Range Expansion of Sea Otters along the California Coast

Stochastic Process Final Project - Brooke Fitzgerald

For my final project I wanted to look at stochastic models and how they are used to describe real world systems. In particular, I wanted to look at models of movement and how you can use randomness and stochasticity to describe the movement of organisms.

When we're talking about modeling organisms, it's important to also talk about the scale at which you're doing so. In general, there are three scales that you can use to describe ecological movement.

The first scale is the microscopic. Modeling ecological systems at the microscopic scale consists of constructing individual trajectories from individual fluctuations. This type of modeling, while it maintains the most amount of detail about the system, it is the most mathematically intensive form of modeling and requires the most amount of input data. A mathematical description of microscopic modeling would be using stochastic differential equations describing the change of each particle and then using stochastic calculus to learn more about them.

The second scale is the mesoscopic. Mesoscopic modeling simplifies microscopic models by representing individual fluctuations as probability density functions. Mesoscopic systems are only really suited for the description of a population of organisms because the probability density functions represent a statistical average of microscopic fluctuations and thus only hold at the population level. A mathematical description of mesoscopic models would be using integral equations to produce probability density functions from averaged fluction of individual trajectories.

The final scale is the macroscopic. As the scales of microscopic and mesoscopic systems reaches an appropriate large limit, both systems converge to the corresponding macroscopic system. Macroscopic systems are the easiest to describe mathematically, as they are modeled with partial differential equations. Any of the information about individual motion is boiled down to the choice of parameters.

For my project I decided to apply different models of ecological movement to the example of otter spread along the coast of California from 1914-1984. In the article

“The Spread of a Reinvading Species: Range Expansion in the California Sea Otter,” authors Lubina and Levin analyzed published and unpublished data to analyze how the otters moved along the coast.

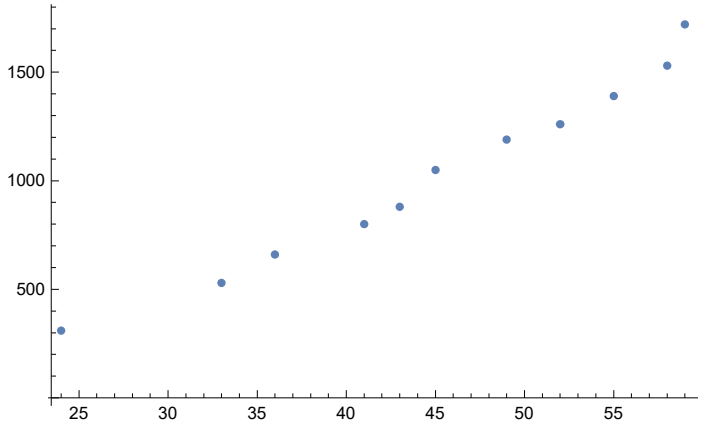
In their article they used various statistical techniques to estimate rates of range expansion, and then used those rates as well as half the rate of change of the mean-squared deviation of individual positions to estimate the diffusion coefficient, which they calculated to be 104 km^2/yr for the entire range.

However, they never actually used the diffusion equation beyond estimating the diffusion coefficient and discussing the implication for future modeling strategies.

I decided to look at two different models and explore their various dynamics. Due to the lack of data on individual trajectories in the paper, I decided to use 2 different macroscopic models in order to explore different ecological scenarios.

```
data = List[{0, 50}, {24, 310}, {33, 530}, {36, 660}, {41, 800}, {43, 880},
   {45, 1050}, {49, 1190}, {52, 1260}, {55, 1390}, {58, 1530}, {59, 1720}];
```

```
ListPlot[data, PlotRange → All]
```



1D General Diffusion Model with Advection

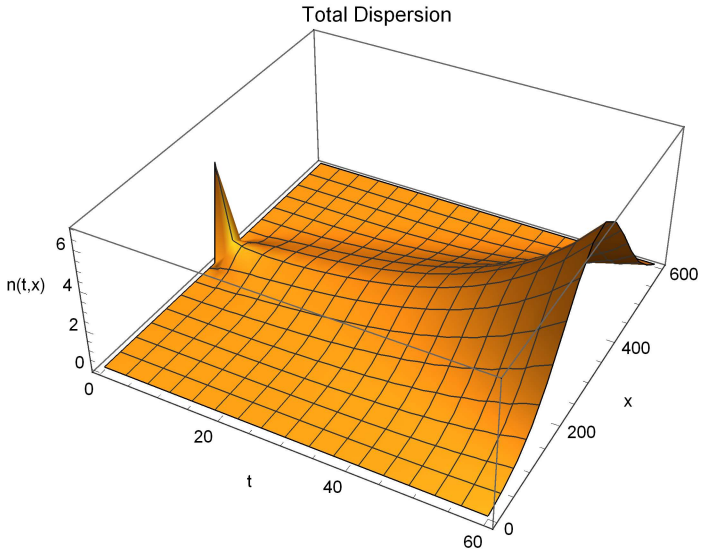
Number density of otter population n(t,x) at time t:

D = coefficient of diffusion, u = advective influence (drift)

$$\frac{\partial n}{\partial t} = f(n, x, t) + D \frac{\partial^2 n}{\partial x^2} - u \frac{\partial n}{\partial x}$$

```
diff = 104;
rloc = .061;
u = 0.5;
```

```
eq = {D[n[x, t], t] == rloc * n[x, t] + diff * D[n[x, t], x, x] - u * D[n[x, t], x],
   n[0, t] == 0, n[600, t] == 0, n[x, 0] == Piecewise[{{5, 295 < x < 305}}, 0]};


Off[NDSolve::mxsst]
sol = NDSolve[eq, n, {t, 0, 60}, {x, 0, 600} ];
Plot3D[Evaluate[n[x, t] /. First[sol]], {t, 0, 60}, {x, 0, 600},
 AxesLabel → {"t", "x", "n(t,x)"}, PlotLabel → "Total Dispersion", PlotRange → All]
```




```
a1 = NIntegrate[Evaluate[n[x, 0] /. First[sol]], {x, 0, 600}];
a2 = NIntegrate[Evaluate[n[x, 24] /. First[sol]], {x, 0, 600}];
a3 = NIntegrate[Evaluate[n[x, 33] /. First[sol]], {x, 0, 600}];
a4 = NIntegrate[Evaluate[n[x, 36] /. First[sol]], {x, 0, 600}];
a5 = NIntegrate[Evaluate[n[x, 41] /. First[sol]], {x, 0, 600}];
a6 = NIntegrate[Evaluate[n[x, 43] /. First[sol]], {x, 0, 600}];
a7 = NIntegrate[Evaluate[n[x, 45] /. First[sol]], {x, 0, 600}];
a8 = NIntegrate[Evaluate[n[x, 49] /. First[sol]], {x, 0, 600}];
a9 = NIntegrate[Evaluate[n[x, 52] /. First[sol]], {x, 0, 600}];
a10 = NIntegrate[Evaluate[n[x, 55] /. First[sol]], {x, 0, 600}];
a11 = NIntegrate[Evaluate[n[x, 58] /. First[sol]], {x, 0, 600}];
a12 = NIntegrate[Evaluate[n[x, 59] /. First[sol]], {x, 0, 600}];
```

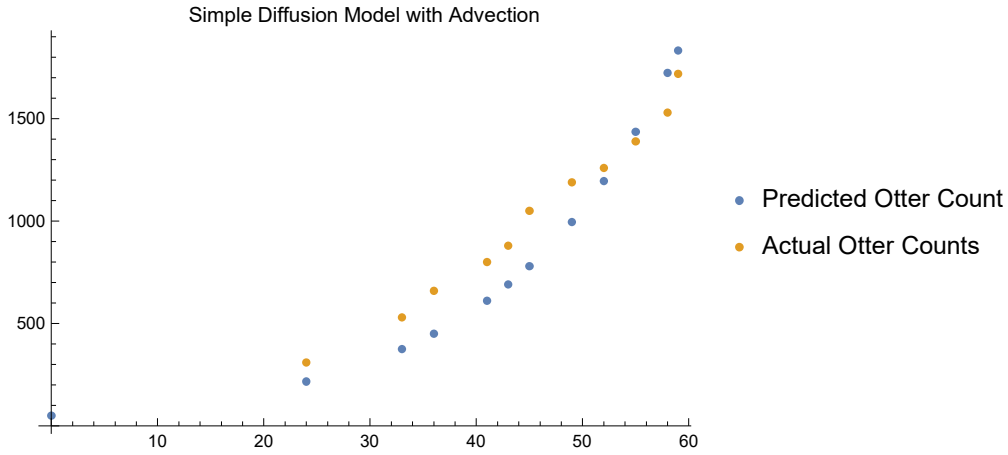
```
diffData = Transpose[{{0, 24, 33, 36, 41, 43, 45, 49, 52, 55, 58, 59},
    {a1, a2, a3, a4, a5, a6, a7, a8, a9, a10, a11, a12}}];
diffData // MatrixForm
```

0	50.4405
24	216.627
33	375.211
36	450.568
41	611.255
43	690.581
45	780.198
49	995.872
52	1195.94
55	1436.23
58	1724.69
59	1833.19

