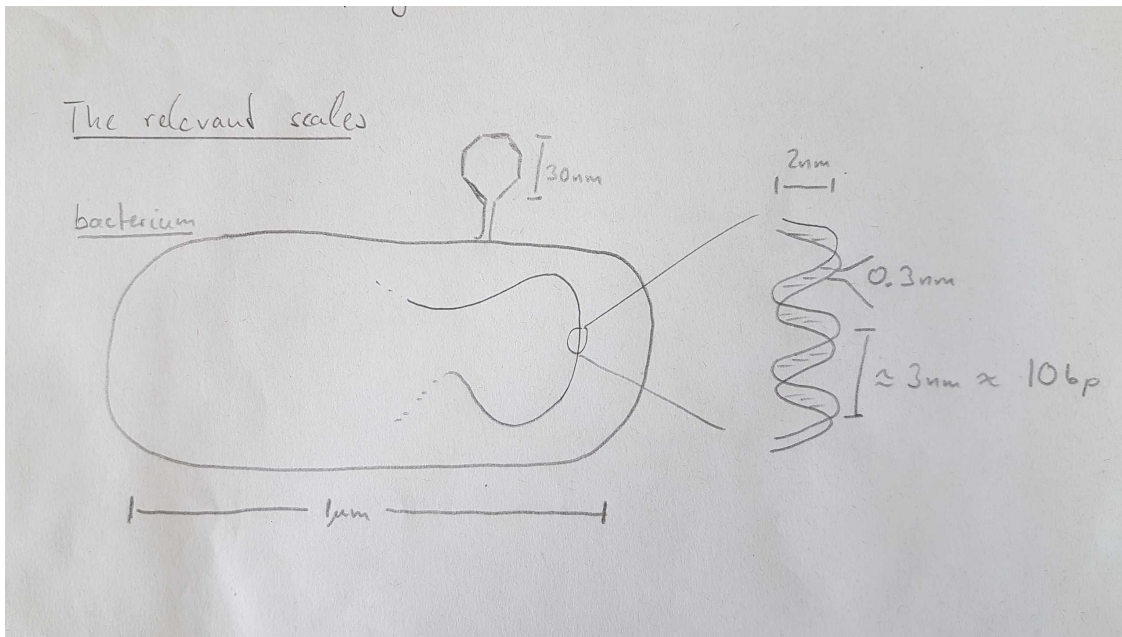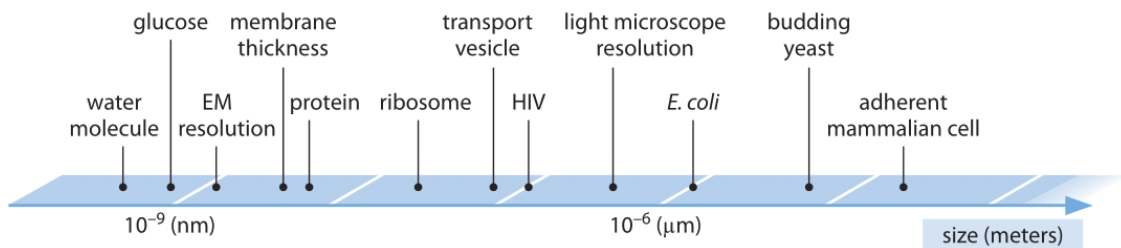# lecture01a_SizesAndLogScales

November 7, 2024

1 Relevant linear dimensions

Life operates on all scales from the sub-nanometer molecules to organisms. The range of these length scales is well illustrated in this graph:

source: Physical Biology of the Cell

Understanding the relevant length scales is crucial for understanding many biological processes and getting a sense of why things are fast, slow etc.

```
[6]: # Note that these numbers are rough estimates and often are only representative
     # values picked from a range. They are intended to give you a sense of the
     # relative sizes but are not an authorative source.
```

```
linear_dimensions = {  # in meters
    "H2O": 2.45e-10,
    "dsDNA base pair height": 3.4e-10,
    "glucose": 9e-10,
    "dsDNA diameter": 2e-9,
    "membrane thickness": 3e-9,
    "ribosome": 2.5e-8,
    "RNA virus": 1e-7,
    "wave length of visible light": 5e-7,
    "bacterium": 1e-6,
    "budding yeast": 5e-6,
    "mammalian cell": 1e-5,
    "human ooctyte": 1e-4,
    "fruit fly egg": 5e-4,
    "chicken egg":5e-2,
    "human": 1.8,
    "blue whale": 25
}

print(f"size of water molecules: {linear_dimensions['H2O']}m")
print(f"size of RNA virus: {linear_dimensions['RNA virus']}m")
```

```
size of water molecules: 2.45e-10m
size of RNA virus: 1e-07m
```

The data structure above is called a "dictionary" as it associates values (numbers measured in meters) to keys. These values can be accessed as `linear_dimensions['H2O']`.

Let's graph these numbers. We can do this with the plotting library `matplotlib`. After the import, the plotting commands are available under the name `plt`.
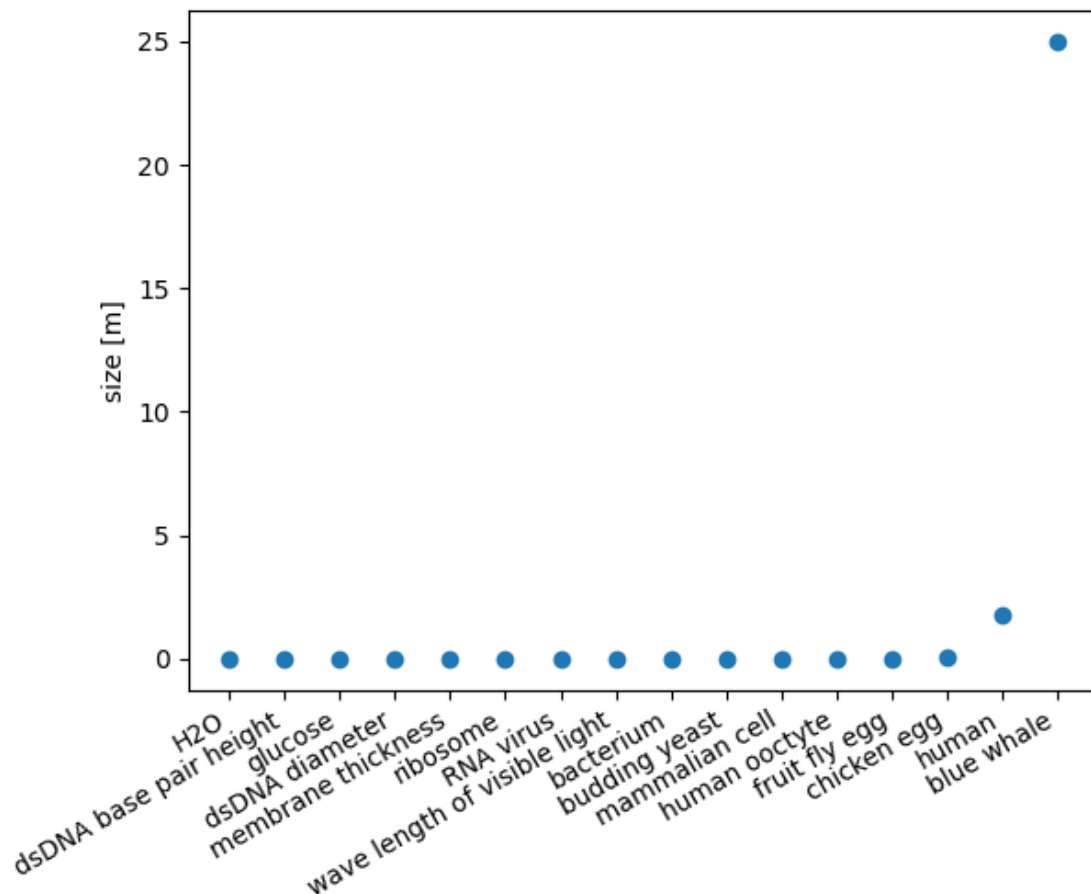
[7]:
```python
import matplotlib.pyplot as plt
```

[8]:
```python
names = list(linear_dimensions.keys())        # make a list of the names to
 ↪label the graph
sizes = [linear_dimensions[k] for k in names]  # make a list of the values for
 ↪plotting
print(names)
print(sizes)
```

```
['H2O', 'dsDNA base pair height', 'glucose', 'dsDNA diameter', 'membrane
thickness', 'ribosome', 'RNA virus', 'wave length of visible light',
'bacterium', 'budding yeast', 'mammalian cell', 'human ooctyte', 'fruit fly
egg', 'chicken egg', 'human', 'blue whale']
[2.45e-10, 3.4e-10, 9e-10, 2e-09, 3e-09, 2.5e-08, 1e-07, 5e-07, 1e-06, 5e-06,
1e-05, 0.0001, 0.0005, 0.05, 1.8, 25]
```
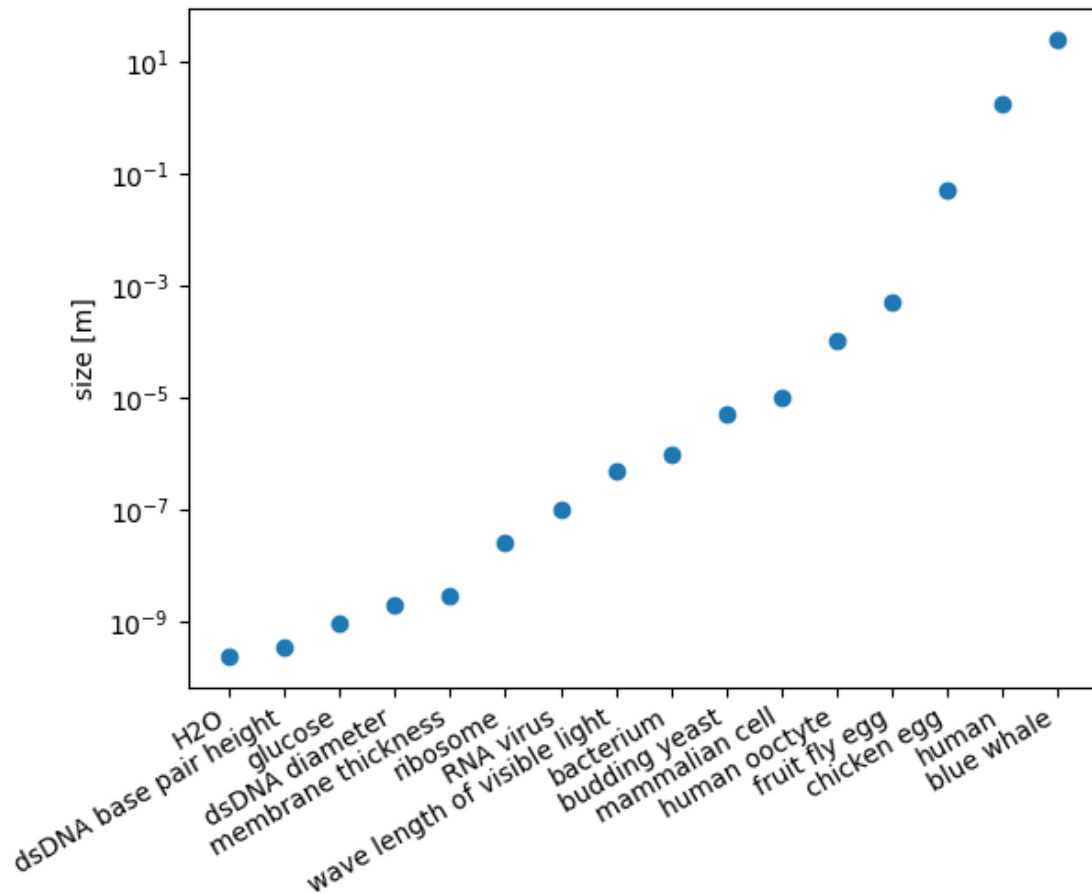
```
[9]: plt.plot(sizes, 'o')   # the 'o' here indicates that we use a circle marker for
      ↪the data
     plt.xticks(range(len(names)), names, rotation=30, ha='right') # label the data
      ↪points
     plt.ylabel('size [m]') # label the y-axis
```

```
[9]: Text(0, 0.5, 'size [m]')
```


As you see, we don't see much. Only for whale and the human it is visible that the values are non-zero. This is not surprising, we are plotting quantities on vastly different scales. To get a better sense of the relative magnitude of points in our data, it is useful to look at these data on a logarithmic scale:

```
[10]: plt.plot(sizes, 'o')
      plt.xticks(range(len(names)), names, rotation=30, ha='right')
      plt.yscale('log')
      plt.ylabel('size [m]')
      plt.show()
```

Now the differences between all data points are clearly visible. One a logarithmic scale, fold changes are additive. Thas it 10 is as far from 1 and 100 is from 10. This fact is a consequence of the fundamental property of logarithms:

$$\log(xy) = \log(x) + \log(y)$$

1.0.1 Additional resources

- video lesson on logarithmic scales by the Khan academy
- Biology by the Numbers by Milo and Phillips, Chapter 1

[ ]:

[ ]: