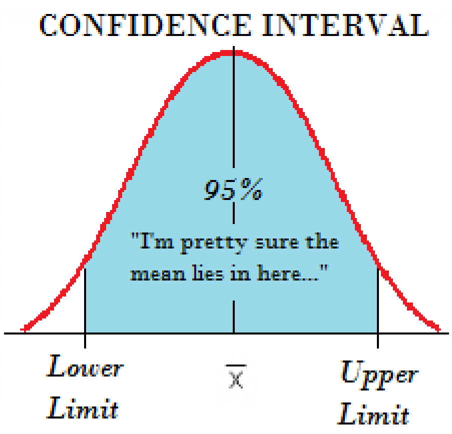
Confidence Interval



Importing necessary Package

In [1]:
```
from pyforest import *
```

Loading Dataset

In [2]:
```
df = pd.read_csv('titanic_train.csv')
df.head()
```

Out[2]:

	PassengerId	Survived	Pclass	Name	Sex	Age	SibSp	Parch	Ticket	Fare	Cabin	Eml
0	1	0	3	Braund, Mr. Owen Harris	male	22.0	1	0	A/5 21171	7.2500	NaN	
1	2	1	1	Cumings, Mrs. John Bradley (Florence Briggs Th...	female	38.0	1	0	PC 17599	71.2833	C85	
2	3	1	3	Heikkinen, Miss. Laina	female	26.0	0	0	STON/O2. 3101282	7.9250	NaN	
3	4	1	1	Futrelle, Mrs. Jacques Heath (Lily May Peel)	female	35.0	1	0	113803	53.1000	C123	
4	5	0	3	Allen, Mr. William Henry	male	35.0	0	0	373450	8.0500	NaN	

In [3]:
```
ages = df.Age.dropna()
ages.head()
```

Out[3]:
```
0    22.0
1    38.0
2    26.0
3    35.0
4    35.0
Name: Age, dtype: float64
```

In [4]:
```
len(ages)
```

Out[4]:
```
714
```

In [5]:
```
avg_age = np.mean(ages)
max_age = np.max(ages)
min_age = np.min(ages)
std_age = np.std(ages)
print(f'Average age: {avg_age}')
print(f'Maximum age: {max_age}')
print(f'Minimum age: {min_age}')
print(f'Standard deviation in age: {std_age}')
```

```
Average age: 29.69911764705882
Maximum age: 80.0
Minimum age: 0.42
Standard deviation in age: 14.516321150817317
```