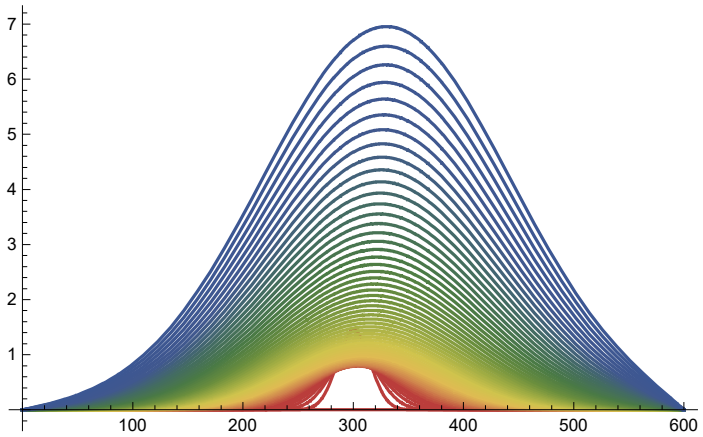
```
diffError = diffData[[All, 2]] - data[[All, 2]];
diffError = Function[x, x^2] /@ diffError;

diffMSE = Mean[diffError]
```

26 290.1

```
ListPlot[{diffData, data}, PlotLegends → {"Predicted Otter Count", "Actual Otter Counts"},
 PlotLabel → "Simple Diffusion Model with Advection"]
```



```
Show[Table[Plot[Evaluate[n[x, tt] /. First[sol] /. t → tt], {x, 0, 600},
   PlotRange → All, PlotStyle → ColorData["DarkRainbow", 1 - tt / 60]], {tt, 0, 60}]]
```




```
FindRoot[Evaluate[n[x, 59] /. First[sol]] == 1, {x, 100}]
FindRoot[Evaluate[n[x, 59] /. First[sol]] == 1, {x, 500}]
```

```
{x → 114.42}
```

```
{x → 541.435}
```

```
diffRange = 541 - 114
diffRangeDiff = (541 - 300) - (300 - 114)
```

```
427
```

```
55
```

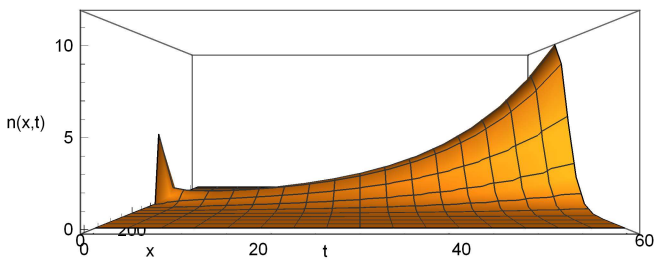
1D Chemotaxis Model with Local Growth

Number density of otter population n(t,x) at time t: $\frac{\partial n}{\partial t} = f(n, x, t) + D \frac{\partial^2 n}{\partial x^2} - \chi \frac{\partial^2 c(x)}{\partial x^2}$, where χ represents the chemical coefficient.

```
chi = .022;
rloc = .061;
```

```
eq = {D[n[x, t], t] == rloc * n[x, t] + diff * D[n[x, t], x, x] + chi * D[(x - 350) * n[x, t], x],
   n[0, t] == 0, n[600, t] == 0, n[x, 0] == Piecewise[{{5, 295 < x < 305}}, 0]};
```

```
sol = NDSolve[eq, n, {t, 0, 60}, {x, 0, 600}];
Plot3D[Evaluate[n[x, t] /. First[sol]], {t, 0, 60},
 {x, 0, 600}, AxesLabel → {"t", "x", "n(x,t)"}, PlotRange → All]
```




```
b1 = NIntegrate[Evaluate[n[x, 0] /. First[sol]], {x, 0, 600}];
b2 = NIntegrate[Evaluate[n[x, 24] /. First[sol]], {x, 0, 600}];
b3 = NIntegrate[Evaluate[n[x, 33] /. First[sol]], {x, 0, 600}];
b4 = NIntegrate[Evaluate[n[x, 36] /. First[sol]], {x, 0, 600}];
b5 = NIntegrate[Evaluate[n[x, 41] /. First[sol]], {x, 0, 600}];
b6 = NIntegrate[Evaluate[n[x, 43] /. First[sol]], {x, 0, 600}];
b7 = NIntegrate[Evaluate[n[x, 45] /. First[sol]], {x, 0, 600}];
b8 = NIntegrate[Evaluate[n[x, 49] /. First[sol]], {x, 0, 600}];
b9 = NIntegrate[Evaluate[n[x, 52] /. First[sol]], {x, 0, 600}];
b10 = NIntegrate[Evaluate[n[x, 55] /. First[sol]], {x, 0, 600}];
b11 = NIntegrate[Evaluate[n[x, 58] /. First[sol]], {x, 0, 600}];
b12 = NIntegrate[Evaluate[n[x, 59] /. First[sol]], {x, 0, 600}];
```

NIntegrate::slwcon : Numerical integration converging too slowly; suspect one of the following: singularity, value of the integration is 0, highly oscillatory integrand, or WorkingPrecision too small. ≫

NIntegrate::ncvb : NIntegrate failed to converge to prescribed accuracy after 9 recursive bisections in x near {x} = {305.85}. NIntegrate obtained 50.440547472039285` and 0.8716380783799866` for the integral and error estimates. ≫

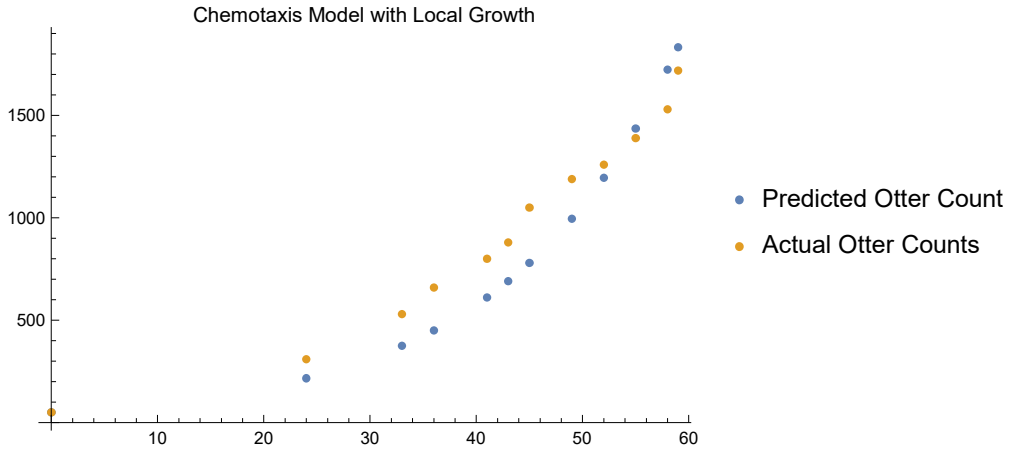
```
chemData = Transpose[{{0, 24, 33, 36, 41, 43, 45, 49, 52, 55, 58, 59},
   {b1, b2, b3, b4, b5, b6, b7, b8, b9, b10, b11, b12}}];
chemData // MatrixForm
```

0	50.4405
24	216.642
33	375.242
36	450.596
41	611.283
43	690.602
45	780.222
49	995.874
52	1195.9
55	1436.08
58	1724.49
59	1832.98

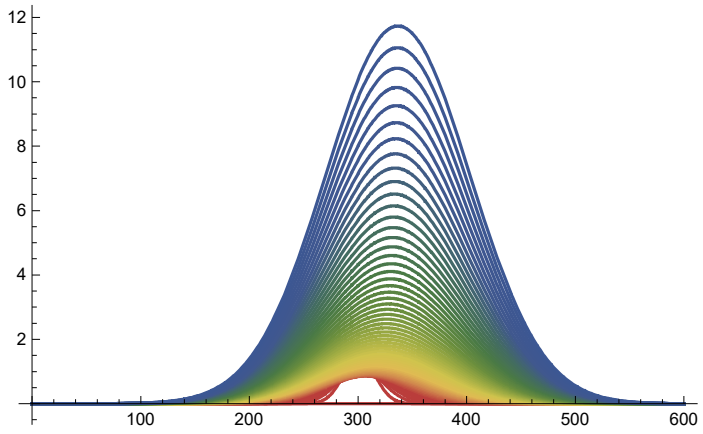
```
chemError = chemData[[All, 2]] - data[[All, 2]];
chemError = Function[x, x^2] /@ chemError;

chemMSE = Mean[chemError]
```

26 274.1

```
26274.07338945004`` × 0.61

ListPlot[{chemData, data}, PlotLegends → {"Predicted Otter Count", "Actual Otter Counts"},
 PlotLabel → "Chemotaxis Model with Local Growth"]
```




```
Show[Table[Plot[Evaluate[n[x, t] /. First[sol] /. t → tt], {x, 0, 600},
    PlotRange → All, PlotStyle → ColorData["DarkRainbow", 1 - tt / 60]], {tt, 0, 60}]]
```




```
FindRoot[Evaluate[n[x, 59] /. First[sol]] == 1, {x, 200}]
FindRoot[Evaluate[n[x, 59] /. First[sol]] == 1, {x, 500}]
```

{x → 191.338}

{x → 481.345}

```
chemRange = (481 - 191)
chemRangeDiff = (481 - 300) - (300 - 191)
```

```
290
```

```
72
```

Conclusions:

As you can see from the graphs above, the diffusion model gives some probability of otters

Thus, it is possible that chemotaxis might play an important role in otter spread.

Sources:

Lubina, John A., and Simon A. Levin. "The spread of a reinvading species: range expansion in the California sea otter." American Natural

Méndez, Vicenç, Daniel Campos, and Frederic Bartumeus. *Stochastic foundations in movement ecology: anomalous diffusion, front propag*