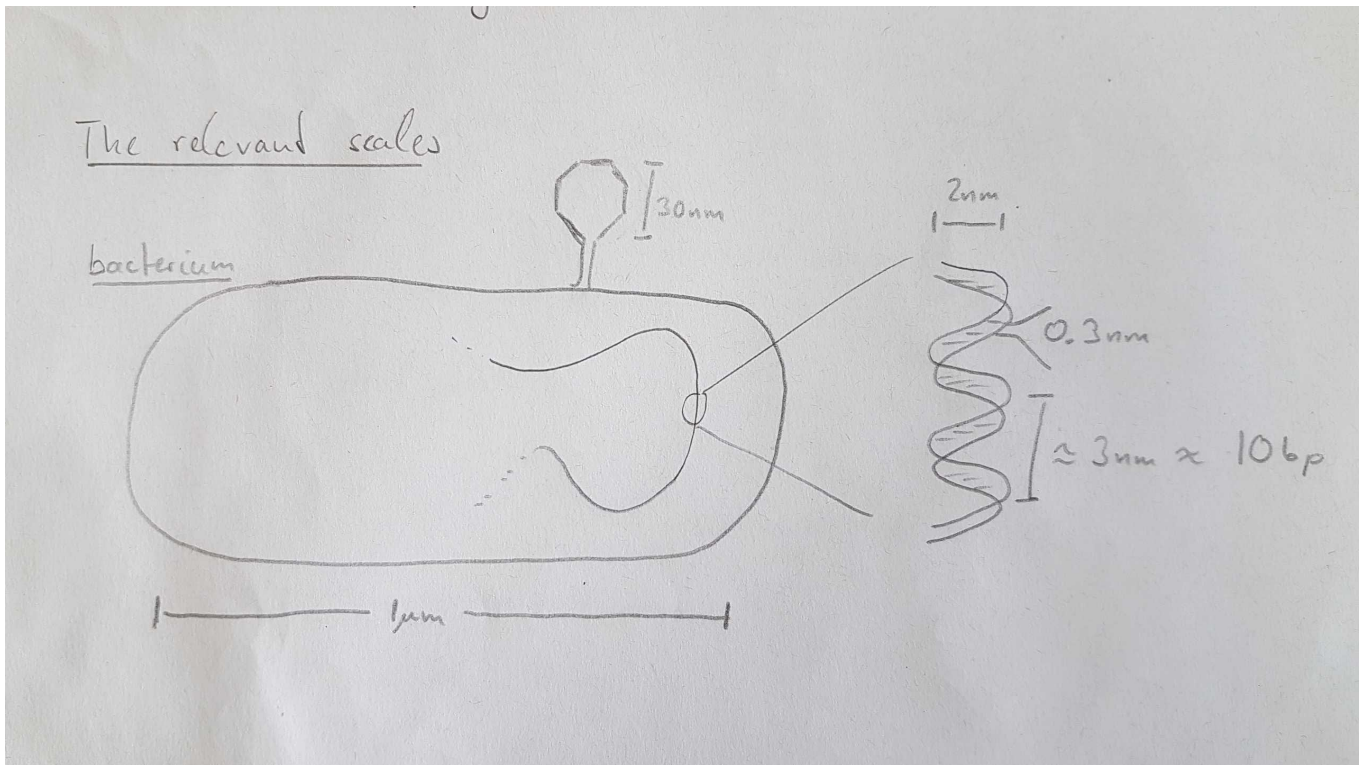
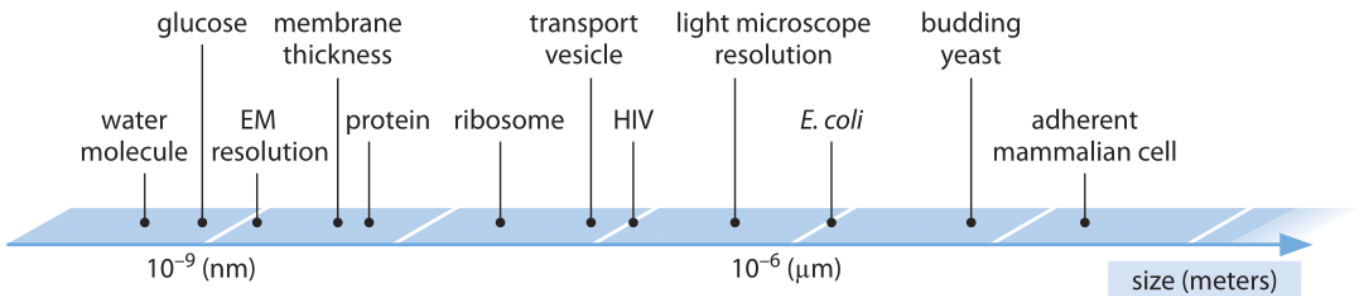


Relevant linear dimensions



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.

In [1]:

```
# 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 authoritative 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 oocyte": 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")
```

```
size of water molecules: 2.45e-10m
```

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`.

In [2]:

```
import matplotlib.pyplot as plt
```

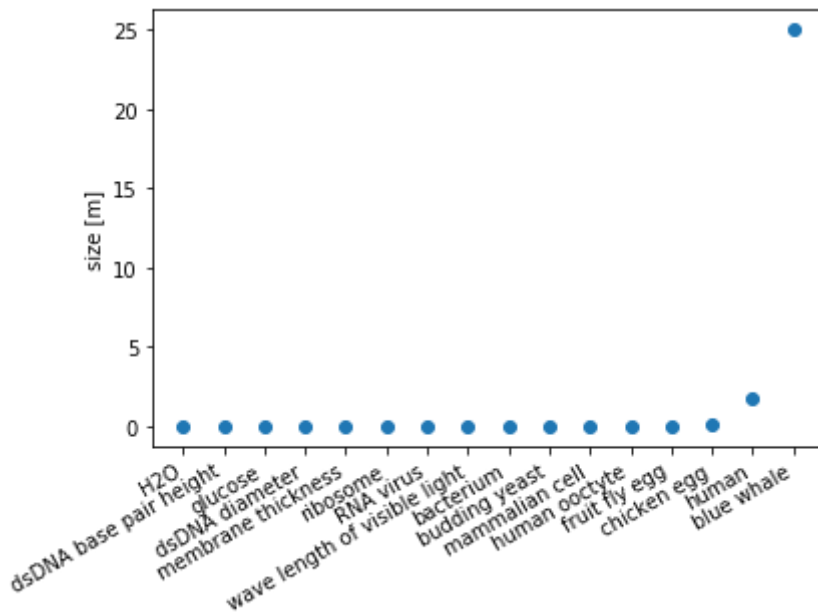
In [3]:

```
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)
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
```

```
['H2O', 'dsDNA base pair height', 'glucose', 'dsDNA diameter', 'membrane thickness', 'ribosome', 'RNA virus', 'wave length of visible light', 'bacterium', 'budding yeast', 'mammalian cell', 'human oocyte', 'fruit fly egg', 'chicken egg', 'human', 'blue whale']
```

Out[3]:

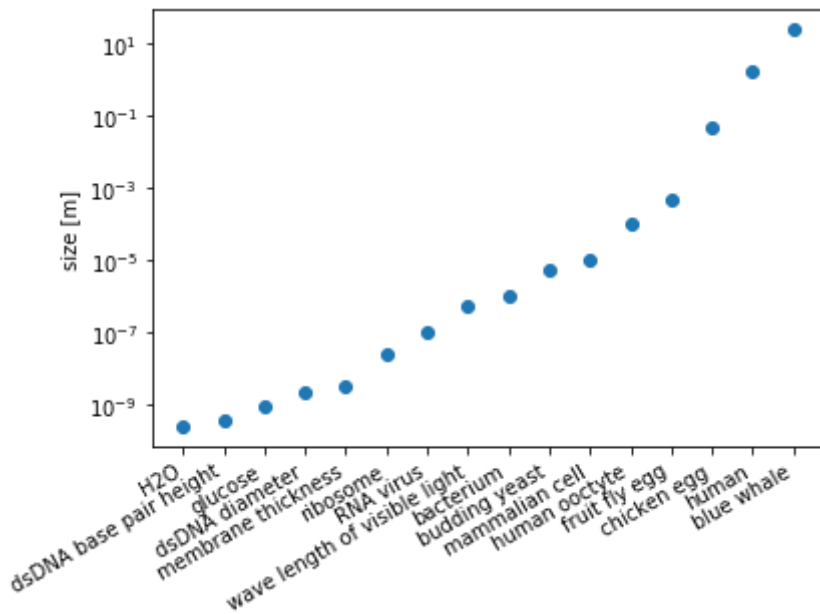
Text(0, 0.5, 'size [m]')



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:

In [4]:

```
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. On a logarithmic scale, fold changes are additive. Thus 10 is as far from 1 as 100 is from 10. This fact is a consequence of the fundamental property of logarithms:

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

Dig deeper

- plot these the size of things in units of the length of a water molecule H_2O and the width of your thumb. These might not be very useful units, but they are perfectly valid.
- plot the logarithm of the sizes instead of the sizes on a logarithmic scale. What happened to the unit?

Additional resources

- video lesson on logarithmic scales by the [Khan academy](https://www.youtube.com/watch?v=sBhEi4L91Sg) (<https://www.youtube.com/watch?v=sBhEi4L91Sg>)
- [Biology by the Numbers](https://www.dropbox.com/s/gvpleqtcv8scro4/cellBiologyByTheNumbersJuly2015.pdf?dl=1) (<https://www.dropbox.com/s/gvpleqtcv8scro4/cellBiologyByTheNumbersJuly2015.pdf?dl=1>) by Milo and Phillips, Chapter 1

In []: