# lab3

May 18, 2021

## 1 Bayesian Learning Lab3

Author : Yunan Dong, Yifan Ding

[57]:
```
import math
import stan
import nest_asyncio
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt

from scipy.stats import multivariate_normal
from sklearn.neighbors import KernelDensity

# config event loop for stan in juypyter
nest_asyncio.apply()
```

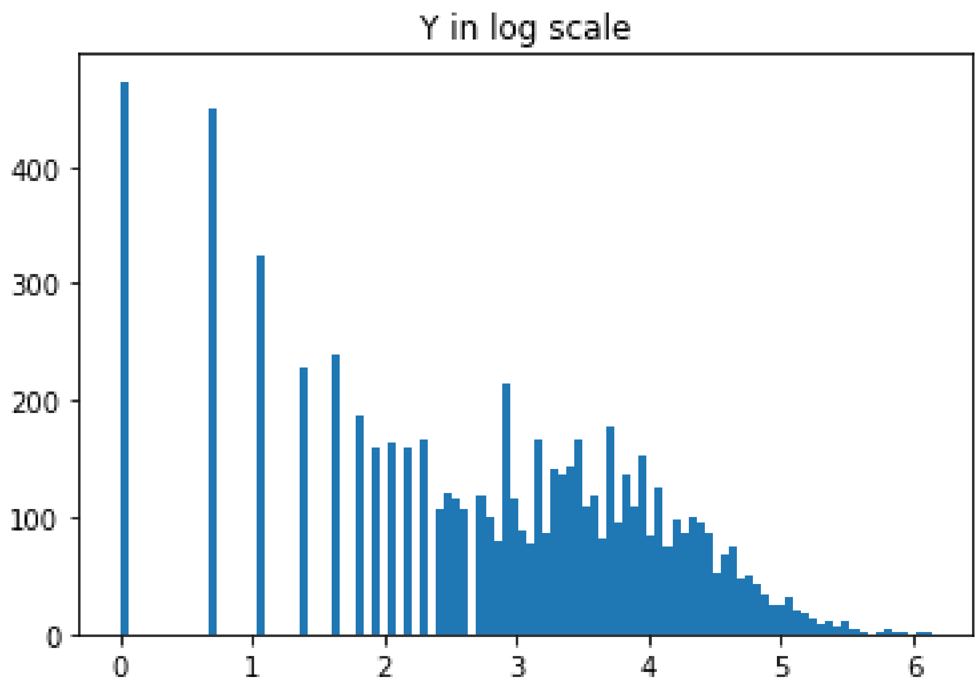
### 1.1 Q1

#### 1.1.1 a)

[58]:
```
with open('rainfall.dat') as f:
    doc = f.readlines()
    for i,j in enumerate(doc):
        doc[i] = int(j.split('\n')[0])
y = np.array(doc)
logy = np.log(y)
```

[59]:
```
# prior parameters
mu0 = np.mean(logy)
tau0_squa = 1
v0 = 4
sigma0_squa = 1

mu = np.random.normal(mu0, np.sqrt(tau0_squa))
sigma_squa = sigma0_squa * v0 / np.random.chisquare(v0, size=1)
```

```python
plt.hist(logy, bins=100)
plt.title('Y in log scale')
plt.show()
```

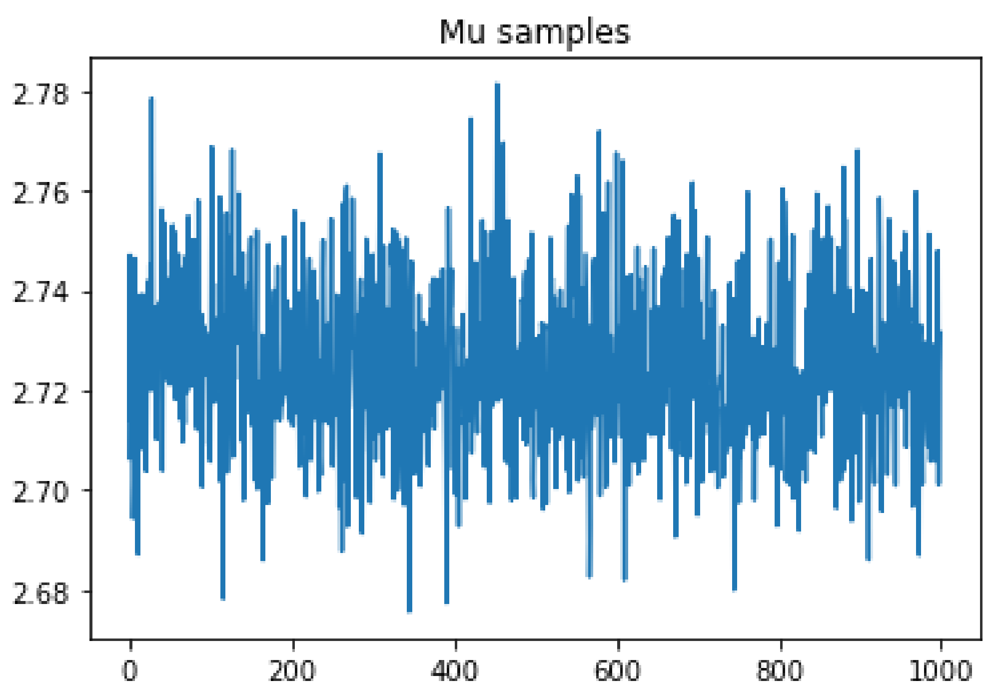


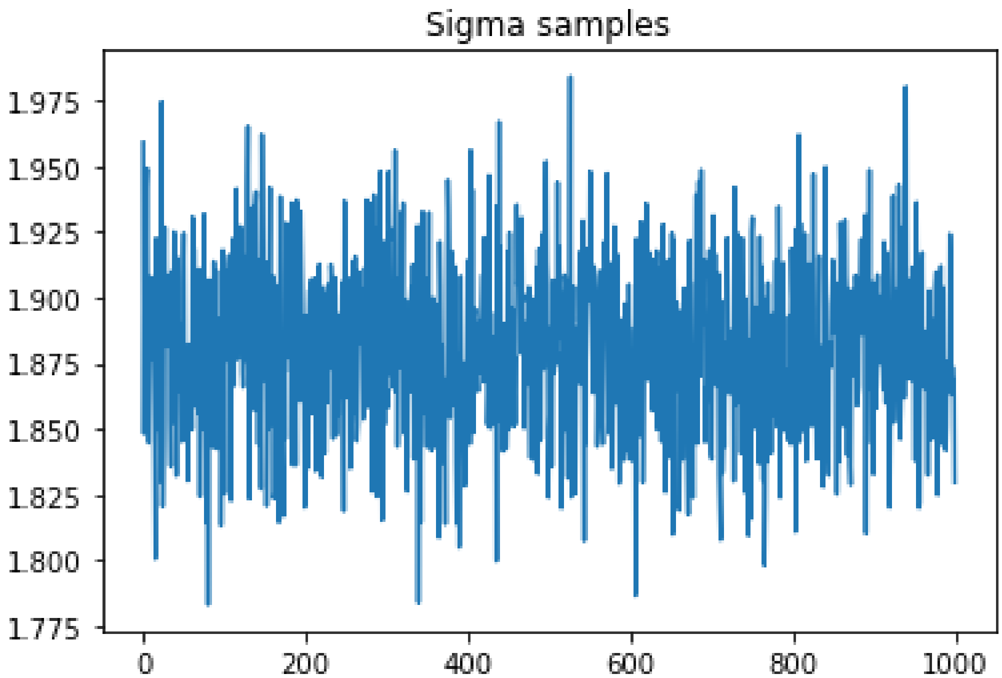

[60]:

```python
steps = 1000
chains = 4
n = len(logy)

chain_collection = []
for i in range(chains):
    mu_collection = []
    sigma_collection = []
    for i in range(steps):

        # update mu
        epsilon = n / sigma_squa
        w = (epsilon) / (epsilon + 1 / tau0_squa)
        mu_n = w * np.mean(logy) + (1 - w) * mu0
        tau_n_squa = 1 / (epsilon + 1 / tau0_squa)
        mu = np.random.normal(mu_n, np.sqrt(tau_n_squa))

        # update sigma
        vn = v0 + n
        sigma_squa_scale = (v0 * sigma0_squa + np.sum((logy - mu)**2)) / vn
```

```
        sigma_squa = sigma_squa_scale * vn / np.random.chisquare(vn, size=1)

        mu_collection.append(mu)
        sigma_collection.append(sigma_squa)

    mu_collection = np.array(mu_collection)
    sigma_collection = np.array(sigma_collection)
    theta_collection = np.concatenate([mu_collection, sigma_collection], axis=1)
    chain_collection.append(theta_collection)
chain_collection = np.array(chain_collection)
```

