.bernoulli(logits = alpha + sr + DR, sample = True)

network = sim_network(m.net.mat_to_edgl(kinship), individual_predictor)

# Predictive model -----
m.data_on_model = dict(
    network = network,
    dyadic_predictors = m.net.mat_to_edgl(kinship),
    focal_individual_predictors = individual_predictor,
    target_individual_predictors = individual_predictor
)

def model(network, dyadic_predictors, focal_individual_predictors, target_individual_predictors):
    N_id = network.shape[0]

    # Block -----
    alpha = m.dist.normal(0,1, sample = True)

```

```
## SR shape = N individuals-----
sr = m.net.sender_receiver(
  focal_individual_predictors,
  target_individual_predictors,
  s_mu = 0.4, r_mu = -0.4
)

# Dyadic shape = N dyads-----
dr = m.net.dyadic_effect(dyadic_predictors, d_sd=2.5) # Diadic effect intercept only

m.dist.bernoulli(logits = alpha + sr + dr, obs=network)

m.fit(model, num_samples = 500, num_warmup = 500, num_chains = 1, thinning = 1)
```