

## Species on Different Islands

### Question:

The Antarctic research scientists are back with another brief. They want to be able to visualize how their data collection counts differ between species and islands.

Specifically, they want to easily compare islands based on the count of different species of penguins they recorded there.

You have the perfect plot - you will layer several bar charts together for easy comparison!

You have been provided a `penguins\_grouped` DataFrame that has the count of samples for each species at each island as well as an `islands` list of the different islands where research was undertaken.

Instructions:

1. View the printed out `penguins\_grouped` DataFrame to see its structure.
2. Create an empty figure object.
3. Loop through the `species`, adding a bar chart trace to the base figure.
4. Set the appropriate y subset and name for the bar chart trace being added.

### Answer:

```
# Create the base figure
fig = go.Figure()
```

```
# Loop through the species
for species in ['Adelie', 'Chinstrap', 'Gentoo']:
    # Add a bar chart trace
    fig.add_trace(go.Bar(
        x=islands,
        y=penguins_grouped[penguins_grouped.Species == species]['Count'],
        name=species
    ))
```

```
# Show the figure
fig.show()
```

### Explanation of the Answer:

The `go.Figure()` initializes an empty figure object. A loop iterates through the species list, and for each species, the DataFrame is filtered to extract the count values corresponding to that species. Each species' data is added as a bar chart trace with the appropriate x-axis values (islands) and y-axis values (counts). Finally, the `fig.show()` method renders the plot with all traces overlaid.