[61]:
```
plt.figure()
plt.plot(mu_collection)
plt.title('Mu samples')
plt.show()

plt.figure()
plt.plot(sigma_collection)
plt.title('Sigma samples')
plt.show()
```






Our Ineffeciency Factor fuction was modified from Pymc's official code of ESS(Effective sample size), the official code is here

[62]:
```
def ineffeciency_factor(x):
    """ Returns estimate of the effective sample size of a set of traces.
    Parameters
    ----------
    x : array-like
      An array containing the 2 or more traces of a stochastic parameter. That␣
↪is, an array of dimension m x n x k, where m is the number of traces, n the␣
↪number of samples, and k the dimension of the stochastic.

    Returns
    -------
    n_eff : float
      Return the effective sample size, :math:`\hat{n}_{eff}`
    Notes
    -----
    The diagnostic is computed by:
      .. math:: \hat{n}_{eff} = \frac{mn}{1 + 2 \sum_{t=1}^T \hat{\rho}_t}
    where :math:`\hat{\rho}_t` is the estimated autocorrelation at lag t, and T
    is the first odd positive integer for which the sum :math:`\hat{\rho}_{T+1}␣
↪+ \hat{\rho}_{T+1}`
    is negative.
    References
```

```python
    ----------
    Gelman et al. (2014)"""

    if np.shape(x) < (2,):
        raise ValueError(
            'Calculation of effective sample size requires multiple chains of␣
↪the same length.')

    try:
        m, n = np.shape(x)
    except ValueError:
        return [effective_n(np.transpose(y)) for y in np.transpose(x)]

    s2 = gelman_rubin(x, return_var=True)

    negative_autocorr = False
    t = 1

    variogram = lambda t: (sum(sum((x[j][i] - x[j][i-t])**2 for i in␣
↪range(t,n)) for j in range(m))
                                / (m*(n - t)))
    rho = np.ones(n)
    # Iterate until the sum of consecutive estimates of autocorrelation is␣
↪negative
    while not negative_autocorr and (t < n):

        rho[t] = 1. - variogram(t)/(2.*s2)

        if not t % 2:
            negative_autocorr = sum(rho[t-1:t+1]) < 0

        t += 1

    return 1 + 2*rho[1:t].sum()



def gelman_rubin(x, return_var=False):
    """ Returns estimate of R for a set of traces.
    The Gelman-Rubin diagnostic tests for lack of convergence by comparing
    the variance between multiple chains to the variance within each chain.
    If convergence has been achieved, the between-chain and within-chain
    variances should be identical. To be most effective in detecting evidence
    for nonconvergence, each chain should have been initialized to starting
    values that are dispersed relative to the target distribution.
    Parameters
    ----------
```

```
    x : array-like
      An array containing the 2 or more traces of a stochastic parameter. That␣
↪is, an array of dimension m x n x k, where m is the number of traces, n the␣
↪number of samples, and k the dimension of the stochastic.

    return_var : bool
      Flag for returning the marginal posterior variance instead of R-hat␣
↪(defaults of False).
    Returns
    -------
    Rhat : float
      Return the potential scale reduction factor, :math:`\hat{R}`
    Notes
    -----
    The diagnostic is computed by:
      .. math:: \hat{R} = \sqrt{\frac{\hat{V}}{W}}
    where :math:`W` is the within-chain variance and :math:`\hat{V}` is
    the posterior variance estimate for the pooled traces. This is the
    potential scale reduction factor, which converges to unity when each
    of the traces is a sample from the target posterior. Values greater
    than one indicate that one or more chains have not yet converged.
    References
    ----------
    Brooks and Gelman (1998)
    Gelman and Rubin (1992)"""

    if np.shape(x) < (2,):
        raise ValueError(
           'Gelman-Rubin diagnostic requires multiple chains of the same length.
↪')

    try:
        m, n = np.shape(x)
    except ValueError:
        return [gelman_rubin(np.transpose(y)) for y in np.transpose(x)]

    # Calculate between-chain variance
    B_over_n = np.sum((np.mean(x, 1) - np.mean(x)) ** 2) / (m - 1)

    # Calculate within-chain variances
    W = np.sum(
        [(x[i] - xbar) ** 2 for i,
         xbar in enumerate(np.mean(x,
                                   1))]) / (m * (n - 1))

    # (over) estimate of variance
    s2 = W * (n - 1) / n + B_over_n
```

```
    if return_var:
        return s2

    # Pooled posterior variance estimate
    V = s2 + B_over_n / m

    # Calculate PSRF
    R = V / W

    return np.sqrt(R)
```

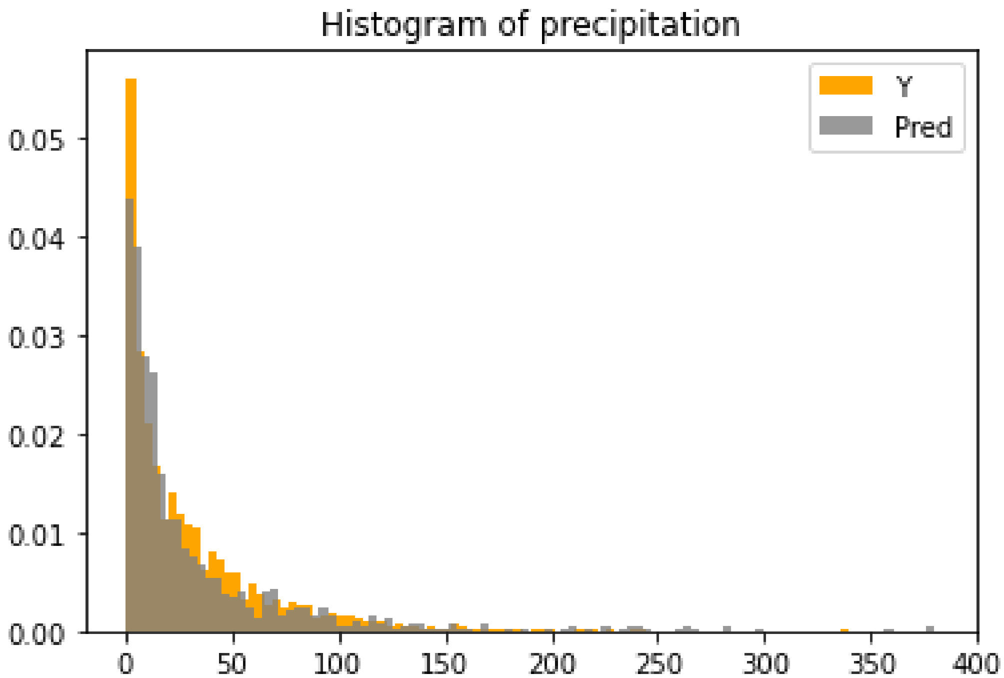
[63]:
```
ineffeciency_factor(chain_collection)
```

[63]: [0.9720755113768855, 0.9479616113805689]

IF-values near 1 therefore suggest this is a very effcient sampler.

#### 1.1.2 b)

[64]:
```
predict = np.random.normal(mu_collection, np.sqrt(sigma_collection))
predict = np.exp(predict)

plt.figure()
plt.hist(y[y<400], bins=100, density=True, color='orange', label='Y')
plt.hist(predict[predict<400], bins=100, density=True, color='gray', ␣
 ↪label='Pred', alpha=0.8)
plt.title('Histogram of precipitation')
plt.legend()
plt.show()
```




Answer: the prediction results matched original data very well except the region close to 0, where original data more dense than predicted results.

### 1.2 Q2

#### 1.2.1 a)

[65]:
```
with open('eBayNumberOfBidderData.dat') as f:
    doc = f.readlines()
    doc = doc[1:]
    for i in range(len(doc)):
        doc[i] = np.array(doc[i].split()).astype(np.float)

doc = np.array(doc)
Y = doc[:, :1]
X = doc[:, 1:]
```

The likelihood of poisson regression

$$lik = \prod_{i=1}^{n} \frac{e^{y_i \beta^T x_i - e^{\beta^T x_i}}}{y_i!}$$

Then minus log likelihood:

$$-loglik = -\sum_{i=1}^{n} y_i\beta^T x_i - e^{\beta^T x_i} - log(y_i!) = -Y^T X\beta + \sum e^{X\beta}$$

Note that $-log(y_i!)$ has nothing to do with $\beta$, thus eliminated.

$$\frac{\partial(-loglik)}{\partial\beta} = -X^T Y + X^T e^{X\beta}$$

[66]:
```
# minus log likelihood
def poisson_lik(X, Y, beta):
    minusloglik = - Y.T @ X @ beta + np.sum(np.exp(X @ beta))
    return minusloglik

# gradiant of minus log likelihood
def grad_loglikli(X, Y, beta):
    grad_loglikli = - X.T @ Y + X.T @ np.exp(X @ beta)
    return grad_loglikli

# numeric optimization
def update_beta(betas, lr, grad, hessian=None):
    # Newton method
    if hessian:
        betas = betas -  lr * np.linalg.inv(hessian) @ grad
    # Gradiant descent
    else:
        betas = betas -  lr * grad
    return betas
```

[67]:
```
betas = np.ones([X.shape[1], 1])
lr = 1e-4
iterations = 1000

for i in range(iterations):
    minuslog_like = poisson_lik(X, Y, betas)
    grad = grad_loglikli(X, Y, betas)
    # hess = hessian(betas, sigma, X)
    betas = update_beta(betas, lr, grad)
print(betas)
```

```
[[ 1.07244139]
 [-0.02054088]
 [-0.3945106 ]
 [ 0.44384269]
 [-0.05219768]
 [-0.22086194]
 [ 0.07067357]
```

```
 [-0.12067802]
 [-1.89409689]]
```

#### 1.2.2 b)

Minus log prior, first and second order derivatives:

$$-logp(\beta) = \frac{1}{2}(\beta - \mu)^T \Sigma^{-1} (\beta - \mu)$$

$$\frac{\partial(-logp(\beta))}{\partial \beta} = \Sigma^{-1}(\beta - \mu)$$

$$\frac{\partial^2(-logp(\beta))}{\partial \beta \partial \beta^T} = \Sigma^{-1}$$

Where $\mu = 0$ and $\Sigma = 100(X^T X)^{-1}$, constant of $-logp(\beta)$ has been eliminated.

Minus log likelihood(copied from section a)), first and second order derivatives:

$$-loglik = -Y^T X\beta + \sum e^{X\beta}$$

$$\frac{\partial(-loglik)}{\partial \beta} = -X^T Y + X^T e^{X\beta}$$

$$\frac{\partial^2(-loglik)}{\partial \beta \partial \beta^T} = X^T (e^{X\beta} .* X)$$

Where .∗ is element wise product, therefore, over all posterior, Jacobian and Hessian:

$$-logp(\beta|X, Y) = \frac{1}{2}(\beta - \mu)^T \Sigma^{-1}(\beta - \mu) - Y^T X\beta + \sum e^{X\beta}$$

$$J = \Sigma^{-1}(\beta - \mu) - X^T Y + X^T e^{X\beta}$$

$$H = \Sigma^{-1} + X^T (e^{X\beta} .* X)$$

[68]:
```
# minus log posterior
def logpoisson_posterior(X, Y, beta, sigma, mu):
    minusloglik = - Y.T @ X @ beta + np.sum(np.exp(X @ beta))
    minprior = 1/2 * (beta - mu).T @ np.linalg.inv(sigma) @ (beta - mu)
    return minusloglik + minprior

# gradiant of minus log posterior
def grad_posterior(X, Y, beta, sigma, mu):
```

```
    grad_loglikli = - X.T @ Y + X.T @ np.exp(X @ beta)
    grad_prior = np.linalg.inv(sigma) @ (beta - mu)
    return grad_loglikli + grad_prior

# hessian of minus log posterior
def hessian_posterior(X, beta, sigma):
    H = np.linalg.inv(sigma) + X.T @ (np.exp(X @ beta) * X)
    return H
```

[69]:
```
betas = np.ones([X.shape[1], 1])
mu = np.zeros(betas.shape)
sigma = 100 * np.linalg.inv(X.T @ X)
lr = 1e-4
iterations = 1000

for i in range(iterations):
    posterior = logpoisson_posterior(X, Y, betas, sigma, mu)
    grad = grad_posterior(X, Y, betas, sigma, mu)
    hess = hessian_posterior(X, betas, sigma,)
    betas = update_beta(betas, lr, grad)
print(betas)
```

```
[[ 1.06984173]
 [-0.02051352]
 [-0.39300269]
 [ 0.44355685]
 [-0.05246213]
 [-0.2212297 ]
 [ 0.07070286]
 [-0.1202211 ]
 [-1.89198651]]
```

[70]:
```
# Std
invhess = np.linalg.inv(hess)
np.sqrt(np.diag(invhess))
```

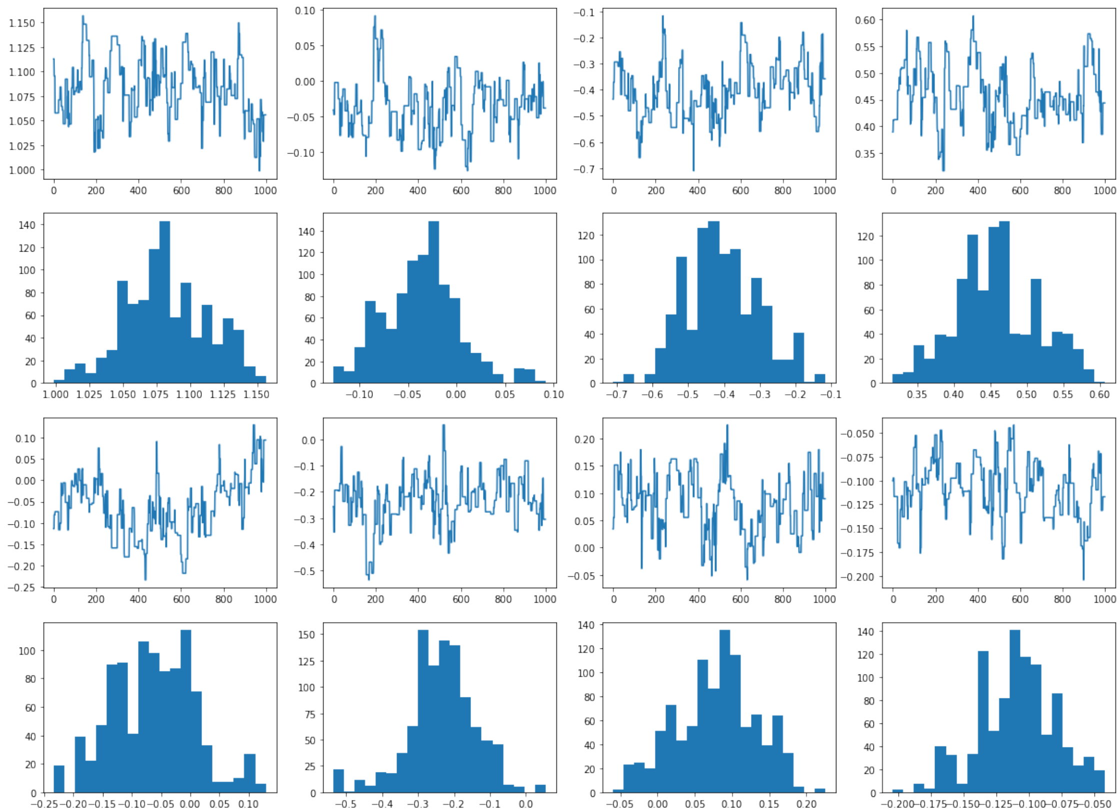
[70]:
```
array([0.03074837, 0.03678417, 0.09227861, 0.05057447, 0.06020457,
       0.09146036, 0.05634756, 0.02895636, 0.07109679])
```

### 1.2.3 c)

[72]:
```
c = 1
sigma_RWM = invhess
# if using original MH rather than random walk
MH = False
#betas = np.ones([X.shape[1], 1])
sample_num = 1000
```

```
betas_collection = []
for i in range(sample_num):
    # propose new betas
    betas_p = np.random.multivariate_normal(betas.reshape(-1), c * sigma_RWM).
↪reshape(-1, 1)
    u = np.random.uniform()

    # log posteriors
    post_proposal = logpoisson_posterior(X, Y, betas_p, sigma, mu)
    post_before = logpoisson_posterior(X, Y, betas, sigma, mu)

    # our posterior is already in minus-log scale
    accept_bound = np.exp(post_before - post_proposal)

    if MH:
        back_p = multivariate_normal.pdf(betas.reshape(-1), mean=betas_p.
↪reshape(-1), cov=c * sigma_RWM)
        trans_p = multivariate_normal.pdf(betas_p.reshape(-1), mean=betas.
↪reshape(-1), cov=c * sigma_RWM)
        accept_bound = accept_bound / trans_p * back_p

    alpha = np.min([1, accept_bound])

    # check the acceptance rate
    if u < alpha:
        betas = betas_p
    betas_collection.append(betas.reshape(-1))

betas_collection = np.array(betas_collection)
```

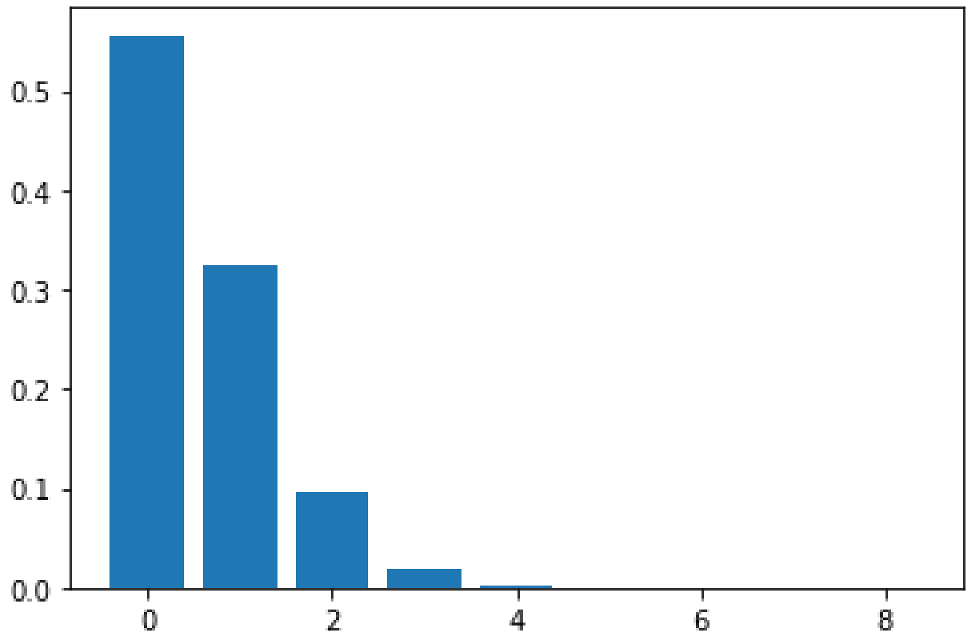
[73]:
```
fig, axs = plt.subplots(4, 4,figsize=(20,15))

for i in range(4):
    axs[0, i].plot(betas_collection[:, i])
    axs[1, i].hist(betas_collection[:, i], bins=20)
    axs[2, i].plot(betas_collection[:, i + 4])
    axs[3, i].hist(betas_collection[:, i + 4], bins=20)
plt.show()
```



### 1.2.4 d)

[74]:
```
auction = np.array([1, 1, 1, 1, 0, 1, 0, 1, 0.7]).reshape(-1, 1)

def possion_reg(x, y, beta):
    prob_y = np.exp(y * beta @ x - np.exp(beta @ x)) / math.factorial(y)
    return np.mean(prob_y)

prob_0 = possion_reg(auction, 0, betas_collection)
print('No bidder :{}'.format(prob_0))


heights = []
for i in range(9):
    height = possion_reg(auction, i, betas_collection)
    heights.append(height)

plt.figure()
plt.bar(x=np.arange(9), height=heights)
plt.show()
```

```
No bidder :0.5560870690836389
```

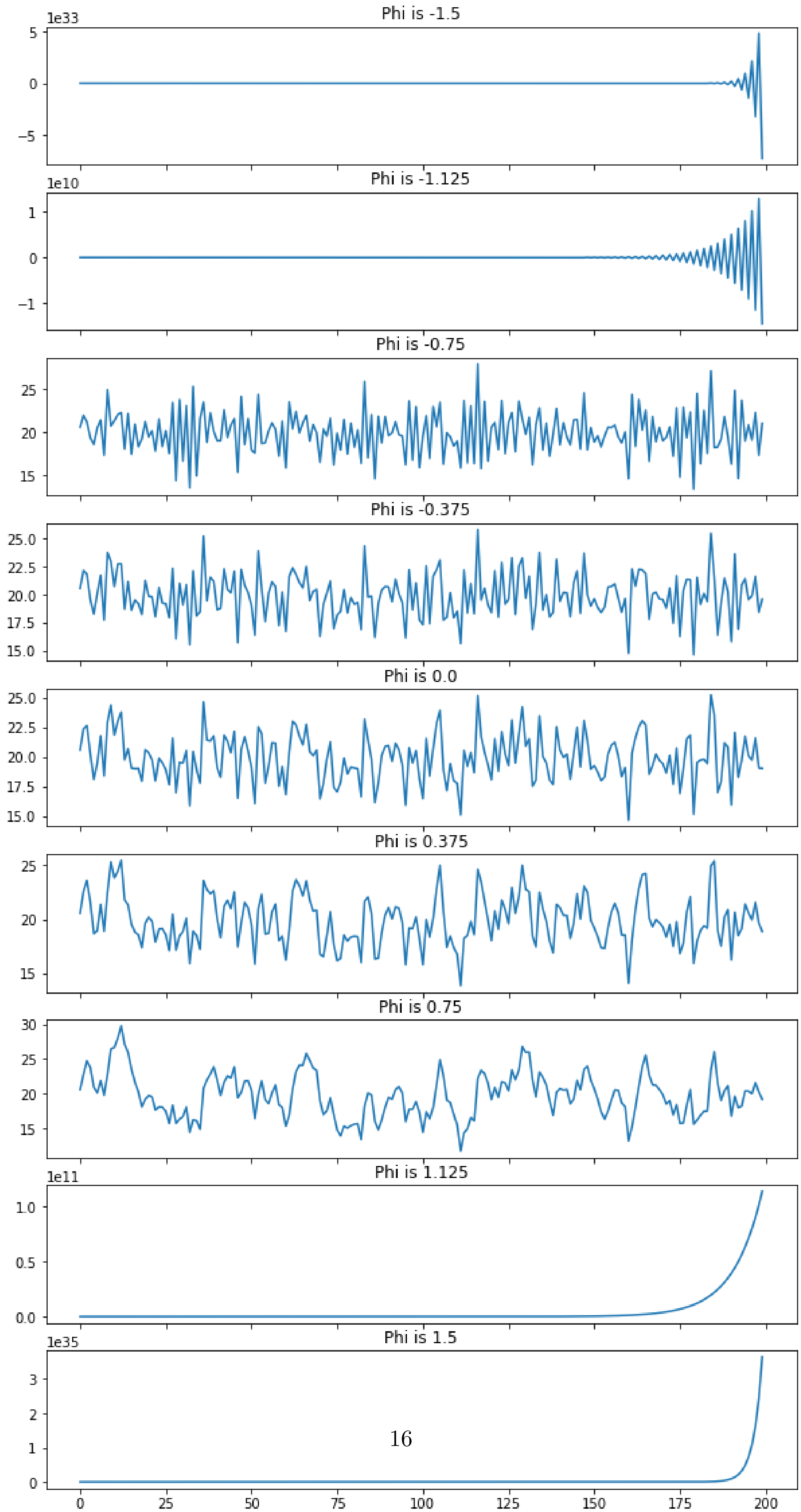



## 2 Q3

#### 2.0.1 a)

[75]:
```
def get_autoreg(x, mu, sigma, phi, T):
    xs = []
    for i in range(T):
        x = mu + phi * (x - mu) + np.random.normal(0, np.sqrt(sigma))
        xs.append(x)

    return np.array(xs)

mu = 20
sigma_2 = 4
T = 200
x0 = mu
phi = np.linspace(-1.5, 1.5, 9)

xs = get_autoreg(x0, mu, sigma_2, phi, T)

fig, axs = plt.subplots(9,figsize=(10,20))
for i in range(9):
    axs[i].plot(xs[:, i])
    axs[i].set_title('Phi is {}'.format(phi[i]))
    axs[i].label_outer()
```

```
plt.show()
```


Phi is -1.5
1e33
Phi is -1.125
1e10
Phi is -0.75
Phi is -0.375
Phi is 0.0
Phi is 0.375
Phi is 0.75
Phi is 1.125
1e11
Phi is 1.5
1e35

AR(1) can generate higher frequency signal when Phi decreases between (-1, 1). When phi is outside of (-1, 1), the process becomes unstable.

#### 2.0.2 b)

**i**

[76]:
```
AR_1 = """
data {
  int<lower=0> N;
  vector[N] y;
}
parameters {
  real mu;
  real phi;
  real<lower=0> sigma;
}

model {
  mu ~ normal(0,100);
  phi ~ normal(0,4);
  sigma ~ scaled_inv_chi_square(1,2);

  for (n in 2:N) {
    y[n] ~ normal(mu + phi * (y[n-1] - mu), sqrt(sigma));
  }
}
"""
phi_x = 0.3
phi_y = 0.9

data_x = {"y": get_autoreg(x0, mu, sigma_2, phi_x, T), "N": T}
data_y = {"y": get_autoreg(x0, mu, sigma_2, phi_y, T), "N": T}
init = {"mu": 0, "phi": 0, "sigma": 100}


posterior = stan.build(AR_1, data=data_x)
fit = posterior.sample(num_chains=1, num_samples=1000, init=[init])
df_x = fit.to_frame()

posterior = stan.build(AR_1, data=data_y)
fit = posterior.sample(num_chains=1, num_samples=1000)
df_y = fit.to_frame()
```

```
Building…
```

```
Building: found in cache, done.Messages from stanc:
Warning at '/var/folders/03/_k7872h17rvg940l_19p5sf40000gp/T/httpstan_bli7ltg0/m
odel_wkpqdsfb.stan', line 13, column 16 to column 19:
  Argument 100 suggests there may be parameters that are not unit scale;
  consider rescaling with a multiplier (see manual section 22.12).
Sampling:   0%
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
```

```
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:  10% (200/2000)
Sampling:  10% (200/2000)
Sampling:  10% (200/2000)
Sampling:  10% (200/2000)
Sampling:  15% (300/2000)
```

```
Sampling:  20% (400/2000)
Sampling:  25% (500/2000)
Sampling:  30% (600/2000)
Sampling:  35% (700/2000)
Sampling:  40% (800/2000)
Sampling:  45% (900/2000)
Sampling: 100% (2000/2000)
Sampling: 100% (2000/2000)
Sampling: 100% (2000/2000), done.
Messages received during sampling:
  Gradient evaluation took 8.2e-05 seconds
  1000 transitions using 10 leapfrog steps per transition would take 0.82
seconds.
  Adjust your expectations accordingly!
  Informational Message: The current Metropolis proposal is about to be rejected
because of the following issue:
  Exception: normal_lpdf: Scale parameter is 0, but must be positive! (in '/var/
folders/03/_k7872h17rvg940l_19p5sf40000gp/T/httpstan_xujku4h4/model_wkpqdsfb.sta
n', line 18, column 4 to column 57)
  If this warning occurs sporadically, such as for highly constrained variable
types like covariance matrices, then the sampler is fine,
  but if this warning occurs often then your model may be either severely ill-
conditioned or misspecified.

Building…


Building: found in cache, done.Messages from stanc:
Warning at '/var/folders/03/_k7872h17rvg940l_19p5sf40000gp/T/httpstan_bli7ltg0/m
odel_wkpqdsfb.stan', line 13, column 16 to column 19:
  Argument 100 suggests there may be parameters that are not unit scale;
  consider rescaling with a multiplier (see manual section 22.12).
Sampling:   0%
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
```

```
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   0% (1/2000)
Sampling:   5% (100/2000)
Sampling:   5% (100/2000)
Sampling:  10% (200/2000)
Sampling:  10% (200/2000)
Sampling:  15% (300/2000)
Sampling:  15% (300/2000)
Sampling:  20% (400/2000)
Sampling:  20% (400/2000)
Sampling:  25% (500/2000)
Sampling:  25% (500/2000)
Sampling:  30% (600/2000)
Sampling:  30% (600/2000)
Sampling:  35% (700/2000)
Sampling:  40% (800/2000)
Sampling:  45% (900/2000)
Sampling:  45% (900/2000)
Sampling: 100% (2000/2000)
Sampling: 100% (2000/2000)
Sampling: 100% (2000/2000), done.
Messages received during sampling:
  Gradient evaluation took 7.2e-05 seconds
  1000 transitions using 10 leapfrog steps per transition would take 0.72
seconds.
  Adjust your expectations accordingly!
```

[77]:
```python
def get_ci(df):
    eti_low = np.percentile(df, 2.5)
    eti_hight = np.percentile(df, 97.5)
    return [round(eti_low, 4), round(eti_hight, 4)]

def get_stats(df):

    ci_mu = get_ci(df['mu'])
    ci_phi = get_ci(df['phi'])
```

```
    ci_sigma = get_ci(df['sigma'])
    mean_mu = np.mean(df['mu'])
    mean_phi = np.mean(df['phi'])
    mean_sigma = np.mean(df['sigma'])
    d = {"mu":[ci_mu, mean_mu], "phi":[ci_phi, mean_phi], "sigma":[ci_sigma,␣
↪mean_sigma]}
    stats = pd.DataFrame(data=d, index=['95 % CI', 'mean'])

    return stats
```

[78]:
```
df_x.describe()
```

[78]:
```
parameters          lp__  accept_stat__    stepsize__  treedepth__  \
count        1000.000000    1000.000000  1.000000e+03  1000.000000
mean         -228.714831       0.926683  7.104316e-01     2.397000
std             1.330734       0.092019  1.121886e-14     0.554706
min          -237.036540       0.387651  7.104316e-01     1.000000
25%          -229.346417       0.896547  7.104316e-01     2.000000
50%          -228.383700       0.960157  7.104316e-01     2.000000
75%          -227.756611       0.994726  7.104316e-01     3.000000
max          -227.122215       1.000000  7.104316e-01     3.000000

parameters   n_leapfrog__  divergent__     energy__           mu          phi  \
count         1000.000000       1000.0  1000.000000  1000.000000  1000.000000
mean             4.998000          0.0   230.235678    19.689371     0.289405
std              2.035716          0.0     1.853588     0.205268     0.072385
min              1.000000          0.0   227.335711    18.952219     0.060243
25%              3.000000          0.0   228.869221    19.563134     0.241992
50%              7.000000          0.0   229.913038    19.684171     0.289717
75%              7.000000          0.0   231.181507    19.834775     0.335038
max              7.000000          0.0   239.393563    20.291169     0.524953

parameters         sigma
count        1000.000000
mean            3.642192
std             0.365328
min             2.619550
25%             3.376488
50%             3.615605
75%             3.882798
max             5.203352
```

[79]:
```
get_stats(df_x)
```

[79]:
```
                      mu               phi             sigma
95 % CI  [19.2678, 20.089]  [0.1445, 0.4275]  [3.0309, 4.4472]
mean               19.6894          0.289405           3.64219
```

[80]:
```
df_y.describe()
```

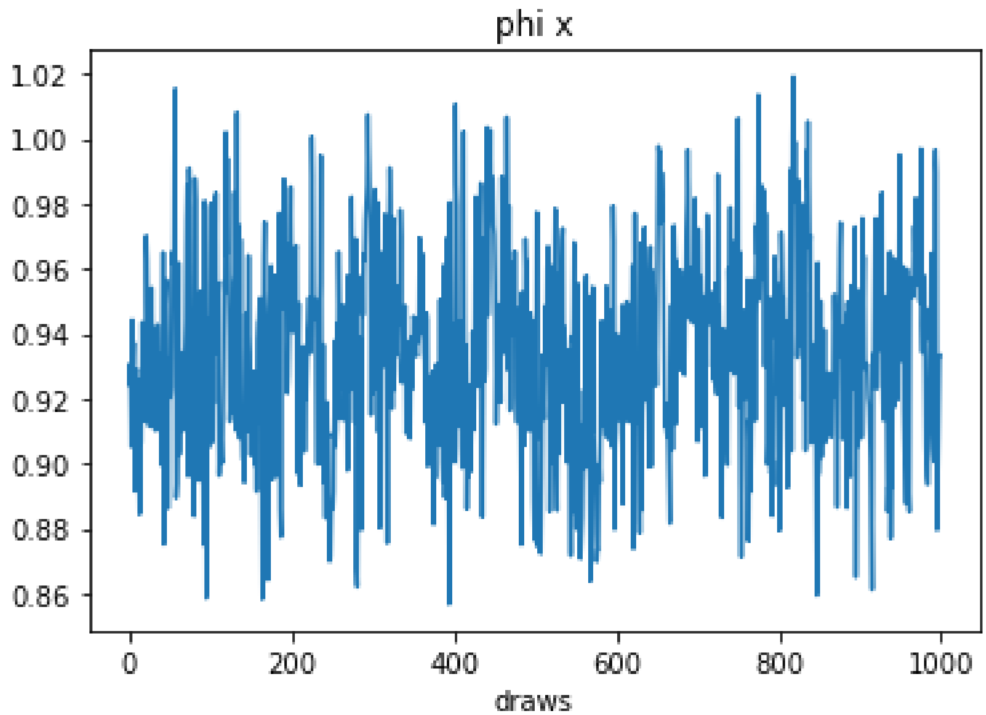
[80]:
```
parameters          lp__  accept_stat__     stepsize__  treedepth__  \
count        1000.000000    1000.000000  1.000000e+03  1000.000000
mean         -227.130026       0.905253  4.744445e-01     2.526000
std             1.371009       0.144176  5.553893e-15     0.556447
min          -233.777173       0.012237  4.744445e-01     1.000000
25%          -227.851944       0.886983  4.744445e-01     2.000000
50%          -226.795288       0.955849  4.744445e-01     3.000000
75%          -226.086098       0.989774  4.744445e-01     3.000000
max          -225.390160       1.000000  4.744445e-01     4.000000

parameters  n_leapfrog__  divergent__    energy__           mu          phi  \
count        1000.000000       1000.0  1000.000000  1000.000000  1000.000000
mean            6.172000          0.0   228.656713    19.725970     0.934107
std             2.223367          0.0     1.851862     3.214392     0.030649
min             1.000000          0.0   225.452567     4.348147     0.856732
25%             5.000000          0.0   227.294239    18.194968     0.911710
50%             7.000000          0.0   228.327613    19.643829     0.933419
75%             7.000000          0.0   229.752130    21.102452     0.955362
max            15.000000          0.0   237.681694    37.296016     1.019203

parameters         sigma
count        1000.000000
mean            3.588954
std             0.377928
min             2.536705
25%             3.314962
50%             3.568717
75%             3.832711
max             5.267277
```

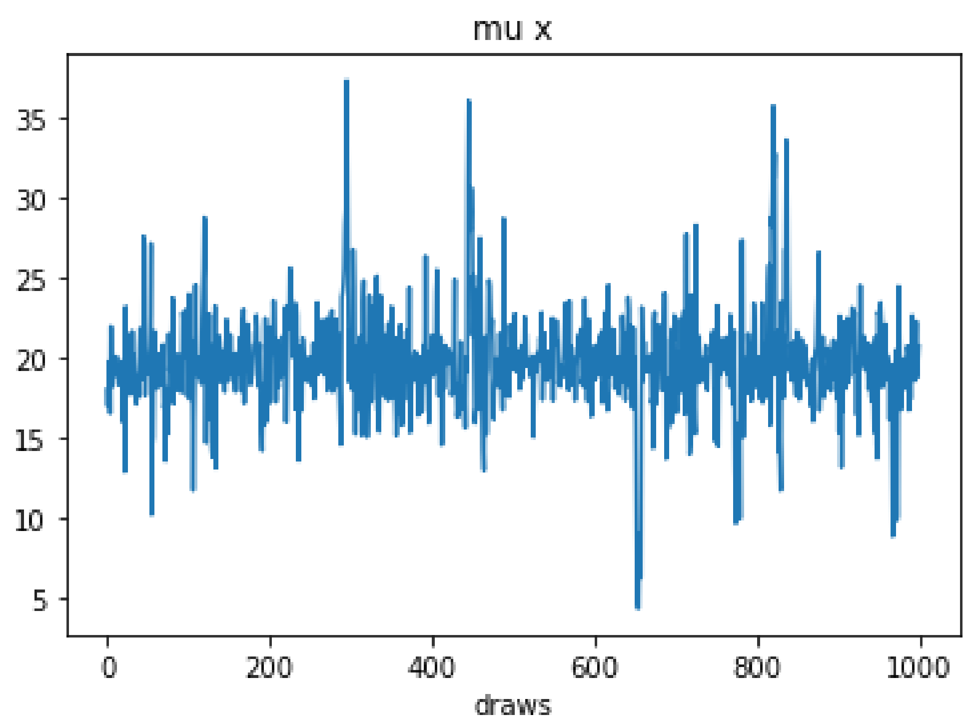
[81]:
```
get_stats(df_y)
```

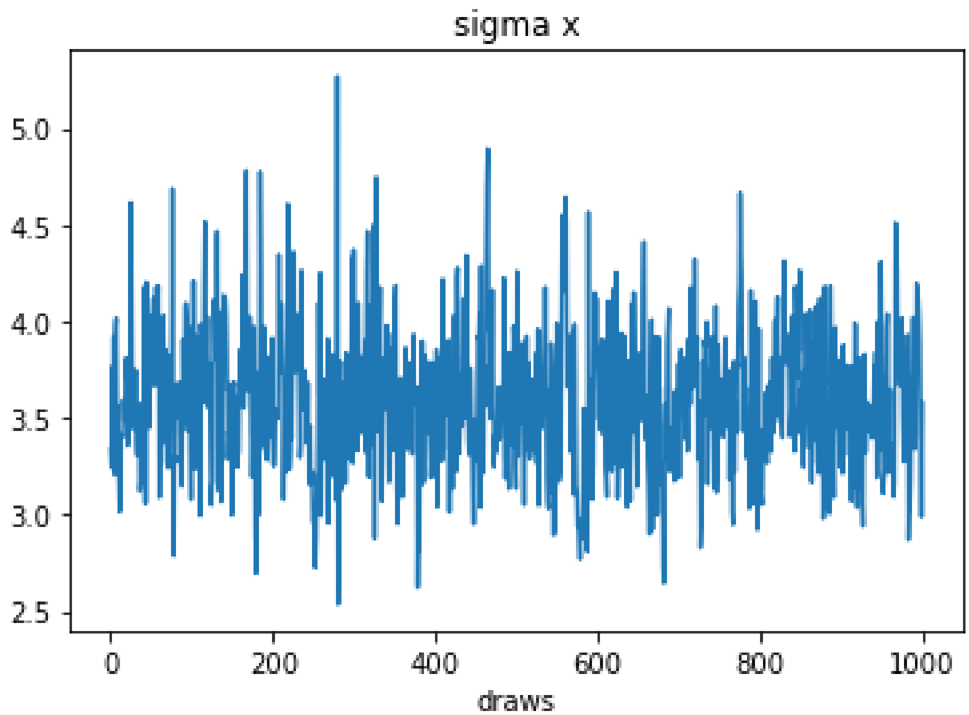
[81]:
```
                             mu               phi             sigma
95 % CI  [13.6912, 27.3167]  [0.8752, 0.9952]  [2.9403, 4.3611]
mean                 19.726          0.934107           3.58895
```

### ii

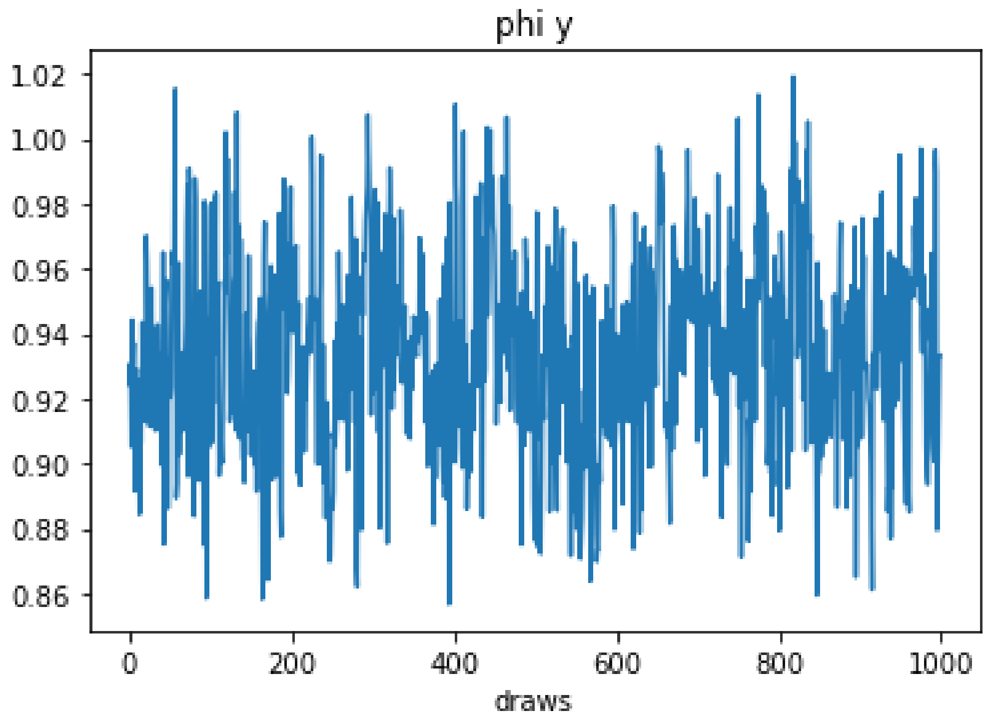
[82]:
```
df_y['phi'].plot(title='phi x')
plt.show()
df_y['mu'].plot(title='mu x')
plt.show()
df_y['sigma'].plot(title='sigma x')
plt.show()
```

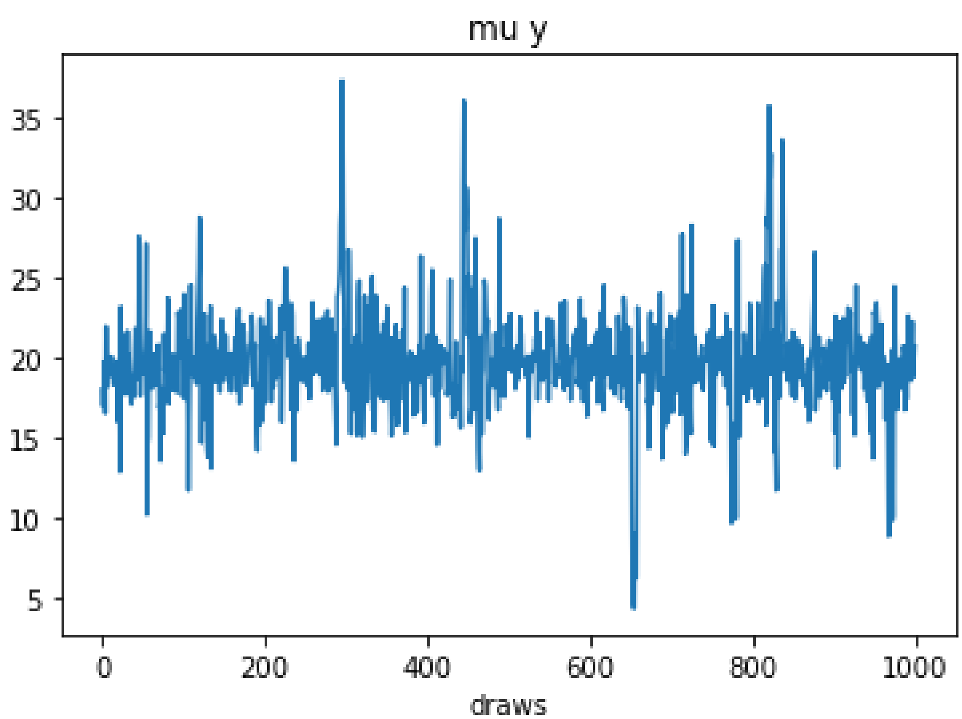

phi x
1.02
1.00
0.98
0.96
0.94
0.92
0.90
0.88
0.86
0
200
400
600
800
1000
draws

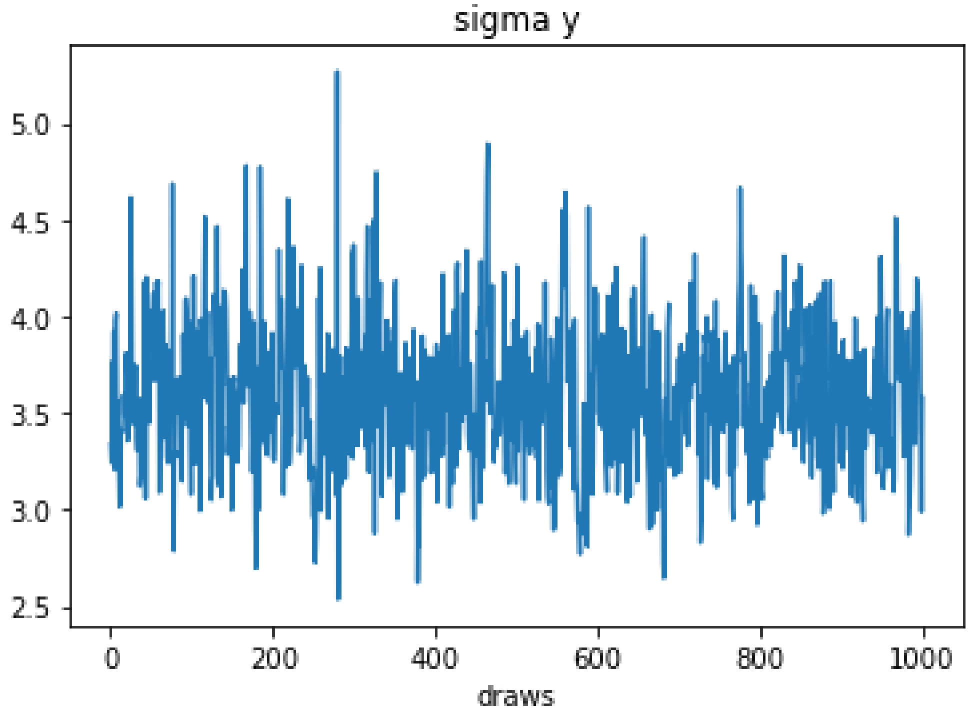

mu x
35
30
25
20
15
10
5
0
200
400
600
800
1000
draws




[83]:
```
df_y['phi'].plot(title='phi y')
plt.show()
df_y['mu'].plot(title='mu y')
plt.show()
df_y['sigma'].plot(title='sigma y')
plt.show()
```

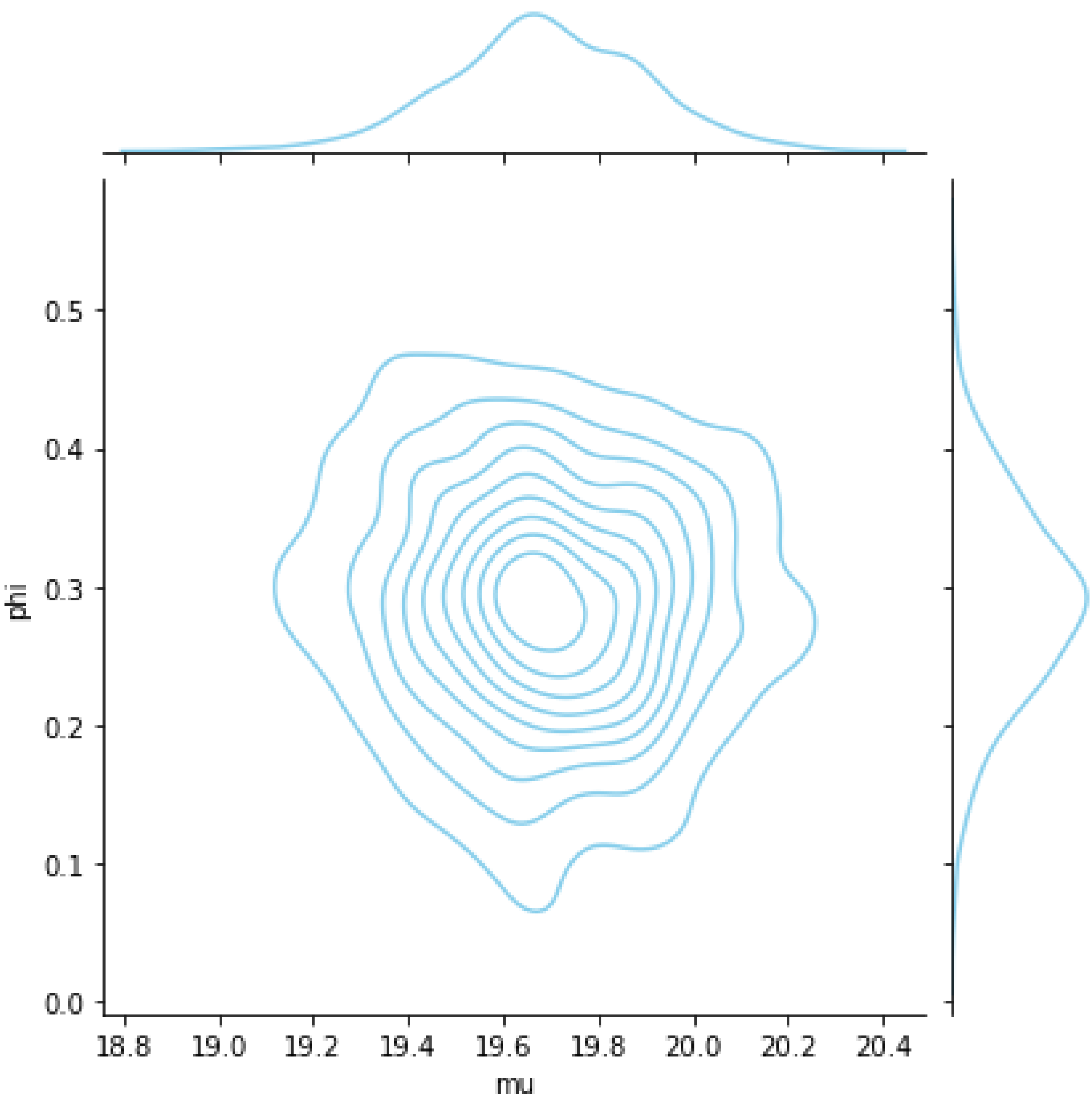

phi y
1.02
1.00
0.98
0.96
0.94
0.92
0.90
0.88
0.86
0
200
400
600
800
1000
draws


mu y
35
30
25
20
15
10
5
0
200
400
600
800
1000
draws



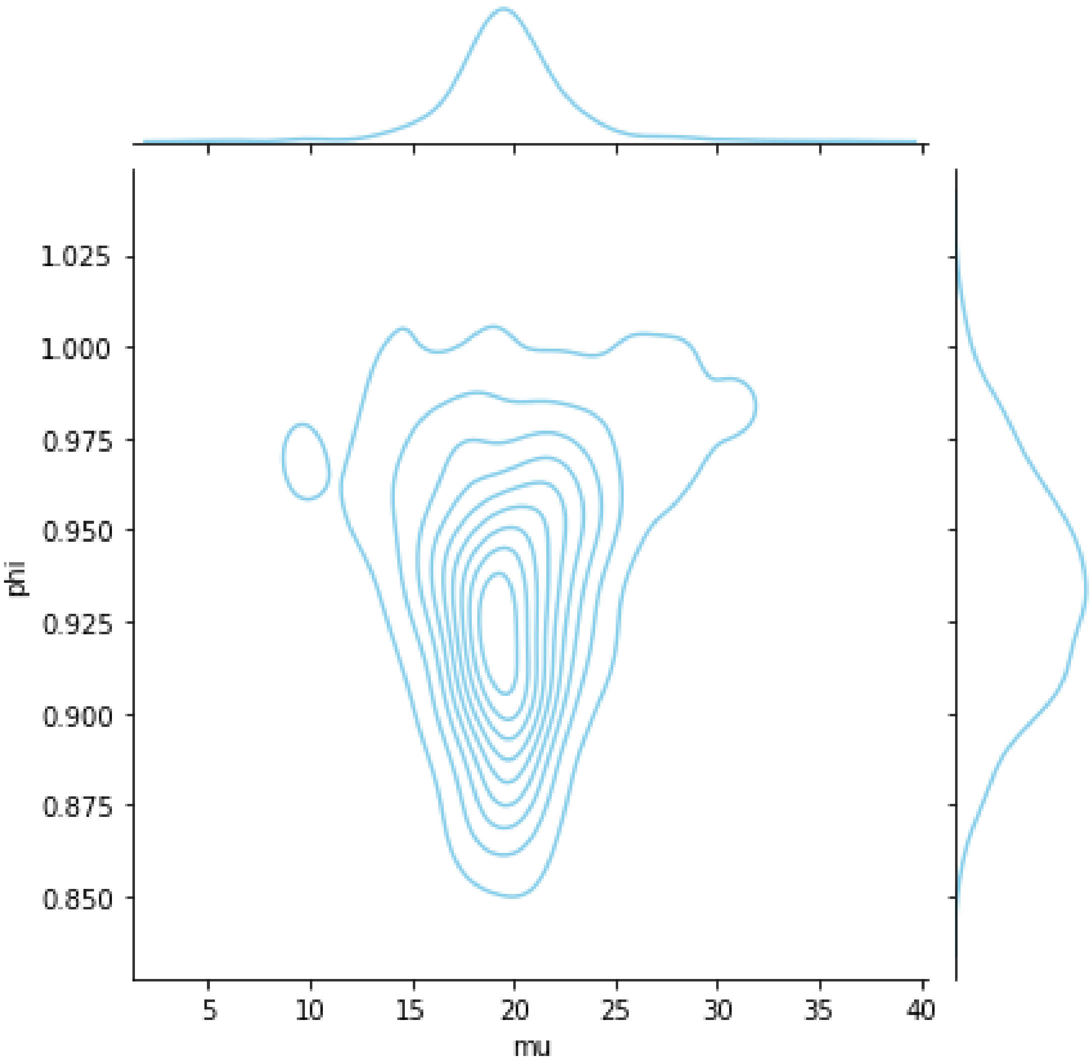

Analytically, joint distribution of $\Phi$ and $\mu$ suppose to be a 2-Dimentional Gaussian distribution, and the sampled joint distributions estimated by kernel density estimation are illustrated below.

[84]:
```
sns.jointplot(x=df_x["mu"], y=df_x["phi"], kind='kde', color="skyblue")
plt.show()
```




[85]:

```
sns.jointplot(x=df_y["mu"], y=df_y["phi"], kind='kde', color="skyblue")
plt.show()
```



1.025
1.000
0.975
0.950
0.925
0.900
0.875
0.850
phi
5
10
15
20
25
30
35
40
mu


```
[ ]:
```