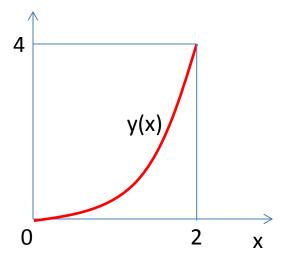
Modeling Uncertainty

Phys 281 – Class 9
Grant Wilson

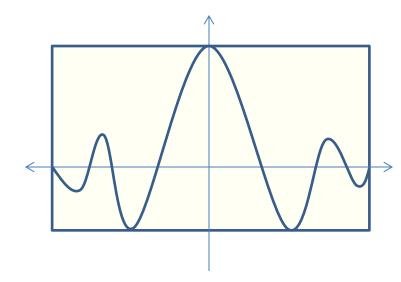
Class 08 Exercises – P1.1

```
#1.1 - Integrate x^2 from 0 to 2 using MC integration
#pick x and y points at random to make npts-ordered pairs
npts = int(1e5)
x1 = np.random.uniform(0,2,npts)
y1 = np.random.uniform(0,4,npts)
box_area = 4.*2.
#here is the function to integrate
def func(x): return x**2
#need the values of y(x1) to compare to y1
yfunc = func(x1)
#now count up the y1 that fall between 0 and y(x1)
count = 0.
for i in range(npts):
  if (y1[i]<yfunc[i]):</pre>
    count = count+1
#the integral is the fraction of the points below y(x1) times the box area
int1 = count/npts * box_area
int_romberg = integrate.romberg(func,0.,2.)
print "Problem 1"
print ' I romberg = ', int romberg
```



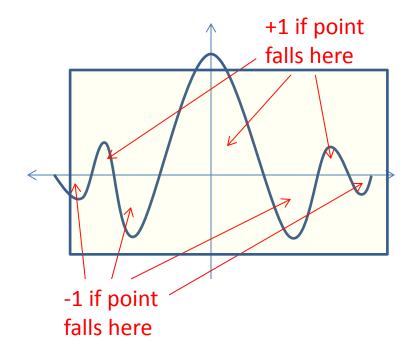
Class 08 Exercises – P1.2

```
#1.2 - Integrate sin(x)/x from -pi to pi using MC integration
npts = int(1e5)
#pick x and y points at random to make npts-ordered pairs
x1 = np.random.uniform(-4.*np.pi,4.*np.pi,npts)
y1 = np.random.uniform(-0.25,1,npts)
box area = 8.*np.pi*1.25
#here is the function to integrate
def func2(x):
  return np.sin(x)/x
#need the values of y(x1) to compare to y1
yfunc = func2(x1)
#now count up the y1 that fall between y(x1) and th x-axis. Points
#that fall above the x-axis should get a +1 while points that fall
#below the x-axis should get a -1. Points that fall outside of
#the function should get 0
count = 0.
for i in range(npts):
  if ((y1[i]<yfunc[i]) and (y1[i]>0)):
    count = count+1
  elif ((y1[i]>yfunc[i]) and (y1[i]<0)):
    count = count-1
```

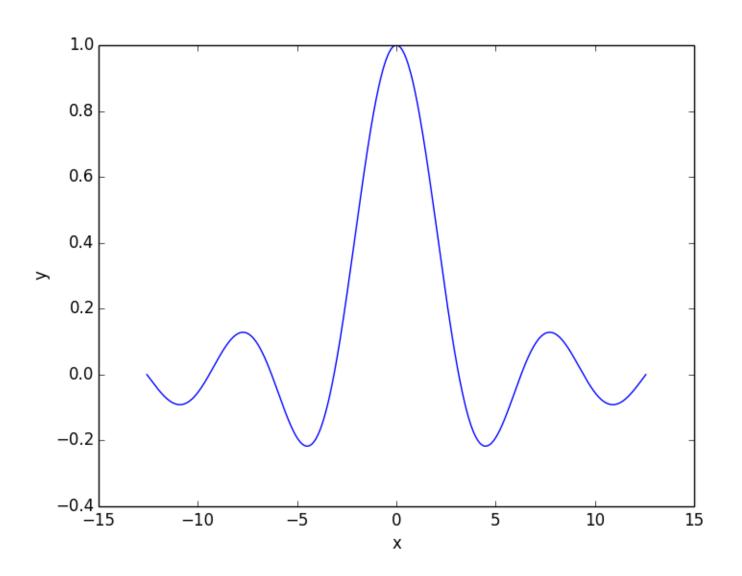


Class 08 Exercises – P1.2

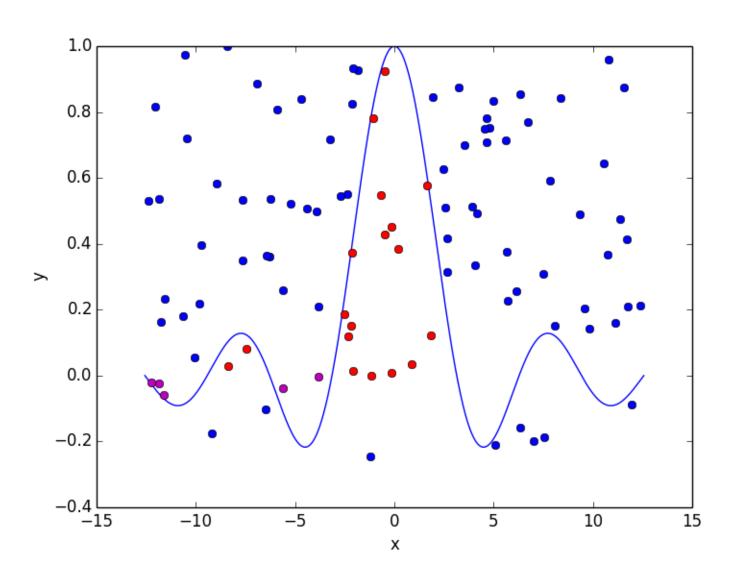
```
#1.2 - Integrate sin(x)/x from -pi to pi using MC integration
npts = int(1e5)
#pick x and y points at random to make npts-ordered pairs
x1 = np.random.uniform(-4.*np.pi,4.*np.pi,npts)
y1 = np.random.uniform(-0.25,1,npts)
box area = 8.*np.pi*1.25
#here is the function to integrate
def func2(x):
  return np.sin(x)/x
#need the values of y(x1) to compare to y1
yfunc = func2(x1)
#now count up the y1 that fall between y(x1) and th x-axis. Points
#that fall above the x-axis should get a +1 while points that fall
#below the x-axis should get a -1. Points that fall outside of
#the function should get 0
count = 0.
for i in range(npts):
  if ((y1[i]<yfunc[i]) and (y1[i]>0)):
    count = count+1
  elif ((y1[i]>yfunc[i]) and (y1[i]<0)):
    count = count-1
```



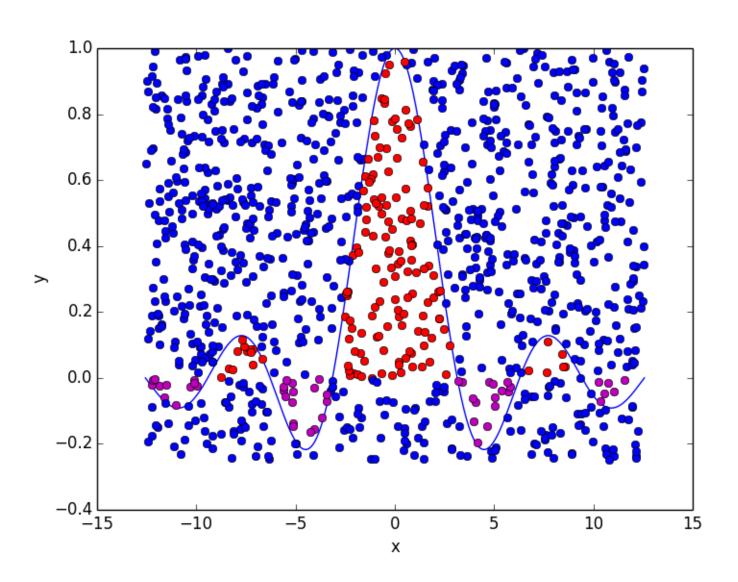
Function to be integrated



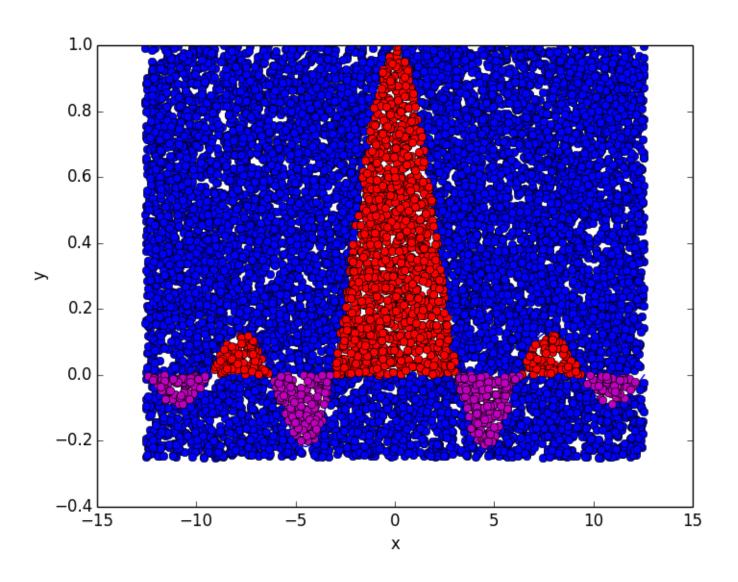
100 points



1000 points



10,000 points



Class 08 Exercises – P2

What needs to be done for P2 is interesting enough that I think I'll make a video short for the approach for the answer. In the meantime, here's the answer:

• Suppose you want to integrate some function $f(\mathbf{x})$ over some subspace \mathcal{C} of an n-dimensional space spanned by \mathbf{x} (note use of bold rather than using a vector sign).

$$I = \int_{\mathcal{C}} d\mathbf{x} \ f(\mathbf{x}) \tag{4}$$

• Monte Carlo integration estimates the integral as

$$\int_{\mathcal{C}} d\mathbf{x} \ f(\mathbf{x}) = V\langle f \rangle \pm V \sqrt{\frac{\langle f^2 \rangle - \langle f \rangle^2}{N}}$$
 (5)

where we define the moments taken over N sample points as

$$\langle f \rangle \equiv \frac{1}{N} \sum_{i=0}^{N-1} f(\mathbf{x}_i)$$

$$\langle f^2
angle \equiv \frac{1}{N} \sum_{i=0}^{N-1} f^2(\mathbf{x}_i)$$

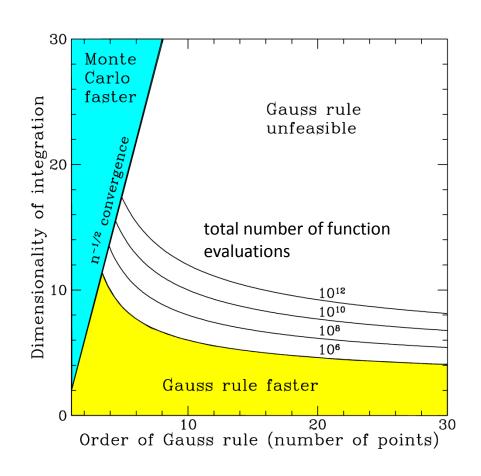
and the volume V encloses the subspace \mathcal{C} .

Choosing your integration approach

Monte Carlo Integration is best used when

- 1. the dimension of the problem is greater than 10
- 2. there is no easy way to write down the limits of the integration

Otherwise, go with Gaussian Quadrature



Modeling Uncertainty

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Simulating probabilities

What does a 1 in 5 chance of something occurring mean?

How could you simulate that?

Given a positive test result, what is the probability that you've actually got the disease?

```
#here is the information about the disease and test
prevalence = 0.1
false_positive_rate = 0.2
false_negative_rate = 0.05
```

#We could calculate this using probability theory, or we could simulate #the process. Let's do the simulation.

```
#set up the trials, one per test
ntrials = 10000
index = np.arange(ntrials)
```

```
#diseased is an array of one element for each trial

#(think of them as different people in the community)

#diseased = 1 implies that the person really does have the disease

#diseased = 0 implies that the person does not have the disease

diseased = np.zeros(ntrials)

u = np.random.rand(ntrials)

for i in index:
```

```
#diseased is an array of one element for each trial
#(think of them as different people in the community)
#diseased = 1 implies that the person really does have the disease
#diseased = 0 implies that the person does not have the disease
diseased = np.zeros(ntrials)
u = np.random.rand(ntrials)
for i in index:
    if (u[i] <= prevalence):
        diseased[i] = 1</pre>
```

```
#at this point, all the diseased=1 people have it, diseased=0 people are clear
#run through them again and apply the test
#test result = 1 implies they have it
#test result = 0 implies they don't
test_result = np.zeros(ntrials)
for i in index:
  if (diseased[i] == 1):
  if (diseased[i] == 0):
```

```
#at this point, all the diseased=1 people have it, diseased=0 people are clear
#run through them again and apply the test
#test result = 1 implies they have it
#test result = 0 implies they don't
test result = np.zeros(ntrials)
for i in index:
  if (diseased[i] == 1):
    #this person has it, what does the test say?
    u = np.random.rand()
                                                                             accounts for false
    if (u <= false_negative_rate):</pre>
                                                                             negatives
      test result[i] = 0
    else:
      test result[i] = 1
  if (diseased[i] == 0):
```

```
#at this point, all the diseased=1 people have it, diseased=0 people are clear
#run through them again and apply the test
#test result = 1 implies they have it
#test result = 0 implies they don't
test_result = np.zeros(ntrials)
for i in index:
  if (diseased[i] == 1):
    #this person has it, what does the test say?
                                                                            accounts for false
    u = np.random.rand()
    if (u <= false negative rate):
                                                                            negatives
      test result[i] = 0
    else:
      test result[i] = 1
  if (diseased[i] == 0):
    #this person doesn't have it, what does the test say?
                                                                            accounts for false
    u = np.random.rand()
    if (u <= false positive rate):
                                                                            positives
      test result[i] = 1
    else:
      test result[i] = 0
```

```
#count up the different kinds of people
diseased_tested_positive = 0.
diseased tested negative = 0.
not diseased tested positive = 0.
not diseased tested negative = 0.
number diseased = 0
for i in index:
  if (diseased[i] == 1 and test result[i] == 1):
          diseased tested positive += 1
  if (diseased[i] == 1 and test result[i] == 0):
          diseased tested negative += 1
  if (diseased[i] == 0 and test result[i] == 1):
          not diseased tested positive += 1
  if (diseased[i] == 0 and test result[i] == 0):
          not diseased tested negative += 1
```

```
#now, given a positive test result, what's the probability you're diseased
probability diseased given positive test =
diseased tested positive/(diseased tested positive +
not diseased tested positive)*100.
probability not diseased given positive test =
not diseased_tested_positive/(not_diseased_tested_positive+diseased_tested_positi
ve)*100.
print "Probability of being diseased given a positive test:
"+str(probability diseased given positive test)+'%'
print "Probability of not being diseased given a positive test:
"+str(probability not_diseased_given_positive_test)+'%'
```

Disease Simulation: Results

False Positive Rate	False Negative Rate	P(sick +)	P(okay +)
20%	5%	35%	65%
10%	5%	50%	50%
1%	5%	92%	8%
0.1%	5%	99%	1%

Probability of being diseased and getting a positive test result.

Probability of being okay and getting a positive test result.

Exercise #1

 Download the code: epidemiology.py from the class Moodle site.

 Modify the program to print out the probability of being sick given a negative test result.

A quick quiz:

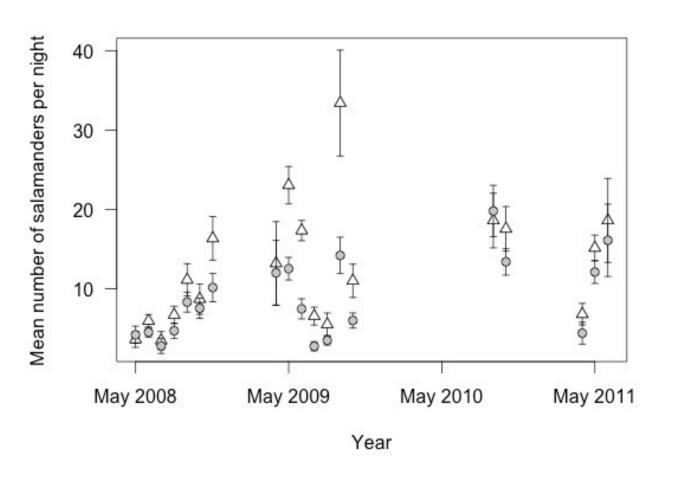
1. What type of number does adding a float and an integer yield?

A quick quiz:

- 1. What type of number does adding a float and an integer yield?
- 2. What type of number does adding a finite and an infinite number yield?

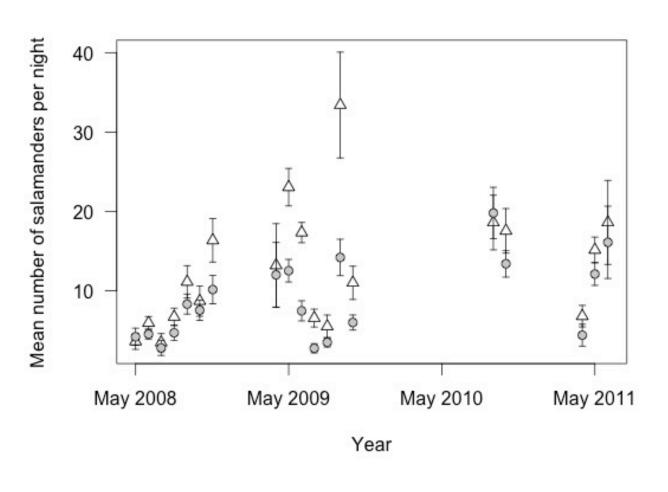
A quick quiz:

- 1. What type of number does adding a float and an integer yield?
- 2. What type of number does adding a finite and an infinite number yield?
- 3. What type of number does adding a random deviate and a "normal" number yield?



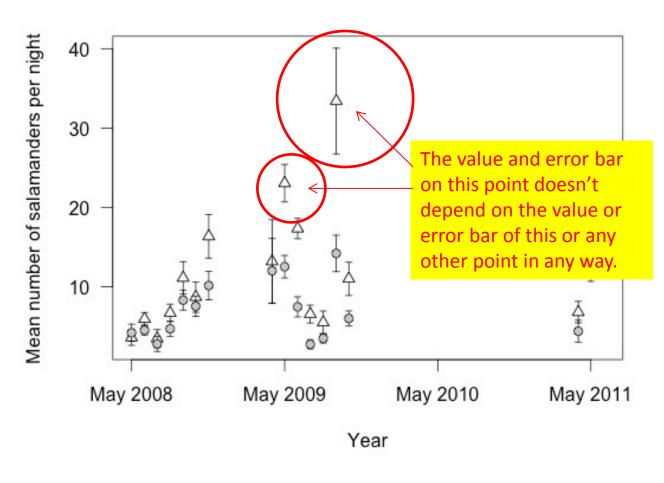
We've all seen plots like this before.

What does it mean to have an error bar?



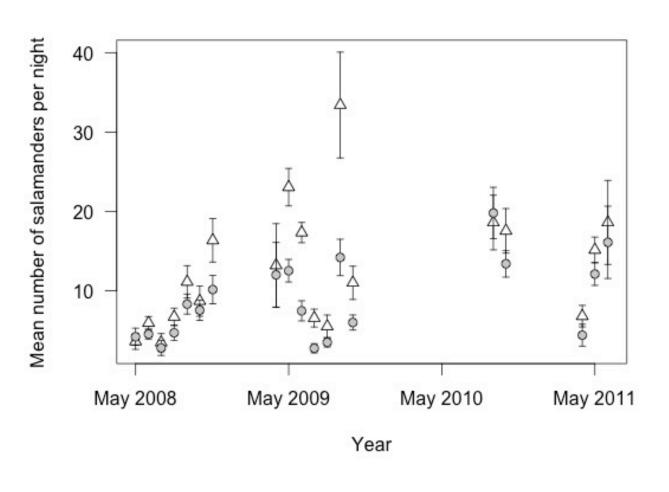
Key assumptions when looking at a plot like this:

- 1. The points are independent.
- 2. The errors are normally distributed.
- 3. The error bars are 1-sigma errors.



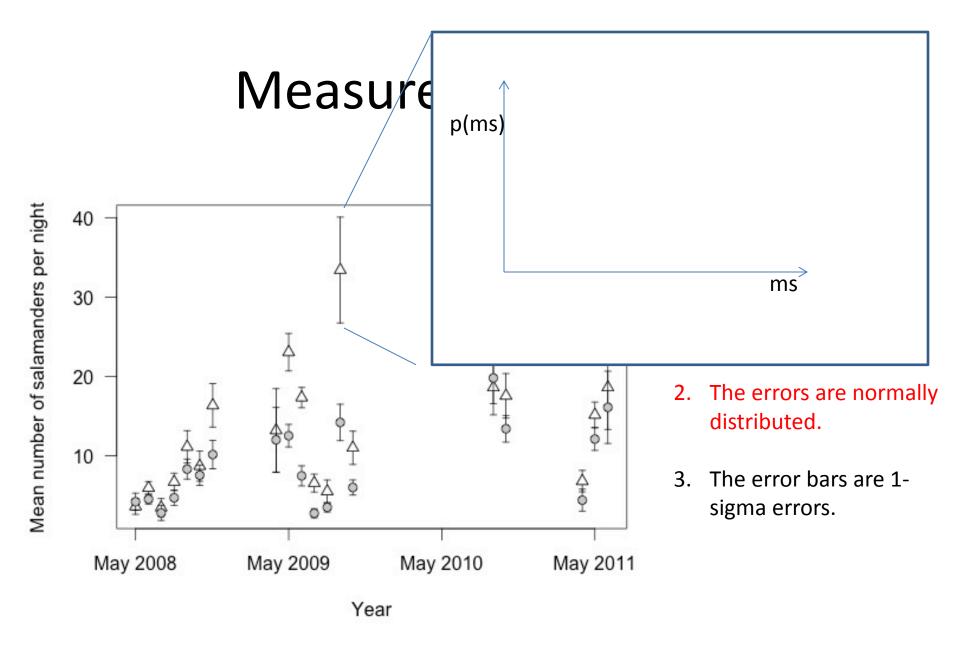
Key assumptions when looking at a plot like this:

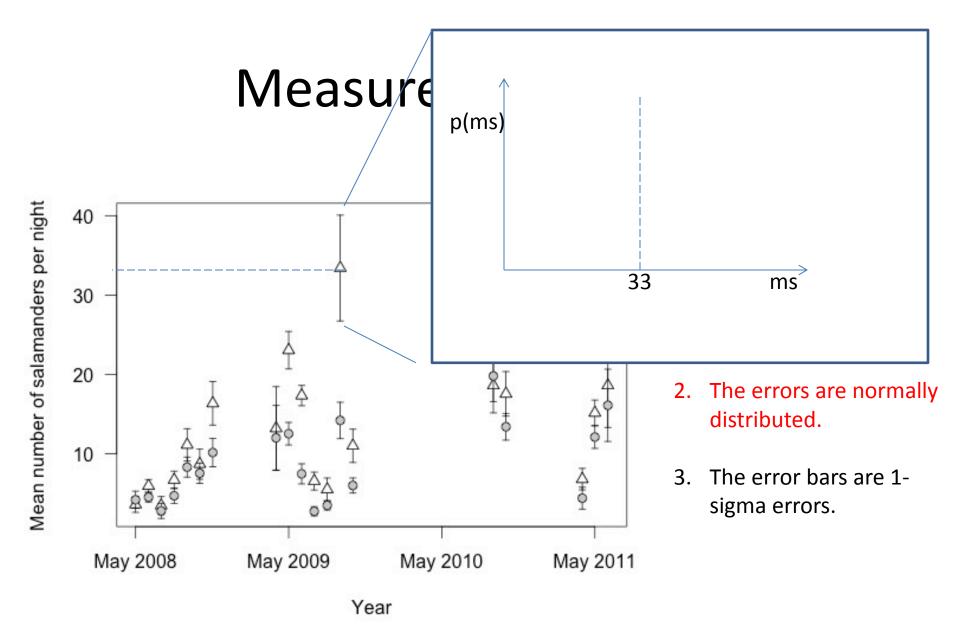
- 1. The points are independent.
- 2. The errors are normally distributed.
- 3. The error bars are 1-sigma errors.

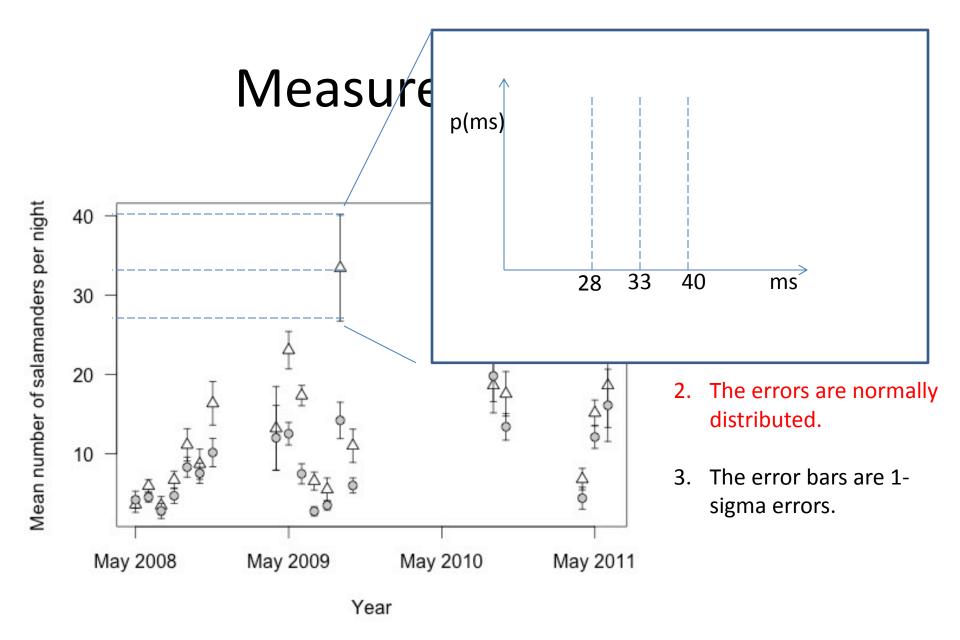


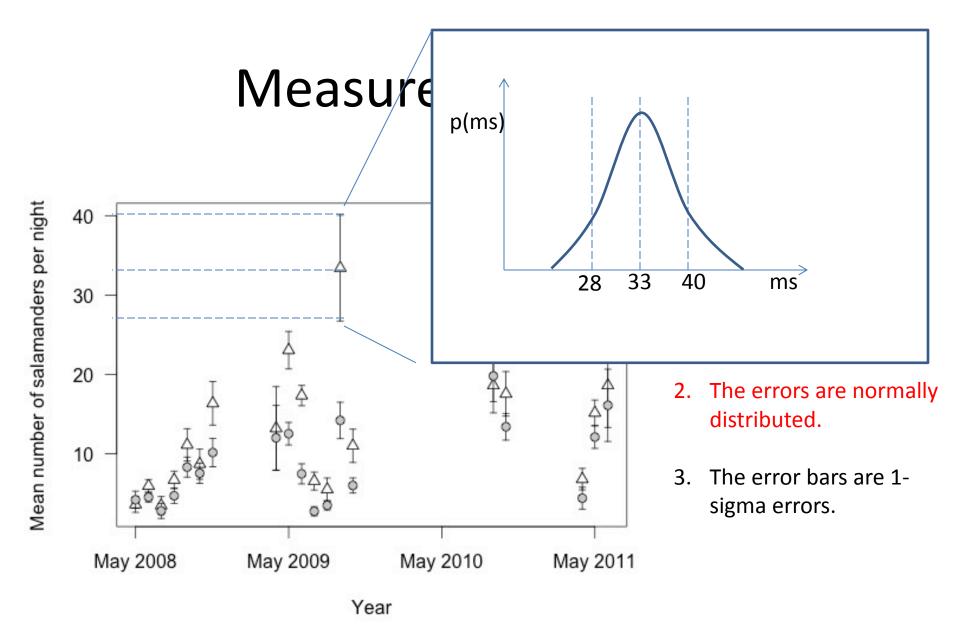
Key assumptions when looking at a plot like this:

- 1. The points are independent.
- 2. The errors are normally distributed.
- 3. The error bars are 1-sigma errors.







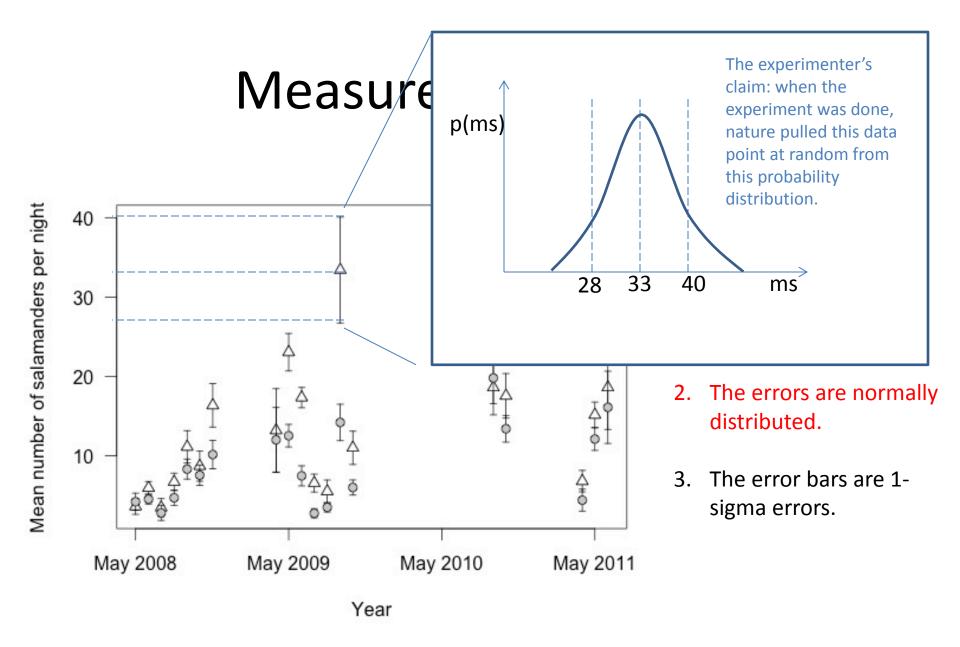


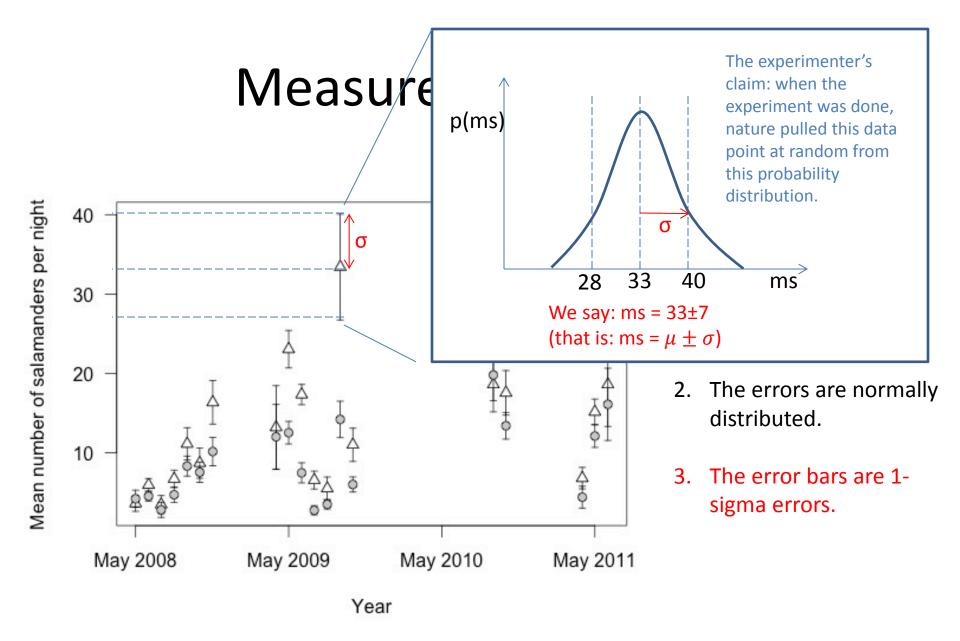
Aside: Why a Normal Distribution?

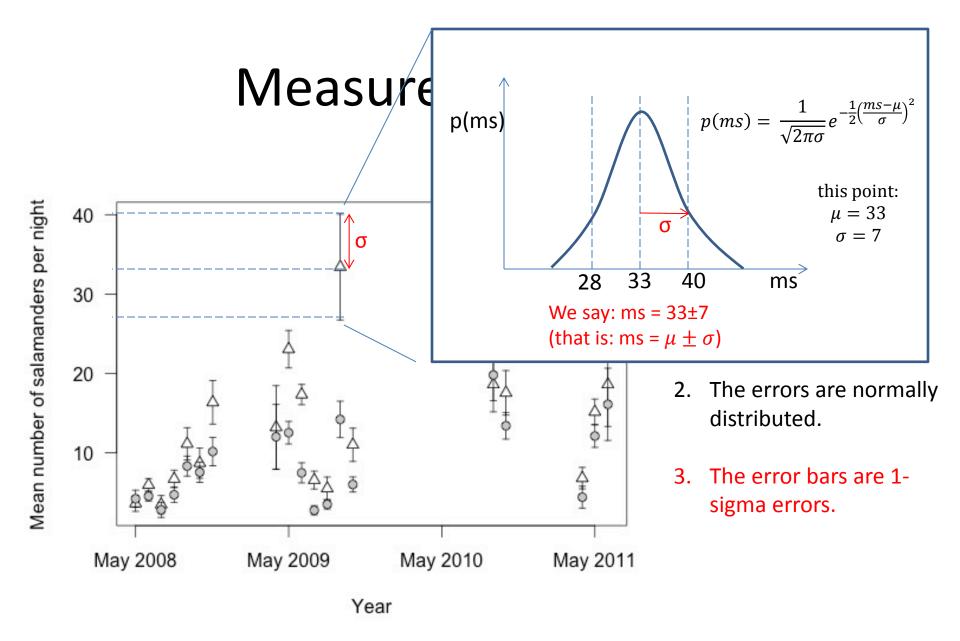
Answer: because of the Central Limit Theorem.

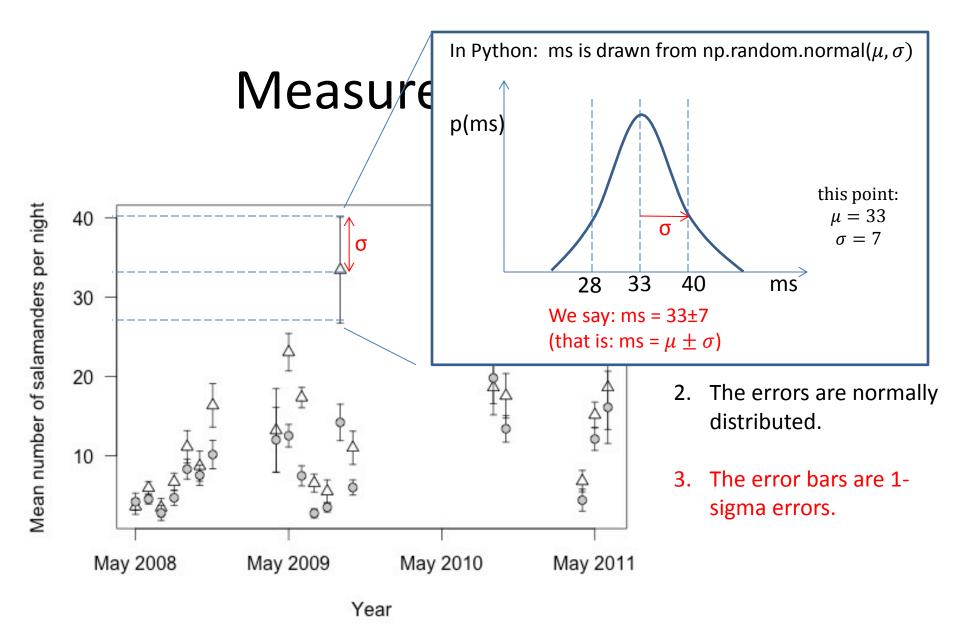
Central limit theorem: The distribution of an average tends to be Normal, even when the distribution from which the average is computed is decidedly non-Normal.

Connection to data and errors: Data points are *typically* made up of the average of many competing random processes. As a result, the central limit theorem states that the underlying probability distribution of each data point is drawn from a Gaussian (normal) distribution.









Connection to Propagation of Uncertainties

 In the discussion in the notes we had the measurement sets [u] and [v] which yielded:

$$-u = \bar{u} \pm \sigma_u$$
; and

$$-v=\bar{v}\pm\sigma_{v}$$

- If, knowing this, we want to draw values from [u] and [v] we can simply do:
 - usim = np.random.normal(\bar{u} , σ_u)
 - vsim = np.random.normal(\bar{v} , σ_v)

Exercise #2

Given measurements of u and v as follows:

$$-u = 10 \pm 4$$

$$-v = 16 \pm 6$$

Use your simulation tools to find the value and error for f(u, v) = u + v.

[Hint: the standard deviation (sigma) of a normally distributed set of data in a numpy array can be found with the array's own std() method. ex, my_gaussian_data.std()]

Simulating propagation of errors

This is enormously powerful.

 Through simulations we can now easily model how errors propagate through incredibly nonlinear systems.

 Of course, the simulations are only as valid as the input assumptions!

Exercise #3

 A student models her data using a standard powerlaw model of the form

$$I(\nu) = A \left(\frac{\nu}{\nu_0}\right)^{\alpha}$$

where $\nu_0 = 10 \pm 3$, $A = 5 \pm 0.5$, $\alpha = 0.9 \pm 0.2$.

What is the value and error of I at $\nu = 5.5$?