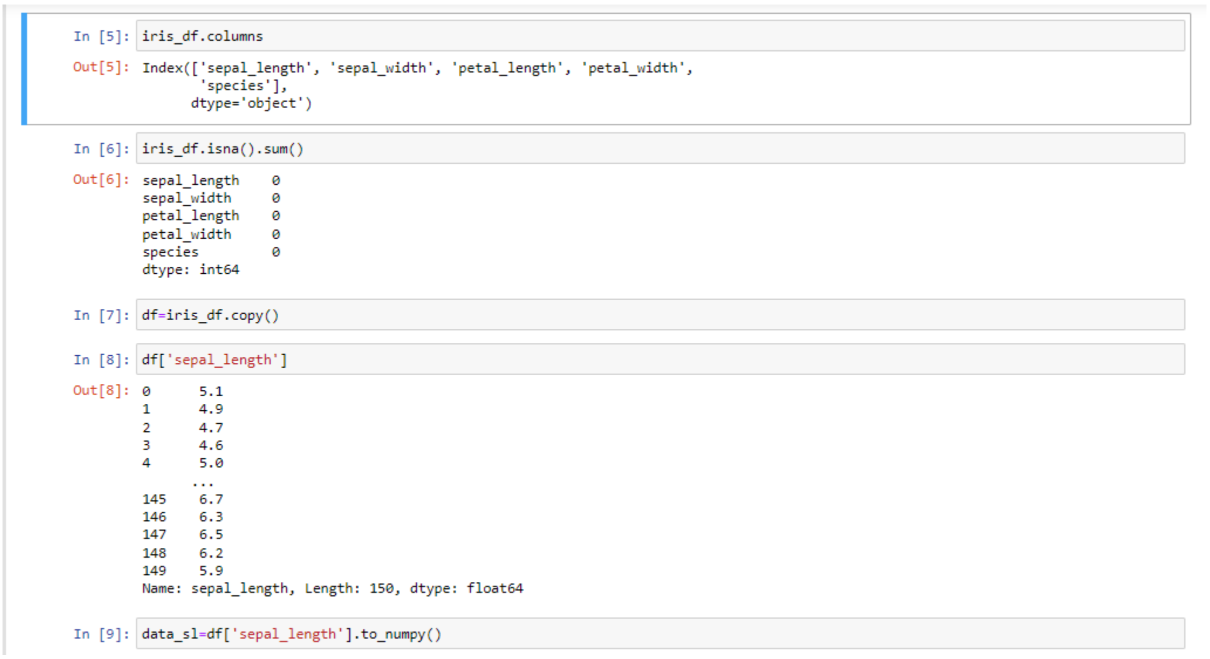
Statistical Modelling Assignment 2

Mahad Ahmed 20i – 0426, Section F

Question 1.

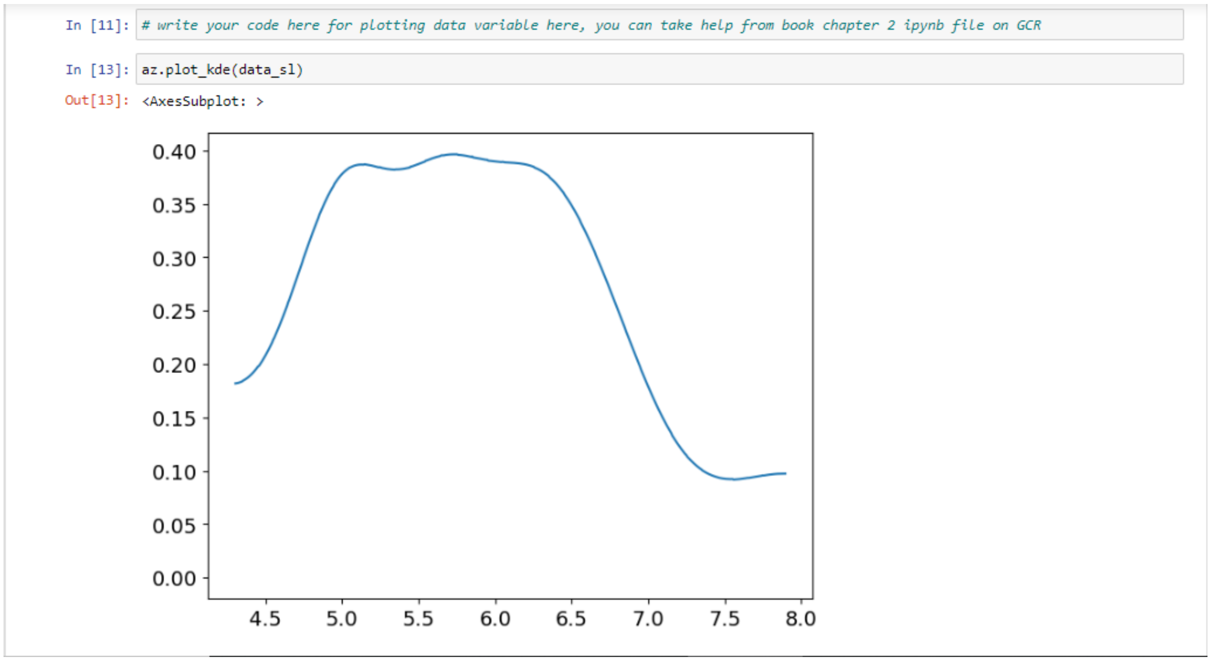
Part A)

Loading the data from the Iris.csv file, getting the sepal width / sepal length columns, converting into a NumPy array.



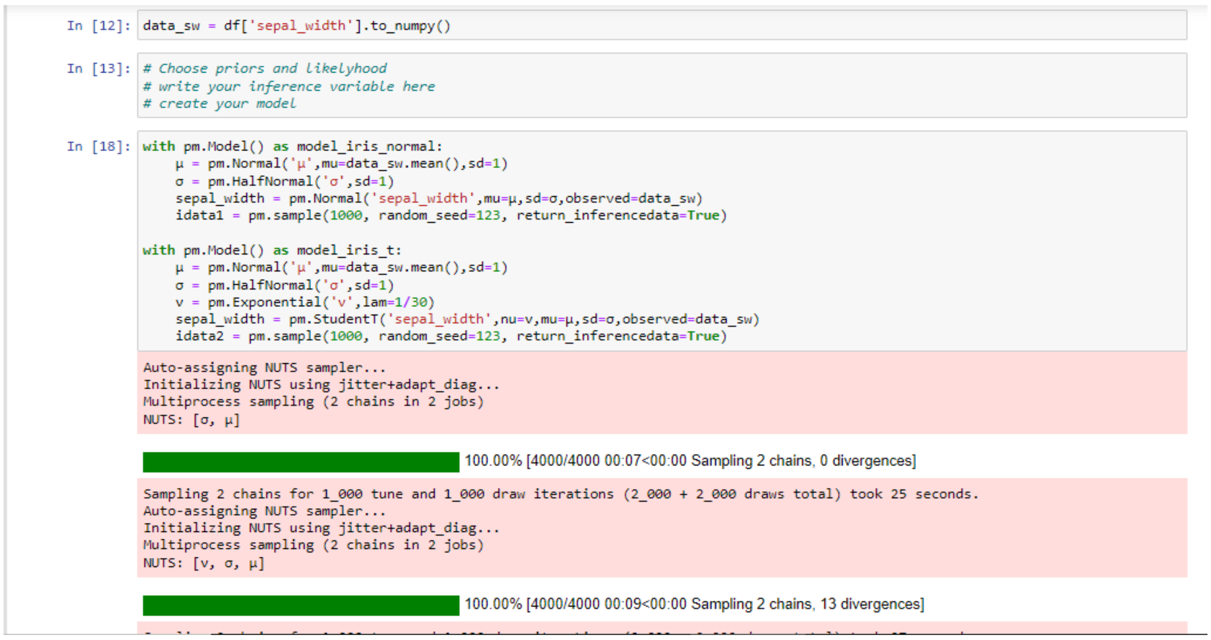
```
In [5]: iris_df.columns

Out[5]: Index(['sepal_length', 'sepal_width', 'petal_length', 'petal_width',
               'species'],
              dtype='object')

In [6]: iris_df.isna().sum()

Out[6]: sepal_length    0
        sepal_width     0
        petal_length    0
        petal_width     0
        species         0
        dtype: int64

In [7]: df=iris_df.copy()

In [8]: df['sepal_length']

Out[8]: 0      5.1
        1      4.9
        2      4.7
        3      4.6
        4      5.0
              ...
        145    6.7
        146    6.3
        147    6.5
        148    6.2
        149    5.9
        Name: sepal_length, Length: 150, dtype: float64

In [9]: data_sl=df['sepal_length'].to_numpy()
```

Plotting the above data on KDE Plot



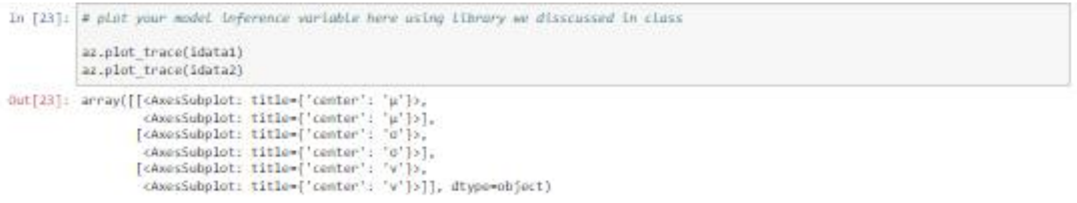
```
In [11]: # write your code here for plotting data variable here, you can take help from book chapter 2 ipynb file on GCR

In [13]: az.plot_kde(data_sl)

Out[13]: <AxesSubplot: >
```

Creating the models for Normal and T distribution (Prior + Likelihood)

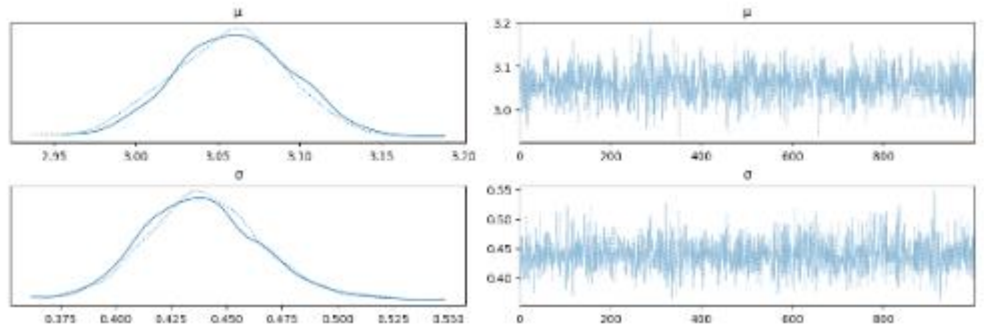


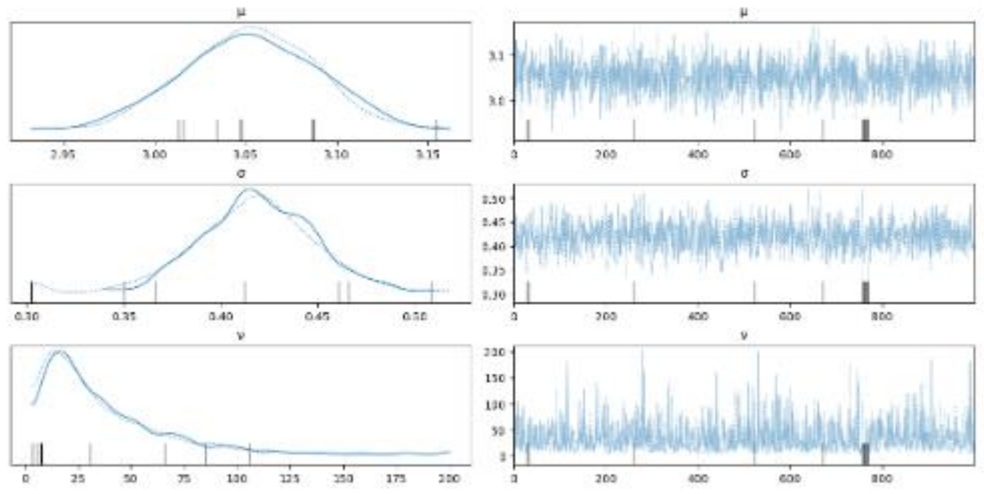
```
In [12]: data_sw = df['sepal_width'].to_numpy()

In [13]: # Choose priors and Likelyhood
         # write your inference variable here
         # create your model

In [18]: with pm.Model() as model_iris_normal:
             μ = pm.Normal('μ',mu=data_sw.mean(),sd=1)
             σ = pm.HalfNormal('σ',sd=1)
             sepal_width = pm.Normal('sepal_width',mu=μ,sd=σ,observed=data_sw)
             idata1 = pm.sample(1000, random_seed=123, return_inferencedata=True)

         with pm.Model() as model_iris_t:
             μ = pm.Normal('μ',mu=data_sw.mean(),sd=1)
             σ = pm.HalfNormal('σ',sd=1)
             v = pm.Exponential('v',lam=1/30)
             sepal_width = pm.StudentT('sepal_width',nu=v,mu=μ,sd=σ,observed=data_sw)
             idata2 = pm.sample(1000, random_seed=123, return_inferencedata=True)

         Auto-assigning NUTS sampler...
         Initializing NUTS using jitter+adapt_diag...
         Multiprocess sampling (2 chains in 2 jobs)
         NUTS: [σ, μ]

         100.00% [4000/4000 00:07<00:00 Sampling 2 chains, 0 divergences]

         Sampling 2 chains for 1_000 tune and 1_000 draw iterations (2_000 + 2_000 draws total) took 25 seconds.
         Auto-assigning NUTS sampler...
         Initializing NUTS using jitter+adapt_diag...
         Multiprocess sampling (2 chains in 2 jobs)
         NUTS: [v, σ, μ]

         100.00% [4000/4000 00:09<00:00 Sampling 2 chains, 13 divergences]
```

Plotting our models



```
In [23]: # plot your model inference variable here using library we disscussed in class

         az.plot_trace(idata1)
         az.plot_trace(idata2)

Out[23]: array([[<AxesSubplot: title={'center': 'μ'}>,
                 <AxesSubplot: title={'center': 'μ'}>],
                [<AxesSubplot: title={'center': 'σ'}>,
                 <AxesSubplot: title={'center': 'σ'}>],
                [<AxesSubplot: title={'center': 'v'}>,
                 <AxesSubplot: title={'center': 'v'}>]], dtype=object)
```





write code here to summarise the results

In [25]:
```
# write code here to summarise the results
```

In [26]:
```
az.summary(idata1)
```

Out[26]:

	mean	sd	hdi_3%	hdi_97%	mcse_mean	mcse_sd	ess_bulk	ess_tail	r_hat
μ	3.058	0.036	2.988	3.119	0.001	0.001	1496.0	1222.0	1.0
σ	0.439	0.026	0.392	0.491	0.001	0.000	1734.0	1236.0	1.0

In [27]:
```
az.summary(idata2)
```

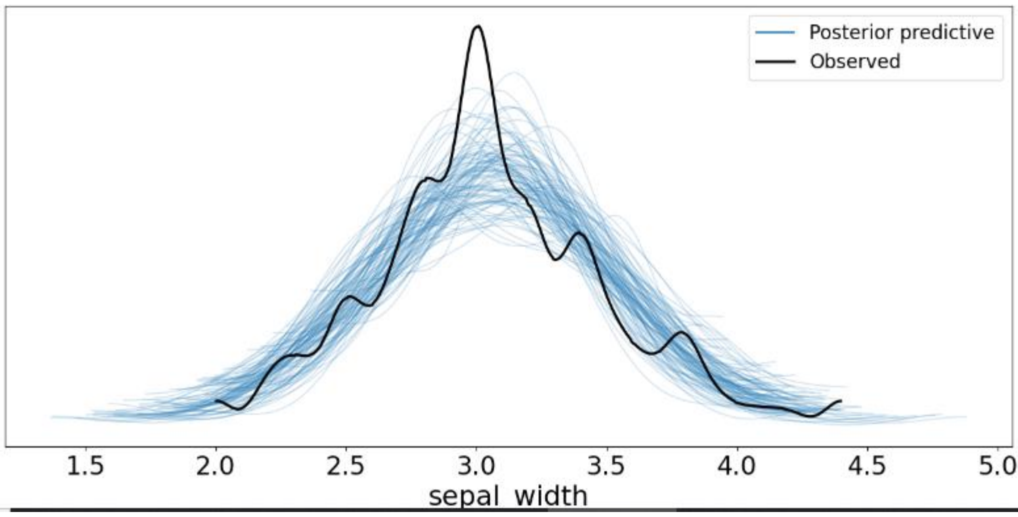
Out[27]:

	mean	sd	hdi_3%	hdi_97%	mcse_mean	mcse_sd	ess_bulk	ess_tail	r_hat
μ	3.052	0.036	2.980	3.113	0.001	0.001	1768.0	1495.0	1.0
σ	0.418	0.030	0.365	0.475	0.001	0.001	893.0	439.0	1.0
ν	35.827	28.321	3.103	88.206	0.841	0.595	858.0	1115.0	1.0

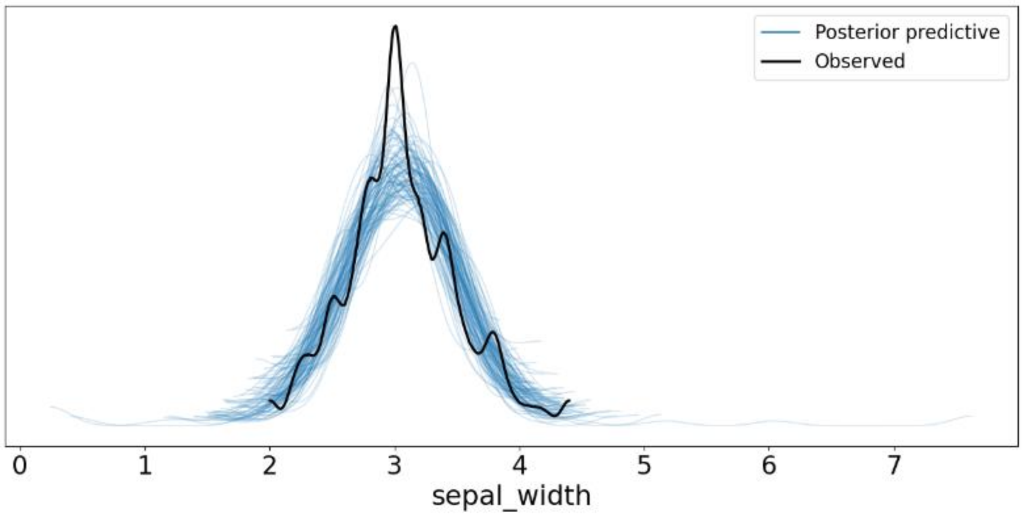
In [28]:
```
y_pred1 = pm.sample_posterior_predictive(idata1, model=model_iris_normal, keep_size=True)
y_pred2 = pm.sample_posterior_predictive(idata2, model=model_iris_t, keep_size=True)
```

```
100.00% [2000/2000 00:12<00:00]

100.00% [2000/2000 00:10<00:00]
```

In [30]:
```
az.concat(idata1, az.from_dict(posterior_predictive=y_pred1), inplace=True)
ax = az.plot_ppc(idata1, num_pp_samples=100, figsize=(12, 6), mean=False)
```



In [31]:
```
az.concat(idata2, az.from_dict(posterior_predictive=y_pred2), inplace=True)
ax = az.plot_ppc(idata2, num_pp_samples=100, figsize=(12, 6), mean=False)
```



You can work on Student T model incase if results are not robust from above model?

```
The results using the T-Distribution are better as it handles the outliers better and has a heavier tail, which is most close
to the observed data in sepal width column. This makes it more Robust and so we can work on it.
```

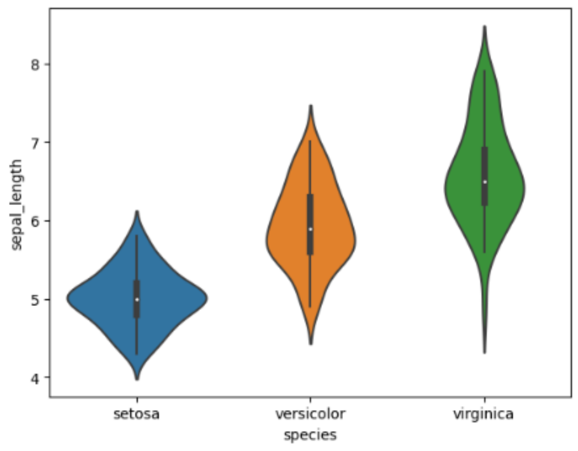
Part B)

Group Comparison

```
In [33]: com = iris_df['sepal_length'].values
         idx = pd.Categorical(df['species'],
                              categories=['versicolor', 'setosa', 'virginica']).codes
         groups = len(np.unique(idx))
```

```
In [34]: sns.violinplot(x='species', y='sepal_length', data=df)
```

```
Out[34]: <AxesSubplot: xlabel='species', ylabel='sepal_length'>
```



```
In [35]: groups
```

```
Out[35]: 3
```

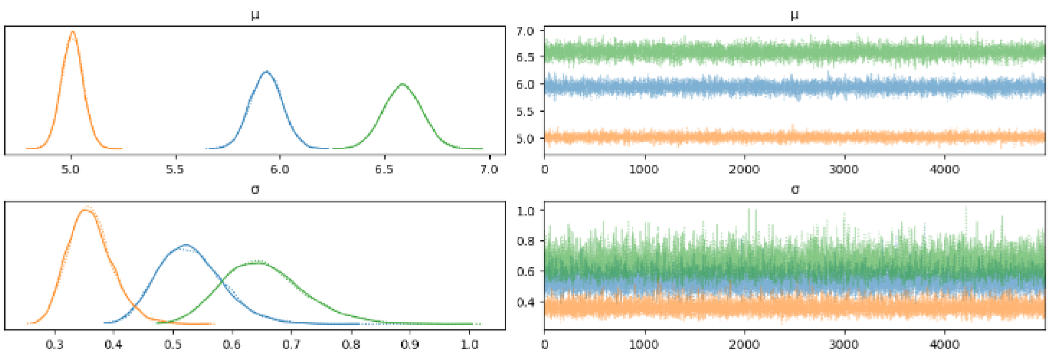
```
In [37]: with pm.Model() as comparing_groups:
           # write code for model
             μ = pm.Normal('μ', mu=0, sd=10, shape=groups)
             σ = pm.HalfNormal('σ', sd=10, shape=groups)
             y = pm.Normal('y', mu=μ[idx], sd=σ[idx], observed=data_sl)
             idata_cg = pm.sample(5000, return_inferencedata=True)


         az.plot_trace(idata_cg)
```

```
Auto-assigning NUTS sampler...
Initializing NUTS using jitter+adapt_diag...
Multiprocess sampling (2 chains in 2 jobs)
NUTS: [σ, μ]
```

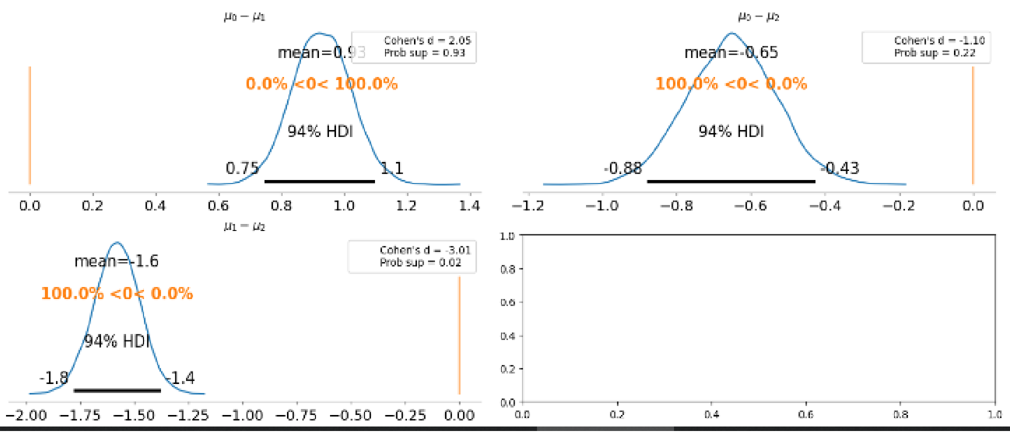
```
100.00% [12000/12000 00:19<00:00 Sampling 2 chains, 0 divergences]
```

```
Sampling 2 chains for 1_000 tune and 5_000 draw iterations (2_000 + 10_000 draws total) took 41 seconds.
```

```
Out[37]: array([[<AxesSubplot: title={'center': 'μ'}>,
                 <AxesSubplot: title={'center': 'μ'}>],
                [<AxesSubplot: title={'center': 'σ'}>,
                 <AxesSubplot: title={'center': 'σ'}>]], dtype=object)
```



```
In [54]: dist = stats.norm()

         _, ax = plt.subplots(3, 2, figsize=(14, 8), constrained_layout=True)

         # comparisons = [(i, j) for i in range(4) for j in range(i+1, 4)]
         # pos = [(k, l) for k in range(3) for l in (0, 1)]

         comparisons = [(i, j) for i in range(3) for j in range(i+1,3)]
         pos = [(k, l) for k in range(2) for l in (0, 1)]

         posterior_cg = idata_cg.posterior.stack(samples={"chain", "draw"})

         for (i, j), (k, l) in zip(comparisons, pos):
             means_diff = posterior_cg["μ"].sel({"μ_dim_0":i}) - posterior_cg["μ"].sel({"μ_dim_0":j})
             d_cohen = (means_diff / np.sqrt((posterior_cg["σ"].sel({"σ_dim_0":i})**2 +
                                              posterior_cg["σ"].sel({"σ_dim_0":j})**2) / 2)).mean().item()
             ps = dist.cdf(d_cohen/(2**0.5))
             az.plot_posterior(means_diff.values, ref_val=0, ax=ax[k, l])
             ax[k, l].set_title(f'$\mu_{i}-\mu_{j}$')
             ax[k, l].plot(
                 0, label=f"Cohen's d = {d_cohen:.2f}\nProb sup = {ps:.2f}", alpha=0)
             ax[k, l].legend()
```



Part C)

```
In [39]: # summarize the inference variable for groups
```

```
In [40]: az.summary(idata_cg)
```

Out[40]:

	mean	sd	hdi_3%	hdi_97%	mcse_mean	mcse_sd	ess_bulk	ess_tail	r_hat
μ[0]	5.935	0.077	5.794	6.082	0.001	0.000	13301.0	8007.0	1.0
μ[1]	5.007	0.052	4.907	5.103	0.000	0.000	13703.0	7795.0	1.0
μ[2]	6.587	0.093	6.416	6.765	0.001	0.001	11534.0	7715.0	1.0
σ[0]	0.530	0.055	0.431	0.632	0.000	0.000	14442.0	7365.0	1.0
σ[1]	0.362	0.038	0.295	0.434	0.000	0.000	15479.0	8112.0	1.0
σ[2]	0.654	0.070	0.527	0.784	0.001	0.000	14884.0	7865.0	1.0

Your results interpretation here

```
In [ ]: # interpret group comparison here
```

We can see from the Cohen D value between Setosa and Virsicolor species is 2.05 which is a moderate value meaning there is a meaningful difference between them. The Cohen D value between Setosa and Virginica is -1.10 and between Virsicolor and Virginica is -3.01 which means there is significant difference in each respective pair.

The 0.93 Probability of superiority between setosa and virsicolor shows that setosa will most probably have a higher sepal width if randomly chosen from the two groups. The probability that Setosa will be larger than a Virginica is 0.22 if they are chosen at random from amongst the two , and between Virsicolor and Virginica is 0.02.

From these conclusions we can say there are significant differences between these groups in sepal width. The virginica group has the highest sepal width, then comes setosa, then comes virsicolor.