

Build in models

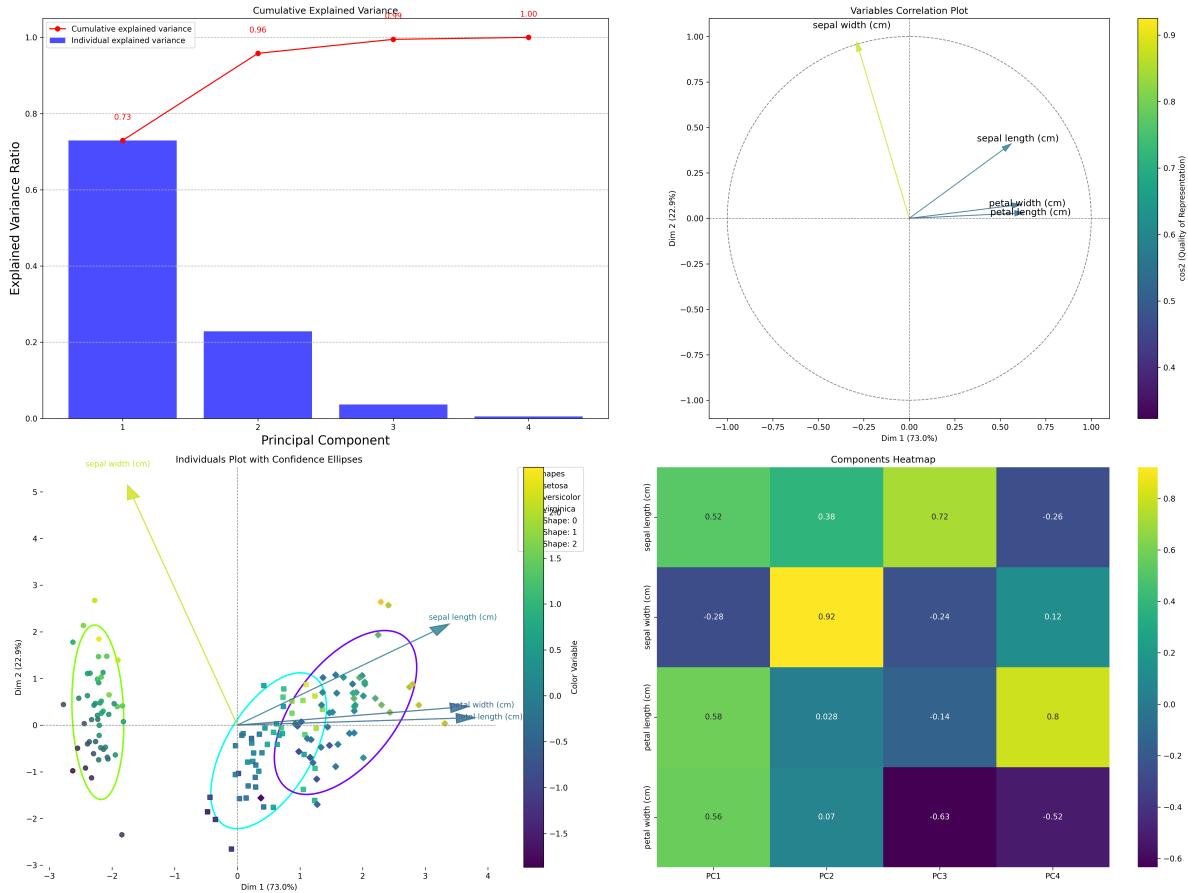
PCA

```
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="ARD"), progress_bar=False) # or robust, sparse, classic, sparse_robust

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

```
m.models.survival.import_covF(  
    m.df.metastasized.values, ['metastasized'])  
# Import time-fixed covariates  
# m.models.survival.import_covV # To import time-varying covariates  
  
m.fit(m.models.survival.model, num_samples=500)  
m.summary()  
  
m.models.survival.plot_surv( beta = 'Hazard_rate_metastasized')
```

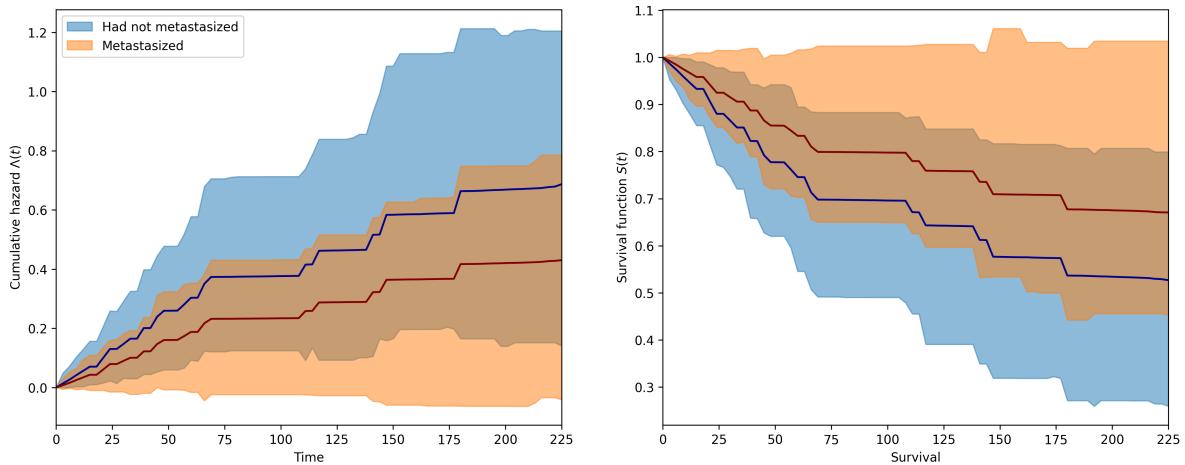
```
jax.local_device_count 16
```

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

```
-----  
Covariates imported: ['metastasized']  
Surv object now has 1 covariates: ['metastasized']
```

```
0%|          | 0/1000 [00:00<?, ?it/s] warmup: 0%|          | 1/1000 [00:01<29:12, 1.75s]
```

Bayesian survival model



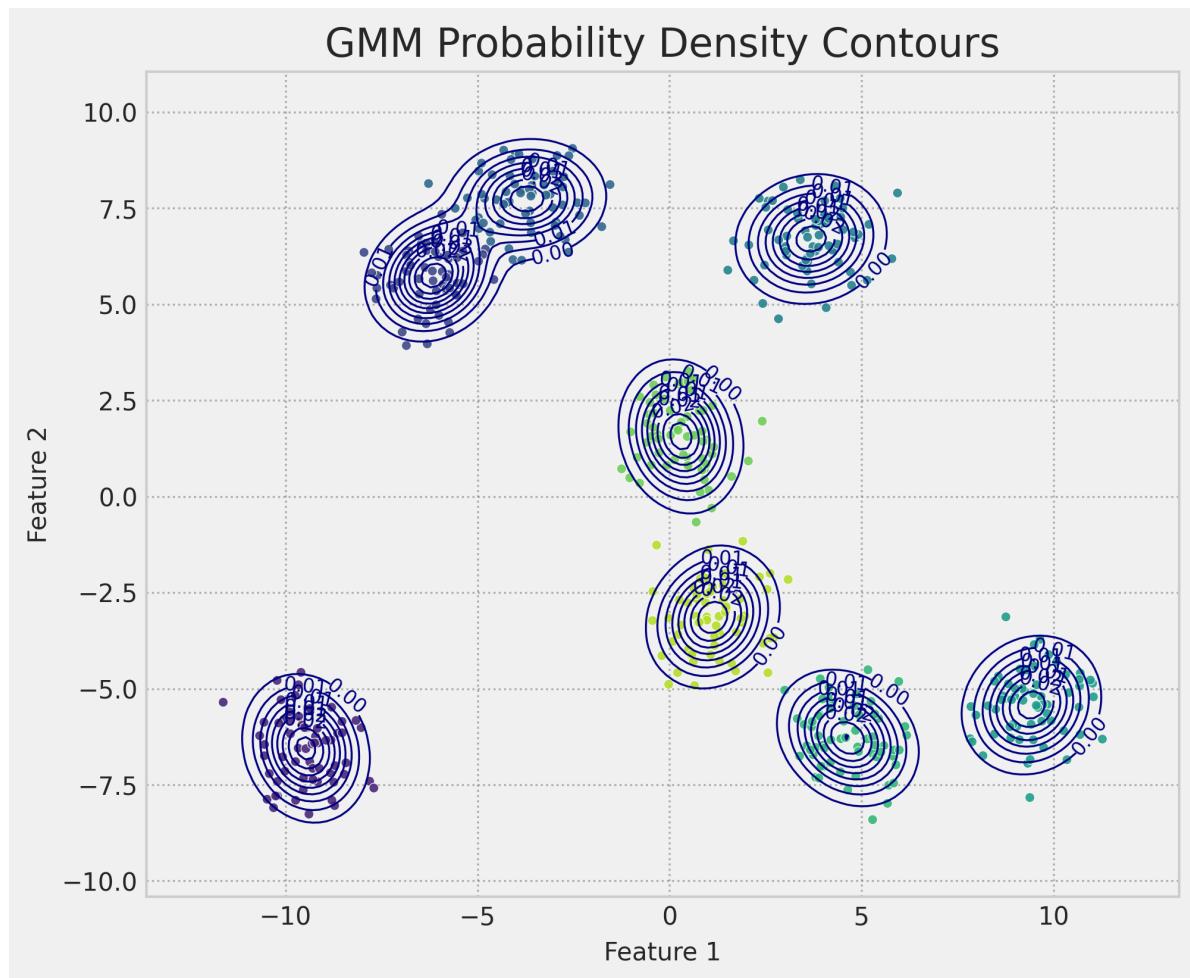
Gaussian Mixture Models

```
from BI import bi
from sklearn.datasets import make_blobs

# 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) # Prebuild plot function for GMM
```

0% | 0/1000 [00:00<?, ?it/s] warmup: 0% | 1/1000 [00:03<1:06:20, 3.98]



Model not supported

Dirichlet Process Mixture Models

Python

```
from BI import bi
from sklearn.datasets import make_blobs

# Generate synthetic data
data, true_labels = make_blobs(
    n_samples=500, centers=8, cluster_std=0.8,
```

```

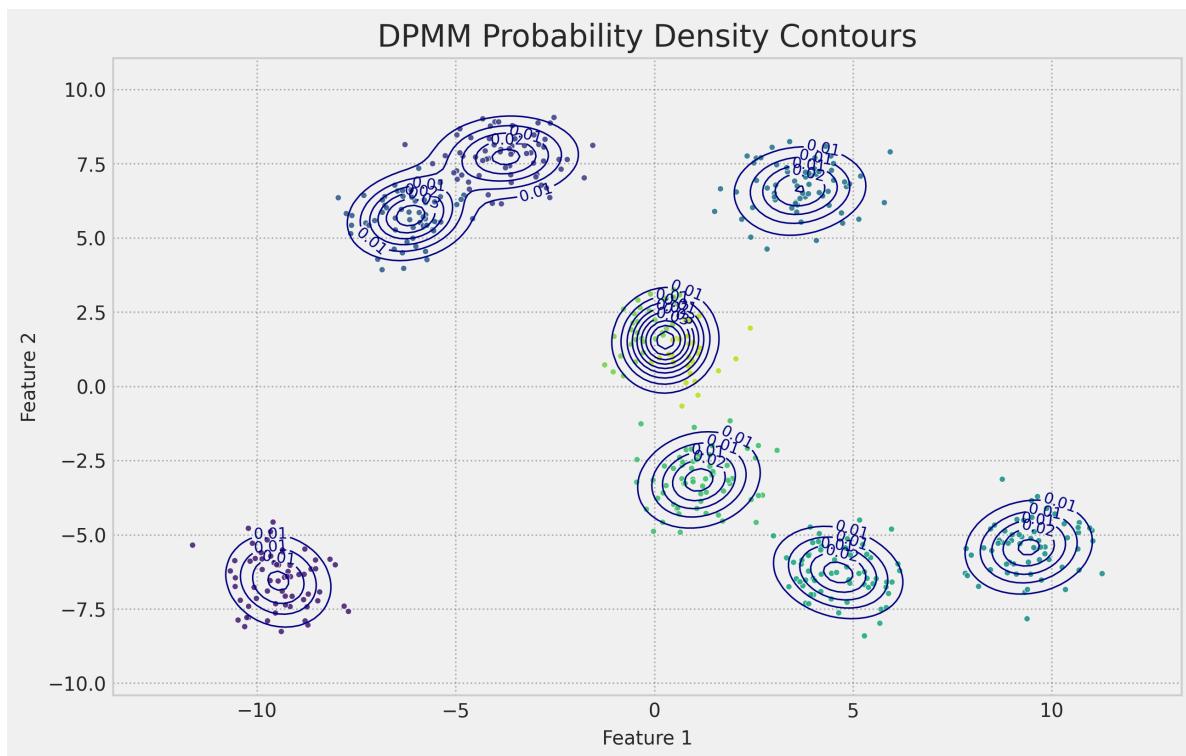
        center_box=(-10,10), random_state=101
    )

m.data_on_model = {"data": data, "T": 10 } # T = Number of maximum cluster to test for
m.fit(m.models.dpmm)
m.plot(X=data,sampler=m.sampler) # Prebuild plot function for GMM

```

0% | 0/1000 [00:00<?, ?it/s] warmup: 0% | 1/1000 [00:03<1:04:07, 3.88]

Model found 9 clusters.



Network Models

Python

```

from BI import bi

# Setup device-----
from BI import bi
# Setup device-----
m = bi(platform='cpu')

m.data_on_model = dict(
    idx = idx,
    Any = Any-1,
    Merica = Merica-1,
    Quantum = Quantum-1,
    result_outcomes = m.net.mat_to_edgl(data['outcomes']),
    kinship = m.net.mat_to_edgl(kinship),
    focal_individual_predictors = data['individual_predictors'],
    target_individual_predictors = data['individual_predictors'],
    exposure_mat = data['exposure']
)

def model(idx, result_outcomes,
          exposure,
          kinship,
          focal_individual_predictors, target_individual_predictors,
          Any, Merica, Quantum):
    # Block -----
    B_any = m.net.block_model(Any,1)
    B_Merica = m.net.block_model(Merica,3)
    B_Quantum = m.net.block_model(Quantum,2)

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

    # Dyadic shape = N dyads-----
    dr = m.net.dyadic_effect(dyadic_predictors)

    m.dist.poisson(jnp.exp(B_any + B_Merica + B_Quantum + sender_receiver + dr), obs = res)

m.fit(model)
summary = m.summary()

```

```

summary.loc[['focal_effects[0]', 'target_effects[0]', 'dyad_effects[0]']]

m.fit(model2)
summary = m.summary()
summary

```

R

```

library(BI)
# Setup platform-----
m=importbi(platform='cpu')

# Import data ----

load(paste(system.file(package = "BI"),'/data/STRAND sim sr only.Rdata', sep = ''))

ids = 0:(model_dat$N_id-1)
idx = m$net$vec_node_to_edgle(jnp$stack(jnp$array(list(ids, ids)), axis = -as.integer(1)))

keys <- c("idx",
         'idxShape',
         "result_outcomes",
         'focal_individual_predictors',
         'target_individual_predictors')

values <- list(
  idx,
  idx$shape[[1]],
  m$net$mat_to_edgl(model_dat$outcomes[, , 1]),
  jnp$array(model_dat$individual_predictors)$reshape(as.integer(1), as.integer(50)),
  jnp$array(model_dat$individual_predictors)$reshape(as.integer(1), as.integer(50))
)
data = py_dict(keys, values, convert = TRUE)
m$data_on_model=data

# Define model -----
model <- function(idx, idxShape, result_outcomes, focal_individual_predictors, target_individual_predictors, N_id = 50, x=0.1/jnp$sqrt(N_id), tmp=jnp$log(x / (1 - x)))

```

```

## Block -----
B = bi.dist.normal(tmp, 2.5, shape=c(1), name = 'block')

#SR -----
sr = m$net$sender_receiver(focal_individual_predictors,target_individual_predictors)

#### Dyadic-----
#dr, dr_raw, dr_sigma, dr_L = m.net.dyadic_random_effects(idx.shape[0], cholesky_density =
dr = m$net$dyadic_effect(shape = c(idxShape))

## SR -----
m$poisson(jnp$exp(B + sr + dr), obs=result_outcomes)
}

# Run MCMC -----
m$fit(model) # Optimize model parameters through MCMC sampling

# Summary -----
summary =m$summary()

summary[rownames(summary) %in% c('focal_effects[0]', 'target_effects[0]', 'block[0]'),]

```