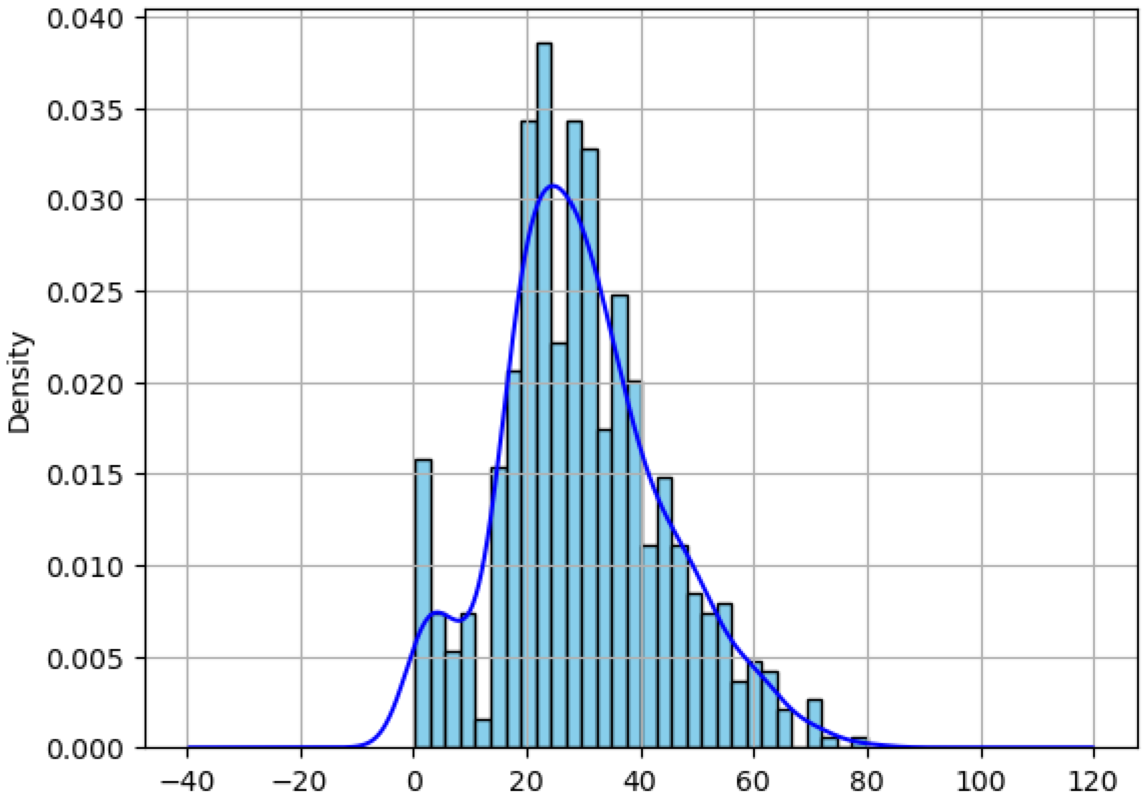
In [6]:
```
ages.describe()
```

Out[6]:
```
count    714.000000
mean      29.699118
std       14.526497
min        0.420000
25%       20.125000
50%       28.000000
75%       38.000000
max       80.000000
Name: Age, dtype: float64
```

Visualizing Age Distribution:

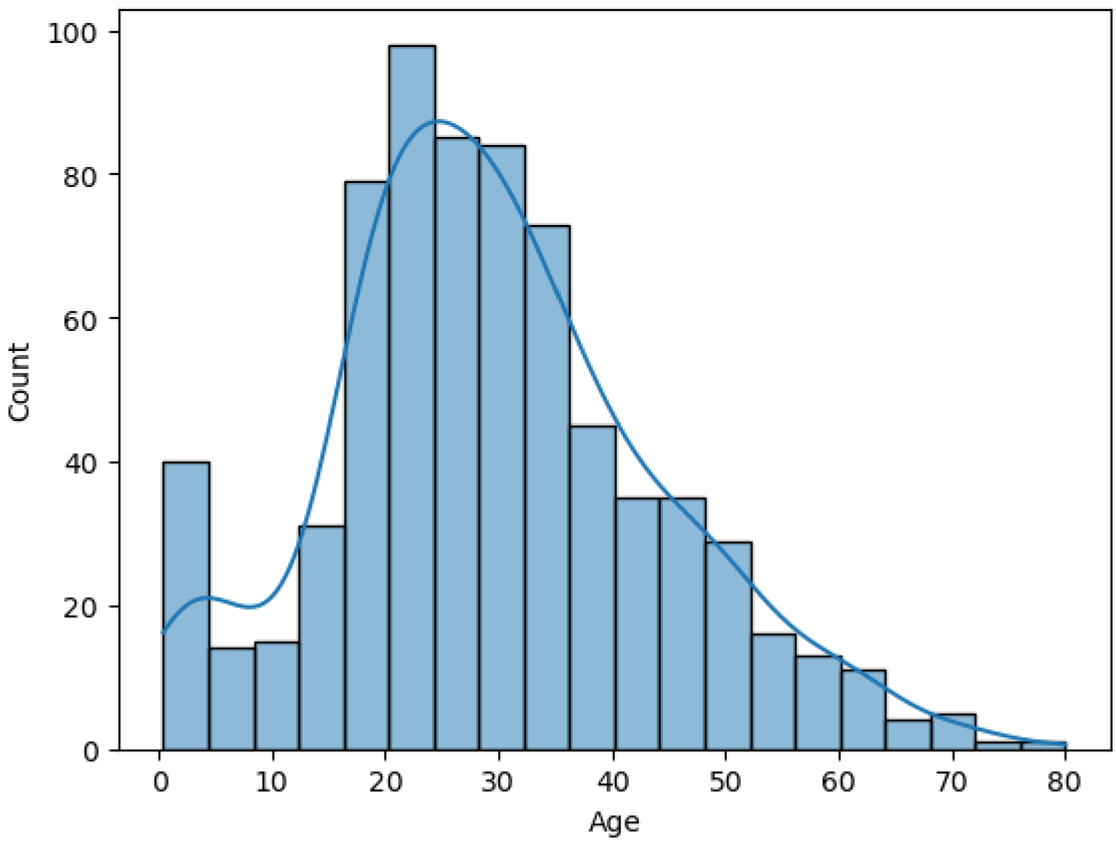
In [7]:
```python
ages.plot(kind='hist', bins=30, grid= True,density=True, edgecolor='black' ,color='sk
ages.plot(kind='kde', color='blue', grid= True)
```

Out[7]: <Axes: ylabel='Density'>



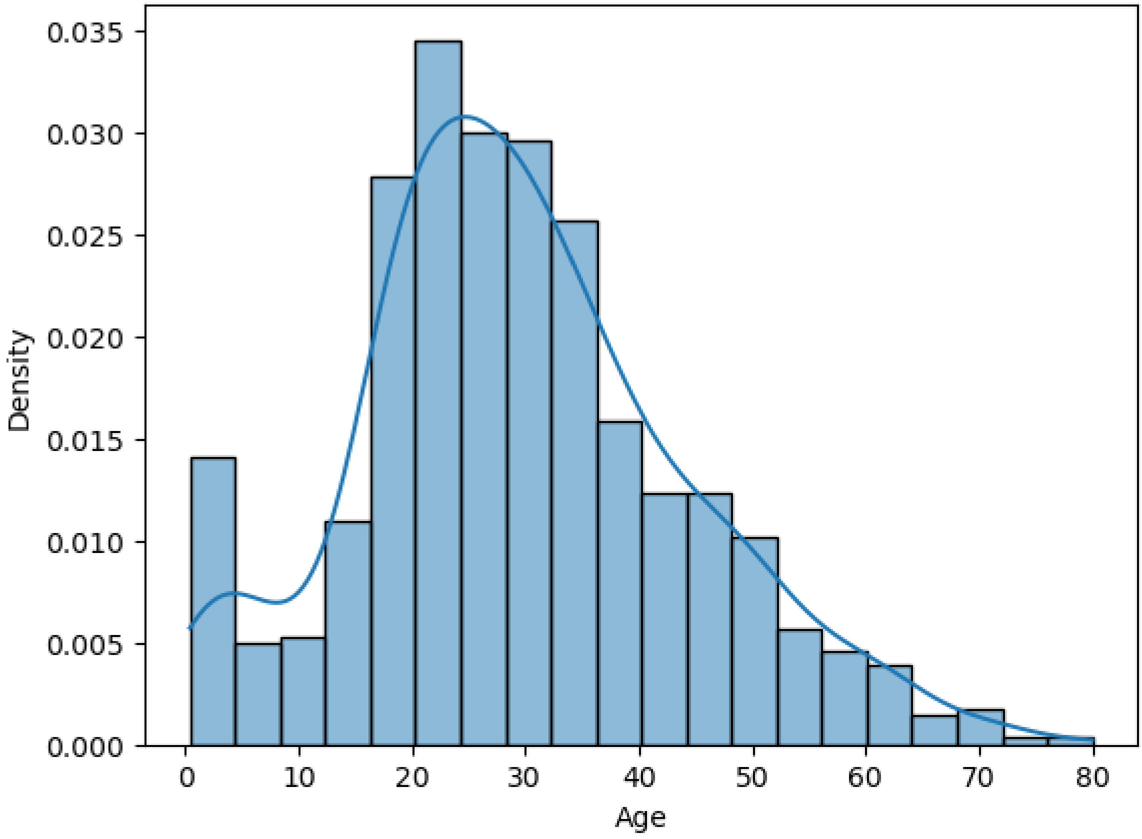
In [8]:
```python
sns.histplot(ages, kde= True)
```

Out[8]: <Axes: xlabel='Age', ylabel='Count'>



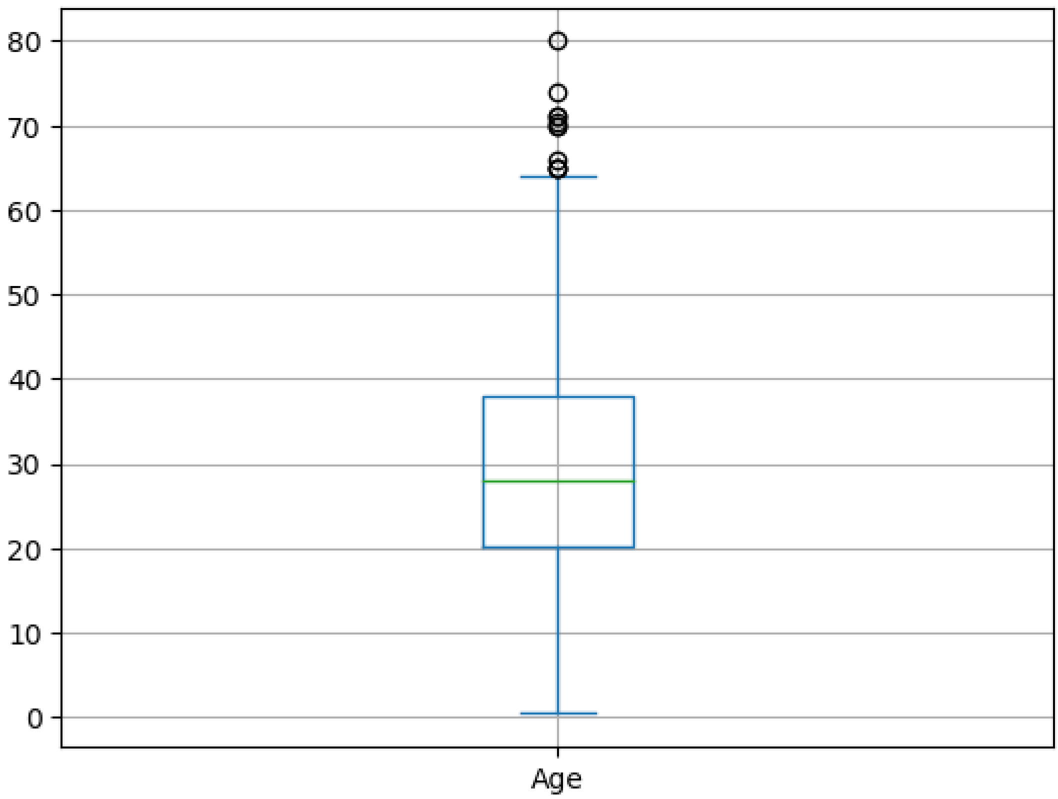
In [9]:
```
sns.histplot(ages, kde= True, stat = 'density')
```

Out[9]: <Axes: xlabel='Age', ylabel='Density'>



In [10]:
```
ages.plot(kind='box',grid= True)
```

Out[10]: <Axes: >



In [11]:
```python
sample_age = ages.sample(10, replace=True)
sample_age
```

Out[11]:
```
852     9.0
851    74.0
494    21.0
645    48.0
615    24.0
632    32.0
672    70.0
183     1.0
141    22.0
16      2.0
Name: Age, dtype: float64
```

In [12]:
```python
avg_sample_age = np.mean(sample_age)
print(f'Average of sample age:{avg_sample_age}')
```

```
Average of sample age:30.3
```

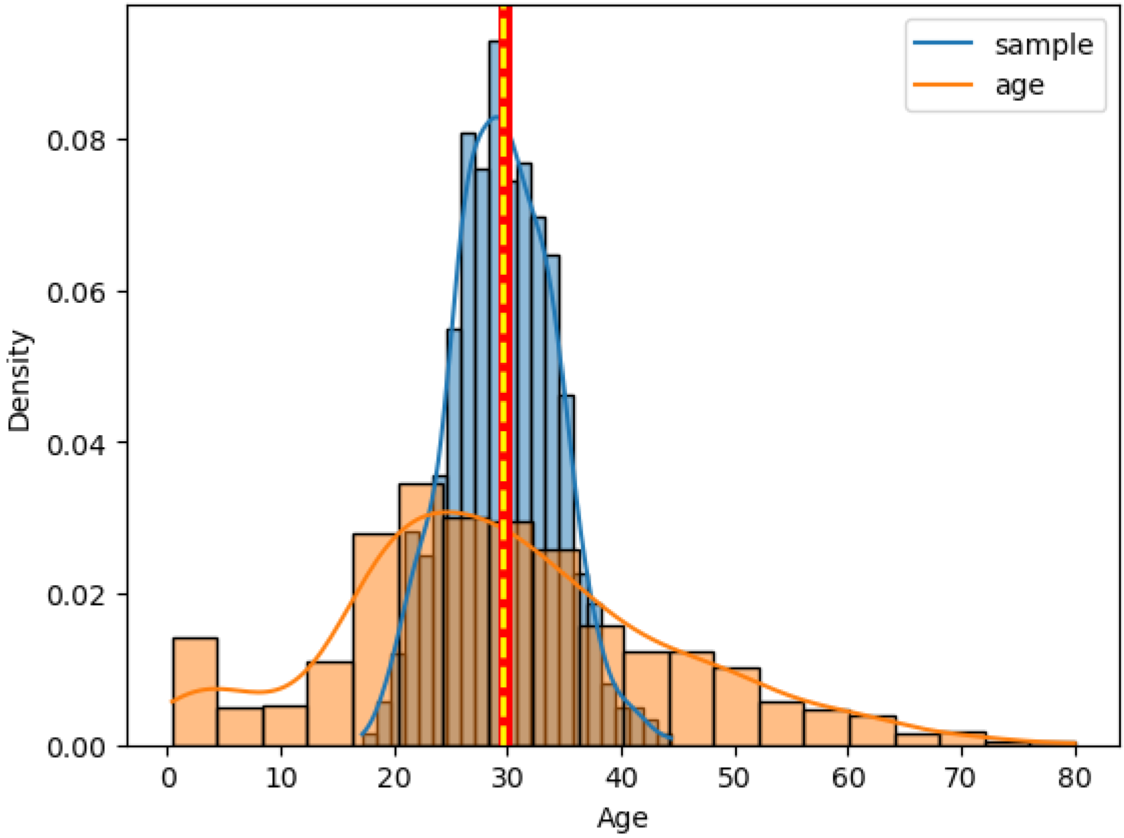
In [13]:
```python
def get_all_sample_means(data, n=10, n_samples=100):

    #
    sample_age = np.random.choice(data,size=(n_samples,n))
    avg_sample_age = np.mean(sample_age, axis=1)
    #
    return avg_sample_age
```

In [14]:
```python
samples = get_all_sample_means(ages,n=10, n_samples=10**3)
samples
```

Out[14]:
```
array([36.4  , 32.9  , 33.3  , 29.3  , 31.2  , 25.525, 31.2  , 31.65 ,
       28.05 , 24.342, 26.2  , 29.2  , 30.9  , 31.9  , 30.842, 32.4  ,
       25.1  , 21.6  , 34.55 , 23.25 , 25.5  , 26.4  , 30.   , 26.2  ,
       29.3  , 32.9  , 26.4  , 23.5  , 36.4  , 30.2  , 32.2  , 30.25 ,
       30.3  , 31.3  , 21.6  , 22.4  , 33.3  , 23.95 , 43.8  , 30.5  ,
       28.35 , 28.942, 32.1  , 37.5  , 31.85 , 25.15 , 33.7  , 36.5  ,
       30.75 , 28.4  , 29.4  , 32.9  , 30.4  , 29.   , 30.35 , 33.4  ,
       25.   , 28.542, 35.5  , 32.9  , 27.1  , 21.85 , 30.875, 26.125,
       42.4  , 24.2  , 25.45 , 33.   , 32.1  , 26.183, 37.2  , 26.9  ,
       24.8  , 28.8  , 26.075, 26.8  , 20.975, 39.95 , 31.55 , 34.4  ,
       23.842, 27.9  , 29.5  , 35.1  , 29.7  , 22.7  , 34.55 , 34.9  ,
       28.6  , 26.55 , 27.5  , 30.9  , 23.392, 22.642, 30.75 , 34.4  ,
       28.45 , 30.8  , 26.6  , 33.85 , 33.   , 29.475, 31.4  , 39.5  ,
       29.2  , 30.5  , 32.4  , 32.25 , 29.8  , 25.15 , 21.4  , 33.6  ,
       25.2  , 28.5  , 31.1  , 25.85 , 28.   , 25.075, 31.983, 22.5  ,
       31.8  , 29.3  , 26.5  , 28.5  , 24.7  , 22.1  , 33.6  , 23.6  ,
       32.5  , 29.   , 22.442, 29.7  , 26.1  , 29.675, 26.5  , 26.992,
       27.35 , 23.55 , 24.4  , 26.   , 30.7  , 31.4  , 33.7  , 28.6  ,
       27.25 , 21.783, 25.6  , 26.2  , 29.2  , 27.1  , 34.   , 34.8  ,
```

In [15]:
```
sns.histplot(samples, kde=True, stat = 'density', )
sns.histplot(ages, kde=True, stat= 'density')
plt.axvline(ages.mean(), color='red', lw=5,)
plt.axvline(samples.mean(), color='yellow', lw=2, ls='--')
plt.legend(['sample','age'])
```

Out[15]: `<matplotlib.legend.Legend at 0x2bd5e449090>`



Bootstarp Sampling

Bootstrapping is a resampling technique that involves generating multiple datasets (bootstrap samples) from a single sample with replacement. Each bootstrap sample is of the same size as the original sample. Bootstrapping is used for various purposes, and its key advantages include:

- **Estimating Population Parameters:** Bootstrapping allows for the estimation of population parameters, such as the mean or standard deviation, by repeatedly resampling from the observed data.
- **Assessing Variability:** By generating multiple bootstrap samples, bootstrapping provides insights into the variability of sample statistics. This is particularly useful for understanding the uncertainty associated with estimated parameters.
- **Creating Confidence Intervals:** Bootstrapping is often employed to construct confidence intervals around sample statistics. These intervals provide a range within which the true population parameter is likely to fall.
- **Handling Non-Normality:** Bootstrapping is robust and does not rely on assumptions of normality. It can be applied to non-normally distributed data, making it versatile for various types of datasets.
- **Model Validation:** In machine learning and model development, bootstrapping can be used for resampling to assess the stability and generalizability of a predictive model.

In [16]:
```
def bootstrap_sample(sample, n_samples=10**4):
    '''
    Bootstrap Sampling is a method that involves drawing of sample data
    repeatedly with replacement from a data source to estimate a population
    parameter.

    Random sampling with replacement.
    '''
    #
    bs_sample_means = get_all_sample_means(
        sample,
        n=len(sample),
        n_samples=n_samples
    )

    return bs_sample_means
```

In [17]:
```
b_sample_means = bootstrap_sample(sample_age)
b_sample_means
```

Out[17]:
```
array([37.9, 19.5, 27.8, ..., 30.9, 29.3, 28.5])
```

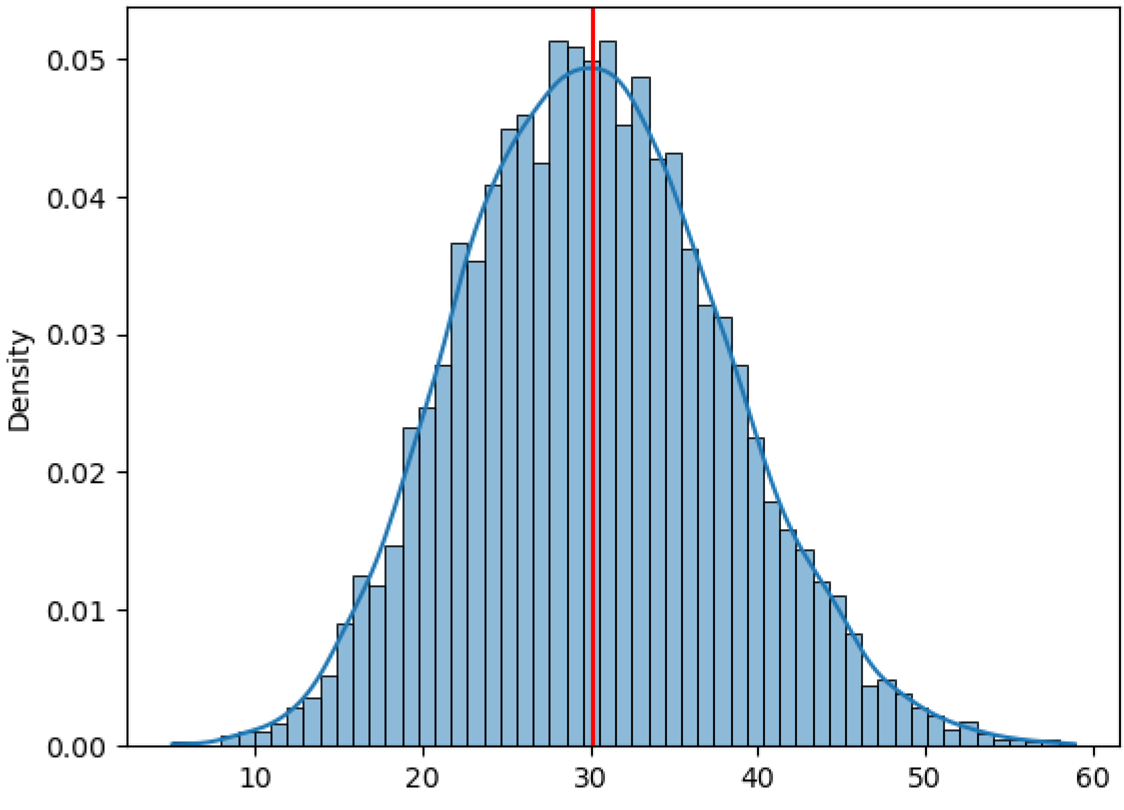
In [18]:
```
len(b_sample_means)
```

Out[18]:
```
10000
```

In [ ]:
```

```

In [19]:
```
sns.histplot(b_sample_means, kde=True, stat = 'density', )
plt.axvline(b_sample_means.mean(), color='red')
```

Out[19]:
```
<matplotlib.lines.Line2D at 0x2bd5f618be0>
```



In [20]:
```
# standard Deviation
mean_bsample = b_sample_means.mean()
sigma = b_sample_means.std()
sigma2= 2* sigma
print(f'mean of bootsrap sampling = {mean_bsample}')
print(f'1st standard deviation of bootsrap sampling = {sigma}')
print(f'2nd standard deviation of bootsrap sampling = {sigma2}')
```

```
mean of bootsrap sampling = 30.230659999999997
1st standard deviation of bootsrap sampling = 7.785627653850394
2nd standard deviation of bootsrap sampling = 15.571255307700788
```

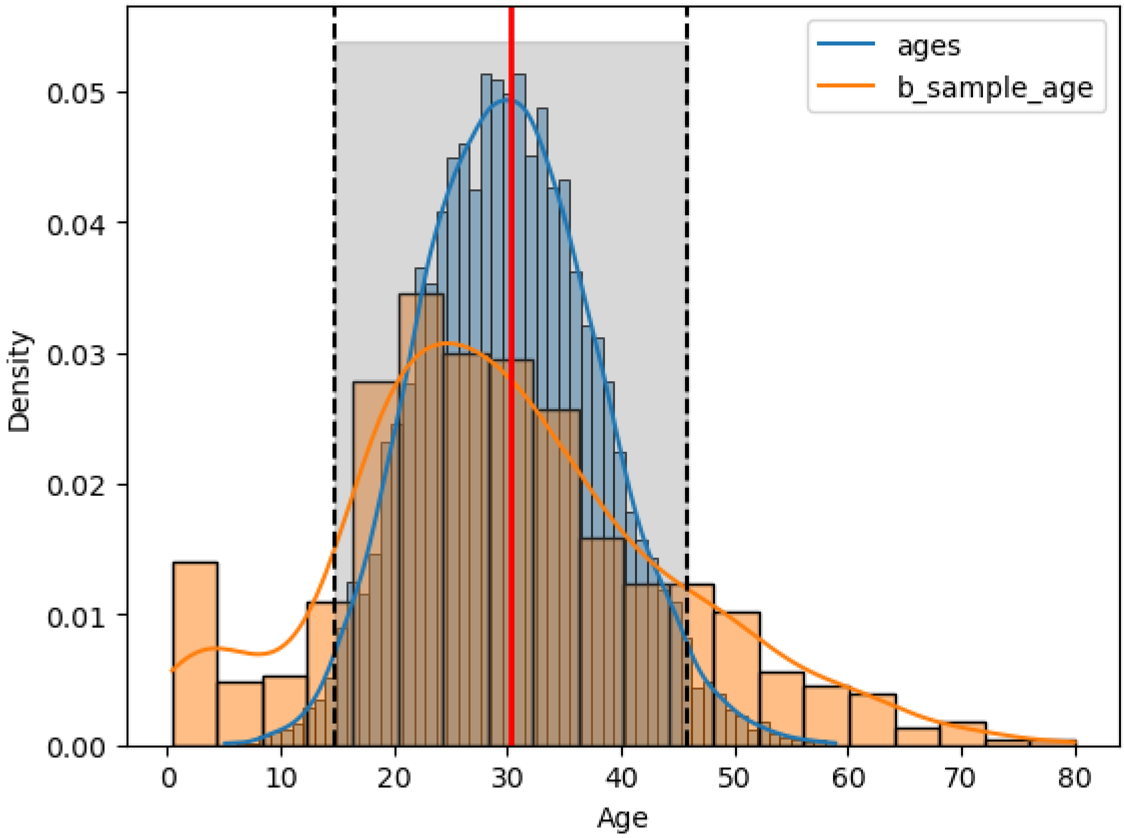
Confidence limits

Confidence limits are a pair of numbers used to describe an estimate or other characteristic of a population. They are the upper and lower boundaries of confidence intervals

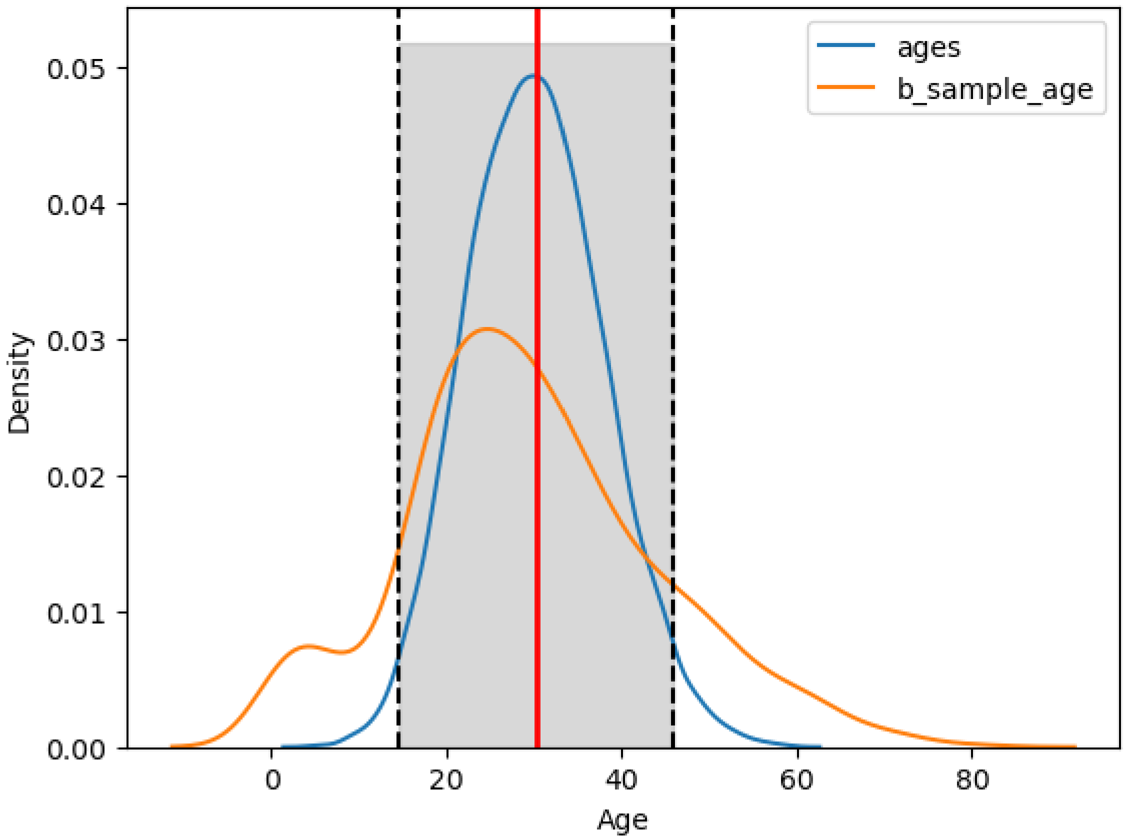
In [21]:
```
upper_limit = mean_bsample +sigma2
lower_limit = mean_bsample- sigma2
confidence_limit =(lower_limit, upper_limit)
print(f'Confidence limit : {confidence_limit}')
```

```
Confidence limit : (14.659404692299209, 45.80191530770078)
```

In [22]:
```
sns.histplot(b_sample_means, kde=True, stat = 'density',)
sns.histplot(ages, kde=True, stat = 'density',)
plt.legend(['ages','b_sample_age'])
plt.axvline(mean_bsample , color='red',lw=2)
plt.axvline(mean_bsample -sigma2 , color='black',ls='--')
plt.axvline(mean_bsample +sigma2 , color='black',ls='--')
plt.fill_betweenx(y=np.linspace(0, plt.ylim()[1], 100),
                  x1=lower_limit, x2=upper_limit, color='gray', alpha=0.3)
plt.show()
```



In [23]:
```
sns.kdeplot(b_sample_means)
sns.kdeplot(ages)
plt.legend(['ages','b_sample_age'])
plt.axvline(mean_bsample , color='red',lw=2)
plt.axvline(lower_limit , color='black',ls='--')
plt.axvline(upper_limit, color='black',ls='--')
plt.fill_betweenx(y=np.linspace(0, plt.ylim()[1], 100),
                  x1=lower_limit, x2=upper_limit, color='gray', alpha=0.3)
plt.show()
```



Finding Confidence Interval

In [24]:
```
import scipy.stats

normal_curve = scipy.stats.norm(mean_bsample,sigma)
normal_curve.cdf(upper_limit) - normal_curve.cdf(lower_limit)
```

Out[24]: 0.9544997361036416

The code primarily focuses on exploring and visualizing the age distribution in the Titanic dataset, performing bootstrap sampling to estimate population parameters, and calculating a confidence interval. The visualizations and statistical measures provide insights into the age characteristics of the dataset, and bootstrap sampling is used to quantify the uncertainty in the estimates.

In [ ]: