Kalman and Bayesian Filters in Python

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Preface

Version 0.0

Not ready for public consumption. In development.

author's note: The chapter on g-h filters is fairly complete as far as planned content goes. The content for the discrete Bayesian chapter, chapter 2, is also fairly complete. After that I have questions in my mind as to the best way to present the statistics needed to understand the filters. I try to avoid the 'dump a semester of math into 4 pages' approach of most textbooks, but then again perhaps I put things off a bit too long. In any case, the subsequent chapters are due a strong editing cycle where I decide how to best develop these concepts. Otherwise I am pretty happy with the content for the one dimensional and multidimensional Kalman filter chapters. I know the code works, I am using it in real world projects at work, but there are areas where the content about the covariance matrices is pretty bad. The implementation is fine, the description is poor. Sorry. It will be corrected.

Beyond that the chapters are much more in a state of flux. Reader beware. My writing methodology is to just vomit out whatever is in my head, just to get material, and then go back and think through presentation, test code, refine, and so on. Whatever is checked in in these later chapters may be wrong and not ready for your use.

Finally, nothing has been spell checked or proof read yet. I wish IPython Notebook had spell check, but it doesn't seem to.

1.1 Motivation

This is a book for programmers that have a need or interest in Kalman filtering. The motivation for this book came out of my desire for a gentle introduction to Kalman filtering. I'm a software engineer that spent almost two decades in the avionics field, and so I have always been 'bumping elbows' with the Kalman filter, but never implemented one myself. They always has a fearsome reputation for difficulty, and I did not have the requisite education. Everyone I met that did implement them had multiple graduate courses on the topic and extensive industrial experience with them. As I moved into solving tracking problems with computer vision the need to implement them myself became urgent. There are classic textbooks in the field, such as Grewal and Andrew's excellent *Kalman Filtering*. But sitting down and trying to read many of these books is a dismal and trying experience if you do not

have the background. Typically the first few chapters fly through several years of undergraduate math, blithely referring you to textbooks on, for example, Itō calculus, and presenting an entire semester's worth of statistics in a few brief paragraphs. These books are good textbooks for an upper undergraduate course, and an invaluable reference to researchers and professionals, but the going is truly difficult for the more casual reader. Symbology is introduced without explanation, different texts use different words and variables names for the same concept, and the books are almost devoid of examples or worked problems. I often found myself able to parse the words and comprehend the mathematics of a definition, but had no idea as to what real world phenomena these words and math were attempting to describe. "But what does that *mean?*" was my repeated thought.

However, as I began to finally understand the Kalman filter I realized the underlying concepts are quite straightforward. A few simple probability rules, some intuition about how we integrate disparate knowledge to explain events in our everyday life and the core concepts of the Kalman filter are accessible. Kalman filters have a reputation for difficulty, but shorn of much of the formal terminology the beauty of the subject and of their math became clear to me, and I fell in love with the topic.

As I began to understand the math and theory more difficulties itself. A book or paper's author makes some statement of fact and presents a graph as proof. Unfortunately, why the statement is true is not clear to me, nor is the method by which you might make that plot obvious. Or maybe I wonder "is this true if R=0?" Or the author provides pseudocode - at such a high level that the implementation is not obvious. Some books offer Matlab code, but I do not have a license to that expensive package. Finally, many books end each chapter with many useful exercises. Exercises which you need to understand if you want to implement Kalman filters for yourself, but exercises with no answers. If you are using the book in a classroom, perhaps this is okay, but it is terrible for the independent reader. I loathe that an author withholds information from me, presumably to avoid 'cheating' by the student in the classroom.

None of this necessary, from my point of view. Certainly if you are designing a Kalman filter for a aircraft or missile you must thoroughly master of all of the mathematics and topics in a typical Kalman filter textbook. I just want to track an image on a screen, or write some code for my Arduino project. I want to know how the plots in the book are made, and chose different parameters than the author chose. I want to run simulations. I want to inject more noise in the signal and see how a filter performs. There are thousands of opportunities for using Kalman filters in everyday code, and yet this fairly straightforward topic is the provenance of rocket scientists and academics.

I wrote this book to address all of those needs. This is not the book for you if you program avionics for Boeing or design radars for Ratheon. Go get a degree at Georgia Tech, UW, or the like, because you'll need it. This book is for the hobbyist, the curious, and the working engineer that needs to filter or smooth data.

This book is interactive. While you can read it online as static content, I urge you to use it as intended. It is written using IPython Notebook, which allows me to combine text, python, and python output in one place. Every plot, every piece of data in this book is generated from Python that is available to you right inside the notebook. Want to double the value of a parameter? Click on the Python cell, change the parameter's value, and click 'Run'. A new plot or printed output will appear in the book.

This book has exercises, but it also has the answers. I trust you. If you just need an answer, go ahead and read the answer. If you want to internalize this knowledge, try to implement the exercise before you read the answer.

This book has supporting libraries for computing statistics, plotting various things related to filters, and for the various filters that we cover. This does require a strong caveat; most of the code is written for didactic purposes. It is rare that I chose the most efficient solution (which often obscures the intent of the code), and in the first parts of the book I did not concern myself with numerical stability. This is important to understand - Kalman filters in aircraft are carefully designed and implemented to be numerically stable; the naive implementation is not stable in many cases. If you are serious about Kalman filters this book will not be the last book you need. My intention is to introduce you to the concepts and mathematics, and to get you to the point where the textbooks are approachable.

Finally, this book is free. The cost for the books required to learn Kalman filtering is somewhat prohibitive even for a Silicon Valley engineer like myself; I cannot believe the are within the reach of someone in a depressed economy, or a financially struggling student. I have gained so much from free software like Python, and free books like those from Allen B. Downey here. It's time to repay that. So, the book is free, it is hosted on free servers, and it uses only free and open software such as IPython and mathjax to create the book.

1.2 Reading the book

There are multiple ways to read this book. However, it is intended to be interactive and I recommend using it in that form. If you install IPython on your computer and then clone this book you will be able to run all of the code in the book yourself. You can perform experiments, see how filters react to different data, see how different filters react to the same data, and so on. I find this sort of immediate feedback both vital and invigorating. You do not have to wonder "what happens if". Try it and see!

If you do not want to do that you can read this book online. the website http://nbviewer.org provides an IPython Notebook server that renders a notebook stored at github (or elsewhere). The rendering is done in real time when you load the book. If you read my book today, and then I make a change tomorrow, when you go back tomorrow you will see that change.

You may access this book via nbviewer at any by using this address:

http://nbviewer.ipython.org/github/rlabbe/Kalman-and-Bayesian-Filters-in-Python/blob/master/Preface.ipynb

If you prefer a PDF, it is available here. I have to generate this PDF manually from the IPython Notebook, and I do not do that for every check in. During the book's development this PDF will often be somewhat out of date. I recommend the nbviewer version above if you can be online while reading.

Finally, you may generate output in a variety of formats. I will not cover how to do that, other than to point you to IPython nbconvert[2]. You can convert this book into static HTML pages, latex, or PDF. While I don't recommend it particularly, it is useful for those that don't want to program and/or are working offline.

1.3 Installation and Software Requirements

If you want to run the notebook on your computer, which is what I recommend, then you will have to have IPython installed. I do not cover how to do that in this book; requirements change based on what other python installations you may have, whether you use a third party package like Anaconda Python, what operating system you are using, and so on.

To use all features you will have to have IPython 2.0 installed, which is released and stable as of April 2014. Most of the book does not require that, but I do make use of the interactive plotting widgets introduced in this release. A few cells will not run if you have an older version installed.

You will need Python 2.7 or later installed. Almost all of my work is done in Python 2.7, but I periodically test on 3.3. I do not promise any specific check in will work in 3.X, however. I do use Python's "from **future** import ..." statement to help with compatibility. For example, all prints need to use parenthesis. If you try to add, say, "print 3.14" into the book your script will fail; you must write "print (3.4)" as in Python 3.X.

You will need a recent version of NumPy, SciPy, and Matplotlib installed. I don't really know what the minimal might be. I have numpy 1.71, SciPy 0.13.0, and Matplotlib 1.3.1 installed on my machines.

Personally, I use the Anaconda Python distribution in all of my work, available here[3]. I am not selecting them out of favoritism, I am merely documenting my environment. Should you have trouble running any of the code, perhaps knowing this will help you.

1.4 Provided Libraries

update: I have created the filterpy project, into which I am slowly moving a lot of this code. Some of the chapters use this project, some do not (yet). It is at https://github.com/rlabbe/filterpy For the time being this book is it's documentation; I cannot spend a lot of time working on the documentation for that library when I am writing this book.

I've not structured anything nicely yet. For now just look for any .py files in the base directory. As I pull everything together I will turn this into a python library, and probably create a separate git project just for the python code.

There are python files with a name like *xxx*_internal.py. I use these to store functions that are useful for the book, but not of general interest. Often the Python is the point and focus of what I am talking about, but sometimes I just want to display a chart. IPython Notebook does not allow you to collapse the python code, and so it sometimes gets in the way. Some IPython books just incorporate .png files for the image, but I want to ensure that everything is open - if you want to look at the code you can.

Some chapters introduce functions that are useful for the rest of the book. Those functions are initially defined within the Notebook itself, but the code is also stored in a Python file that is imported if needed in later chapters. I do document when I do this where the function is first defined. But this is still a work in progress.

1.5 License

1.6 Contact

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1.7 Resources

[1] http://www.greenteapress.com/ [2] http://ipython.org/ipython-doc/rel-1.0.0/interactive/nbconvert.html [3] https://store.continuum.io/cshop/anaconda/

Chapter 2

The g-h Filter

2.1 Building Intuition via Thought Experiments

Imagine that we live in a world without scales - the devices you stand on to weigh yourself. One day at work a coworker comes running up to you and announces her invention of a 'scale' to you. After she explains, you eagerly stand on it and announce the results: "172 lbs". You are ecstatic - for the first time in your life you know what you weigh. More importantly, dollar signs dance in your eyes as you imagine selling this device to weight loss clinics across the world! This is fantastic!

Another coworker hears the commotion and comes over to find out what has you so excited. You explain the invention and once again step onto the scale, and proudly proclaim the result: "161 lbs." And then you hesitate, confused.

"It read 172 lbs just a few seconds ago" you complain to your coworker.

"I never said it was accurate," she replies.

Sensors are inaccurate. This is the motivation behind a huge body of work in filtering, and solving this problem is the topic of this book. I could just provide the solutions that have been developed over the last half century, but these solutions developed by asking very basic, fundamental questions into the nature of what we know and how we know it. Before we attempt the math, let's follow that journey of discovery, and see if it does not inform our intuition about filtering.

Try Another Scale Is there any way we can improve upon this result? The obvious, first thing to try is get a better sensor. Unfortunately, your co-worker informs you that she has built 10 scales, and they all operate with about the same accuracy. You have her bring out another scale, and you weigh yourself on one, and then on the other. The first scale (A) reads "160 lbs", and the second (B) reads "170 lbs". What can we conclude about your weight?

Well, what are our choices?

- We could choose to only believe A, and assign 160lbs to our weight estimate.
- we could choose to only believe B, and assign 170lbs to our weight.
- We could choose a number less than either A or B
- We could choose a number greater than either A or B

- We could choose a number between A and B

The first two choices are plausible, but we have no reason to favor one scale over the other. Why would we choose to believe A more than B? We have no reason for such a belief. The third and fourth choices are irrational. The scales are admittedly not very accurate, but there is no reason at all to choose a number outside of the range of what they measure. The final choice is the only reasonable one. If both scales are inaccurate, and as likely to give a result above my actual weight as below it, more often than not probably the answer is somewhere between A and B.

In mathematics this concept is formalized as *expected value*, and we will cover it in depth later. For now ask yourself what would be the 'usual' thing to happen if we made one million separate readings. Some of the times both scales will read too low, sometimes that will both read too high, and the rest of the time they will straddle the actual weight. If they straddle the actual weight then certainly we should choose a number between A and B. If they don't straddle then we don't know if they are both too high or low, but by choosing a number between A and B we at least mitigate the effect of the worst measurement. For example, suppose our actual weight is 180 lbs. 160 lbs is a big error. But if we choose a weight between 160 lbs and 170 lbs our estimate will be better than 160 lbs. The same argument holds if both scales returned a value greater than the actual weight.

We will deal with this more formally later, but for now I hope it is clear that our best estimate is just the average of A and B. $\frac{160+170}{2} = 165$.

Let's play 'what if' some more. What if we are now told that A is three times more accurate than B? Consider the 5 options we listed above. It still makes no sense to choose a number outside the range of A and B, so we will not consider those. It perhaps seems more compelling to choose A as our estimate - after all, we know it is more accurate, why not just use it instead of B? Can B possibly improve our knowledge over A alone?

The answer, perhaps counter intuitively, is yes, it can. Consider this case. We know scale A is accurate to 1 lb. In other words, if we weight 170 lbs, it could report 169, 170, or 171 lbs. We know that scale B is accurate to 9 lbs. We do a reading, and A=160, and B=170. What should we estimate our weight to be?

Well, if we say 160 lbs we would be wrong, because B can only be 9 pounds off, and 170 lbs - 160 lbs is 10 lbs. 160 is not a possible measurement for B. In fact, the only number that satisfies all of the constraints is 161 lbs. That is 1 lb within the reading of A, and 9 lbs within the reading of B.

This is an important result. With two relatively inaccurate sensors we were able to deduce an extremely accurate result. Now sure, that was a specially constructed case, but it generalizes. What if A is accurate to 3 lbs, B is accurate to 11 lbs, and we get the measurements of A=160 lbs and B=170 lbs? The result can only be from 159 lbs to 163 lbs, which is better than the range of 157 lbs to 163 lbs that is the range of values that A alone allows.

So two sensors, even if one is less accurate than the other, is better than one.

However, we have strayed from our problem. No customer is going to want to buy multiple scales, and besides, we initially started with an assumption that all scales were equally (in)accurate.

So, what if I have one scale, but I weigh myself many times? We concluded that if we had two scales of equal accuracy we should average the results of their measurements. What if I weigh myself 1,000,000 times with one scale? We have already stated that the scale is equally likely to return a number too large as it is to return one that is too small. I will not prove it, but it can be proved that the average of a large number of weighings will be extremely close to my actual weight. Consider a simple case - the scale is accurate to within 1 lb. If I weigh 170, it will return one of either 169, 170, or 171. The average of a bunch of 170 is 170, so we can exclude those. What is left is measurements of 169 and 171. But we know there will be as many 169s as there are 171s. The average of those will also be 170, and so the average of all must be 170, my true weight. It's not that hard to extend this to any arbitrary accuracy.

Okay, great, we have an answer! But it is not a very good answer. No one has the patience to weigh themselves a million, or even a hundred times.

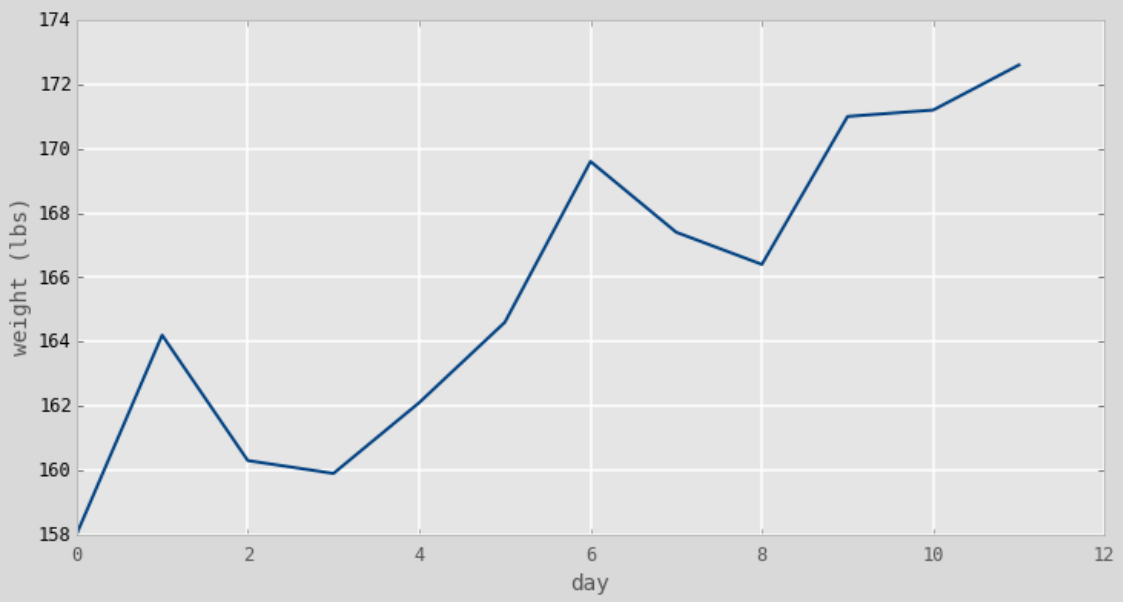
So, let's play 'what if' again. What if you measured your weight once a day, and got the readings 170, 161, and then 169. Did you gain weight, lose weight, or is this all just noisy measurements?

We really can't say. The first measurement was 170, and the last was 169, implying a 1 lb loss. But if the scale is only accurate to 10 lbs, that is explainable by noise - bad measurements. I could have actually gained weight; maybe my weight on day one was 165 lbs, and on day three it was 172. It is possible to get those weight readings with that weight gain. My scale tells me I am losing weight, and I am actually gaining weight!

Shall we give up? No, let's play 'what if'. Suppose I take a different scale, and I get the following measurements: 169, 170, 169, 171, 170, 171, 169, 170, 169, 170. What does your intuition tell you? It is possible, for example, that you gained 1 lb each day, and the noisy measurements just happens to look like you stayed the same weight. Equally, you could have lost 1 lb a day and gotten the same readings. But is that likely? How likely is it to flip a coin and get 10 heads in a row? Not very likely. We can't prove it, but it seems pretty likely that my weight held steady.

Another what if: what if the readings were 158.0, 164.2, 160.3, 159.9, 162.1, 164.6, 169.6, 167.4, 166.4, 171.0? Let's look at a chart of that and then answer some questions.

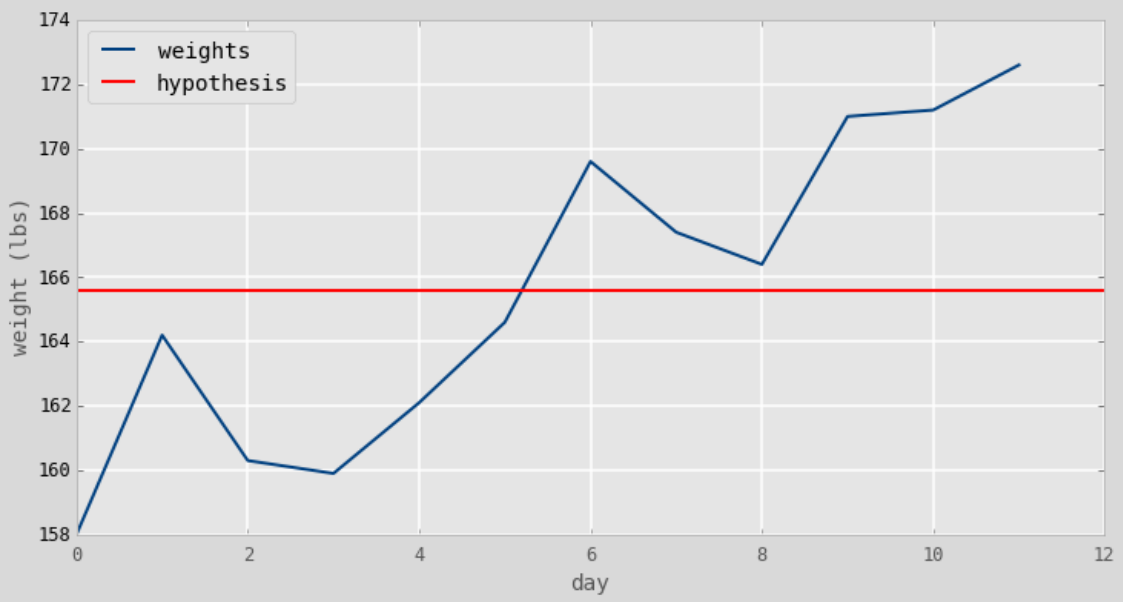
```
In [2]: weights = [158.0, 164.2, 160.3, 159.9, 162.1, 164.6,
                  169.6, 167.4, 166.4, 171.0, 171.2, 172.6]
        plt.plot(weights)
        plt.xlabel('day')
        plt.ylabel('weight (lbs)')
        plt.show()
```



Does it 'seem' likely that I lost weight and this is just really noisy data? Not really. Does it seem likely that I held the same weight? Again, no. This data trends upwards over time; not evenly, but definitely upwards. Lets look at that in a chart. We can't be sure, but that surely looks like a weight gain, and a significant weight gain at that. Let's test this assumption with some more plots. It is often easier to 'eyeball' data in a chart versus a table.

So let's look at two hypotheses. First, let's assume our weight did not change. To get that number we agreed that we should just average all the measurements. Let's look at that.

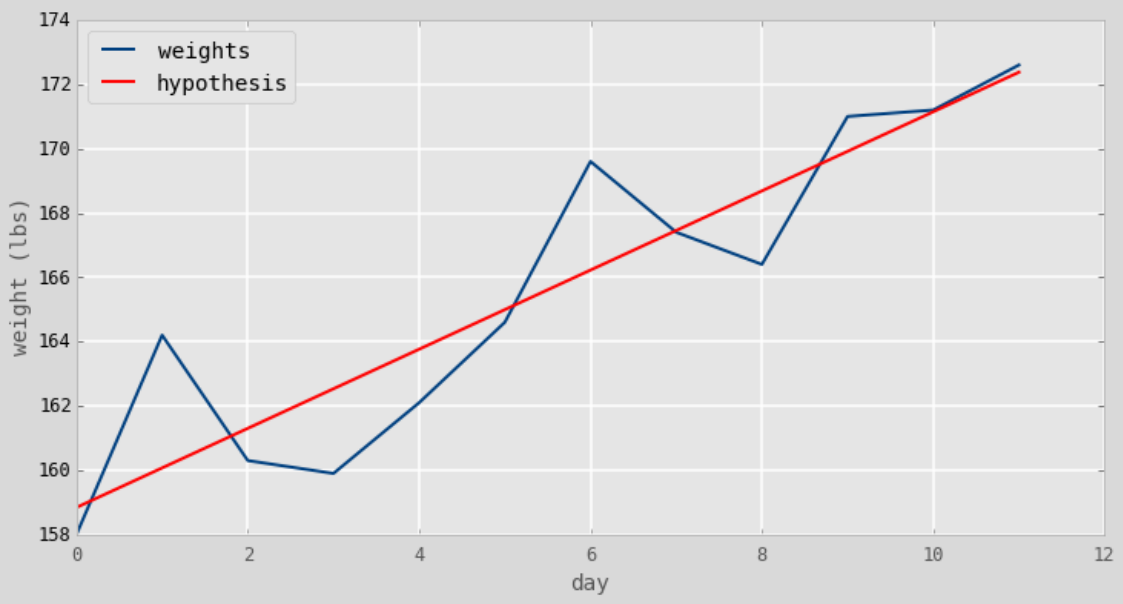
```
In [3]: import numpy as np
        ave = np.sum(weights) / len(weights)
        plt.plot(weights,label='weights')
        plt.plot([0,12], [ave,ave], c='r', label='hypothesis')
        plt.xlabel('day')
        plt.ylabel('weight (lbs)')
        plt.legend(loc='best')
        plt.show()
```



That doesn't look very convincing.

Now, let's assume we we gained weight. How much? I don't know, but numpy does! We just want to draw a line through the measurements that looks 'about' right. numpy has functions that will do this according to a rule called "least squares fit". Let's not worry about the details of that computation, or why we are writing our own filter if numpy provides one, and just plot the results.

```
In [4]: xs = range(len(weights))
        line = np.poly1d(np.polyfit(xs, weights, 1))
        plt.plot(weights, label='weights')
        plt.plot (xs, line(xs), c='r', label='hypothesis')
        plt.xlabel('day')
        plt.ylabel('weight (lbs)')
        plt.legend(loc='best')
        plt.show()
```



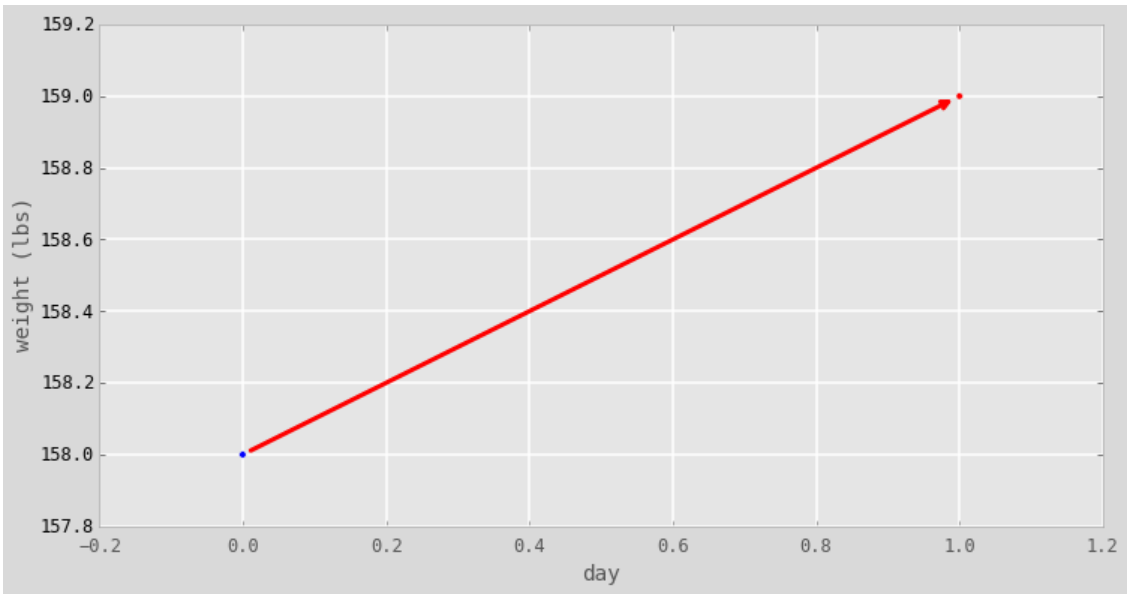
This looks much better, at least to my eyes. It seems far more likely to be true that I gained weight than I didn't gain any weight. Did I actually gain 13 lbs? Who can say? That seems impossible to answer.

"But is it impossible?" pipes up a coworker.

Let's try something crazy. Let's just assume that I know I am gaining about one lb a day. It doesn't matter how I know that right now, just assume I know it somehow. Maybe I am eating a 6000 calorie a day diet, which would result in such a weight gain. Or maybe there is another way to estimate the weight gain. Let's just see if we can make use of such information if it was available.

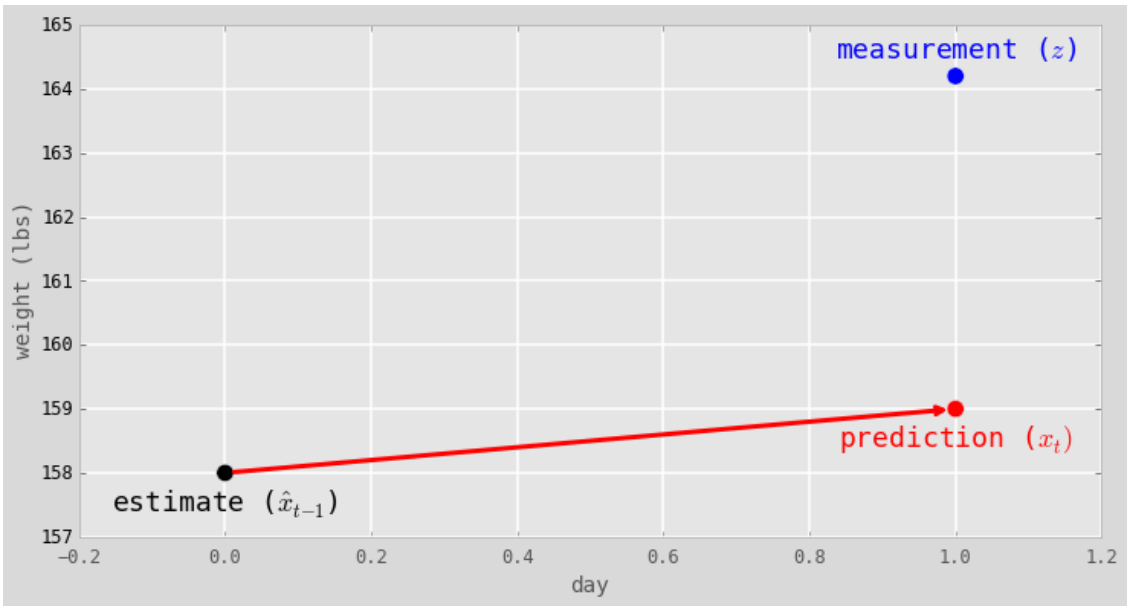
The first measurement was 158. We have no way of knowing any different, so let's just accept that as our estimate. If our weight today is 158, what will it be tomorrow? Well, we think we are gaining weight at 1 lb/day, so our prediction is 159, like so:

```
In [5]: # a lot of the plotting code is not particularly useful to read, so for each c
        # I have placed the uninteresting code in a file named xxx_internal. I import
        # file and call whatever function I need.
        import gh_internal
        gh_internal.plot_estimate_chart_1()
```



Okay, but what good is this? Sure, we could just assume the 1 lb/day is accurate, and just predict our weight for 10 days, but then why use a scale at all if we don't incorporate its readings? So let's look at the next measurement. We step on the scale again and it displays 164.2 lbs.

```
In [6]: gh_internal.plot_estimate_chart_2()
```



Here the measurement is in blue, the previous estimate (output of the filter) is black, and the estimate is red. So we have a problem. Our prediction doesn't match our measurement.

But, that is what we expected, right?. If the prediction was always exactly the same as the measurement, it would not be capable of adding any information to the filter.

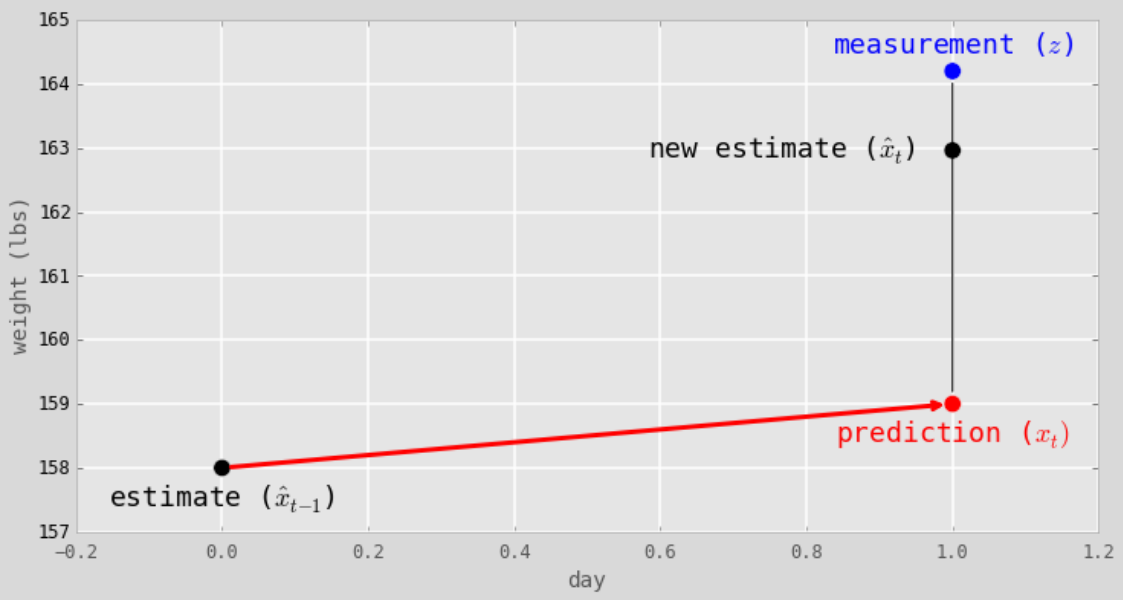
The key insight to this entire book follows. Read it carefully!

So what do we do? If we only take data from the measurement than the prediction will not affect the result. If we only take data from the prediction then the measurement will be ignored. If this is to work we need to take some kind of blend of the prediction and measurement.

Blending two values - this sounds a lot like the two scale problem earlier. Using the same reasoning as before we can see that the only thing that makes sense is to choose a number between the prediction and the measurement. For example, an estimate of 165 makes no sense, nor does 157. Our estimates should like between 159 (the prediction) and 164.2 (the measurement).

Should it be half way? Maybe, but in general it seems like we might know that our prediction is more or less accurate compared to the measurements. Probably the accuracy of our prediction differs from the accuracy of the scale. Recall what we did when A was much more accurate than B - we scaled the answer to be closer to A than B. Let's look at that in a chart.

```
In [7]: gh_internal.plot_estimate_chart_3()
```



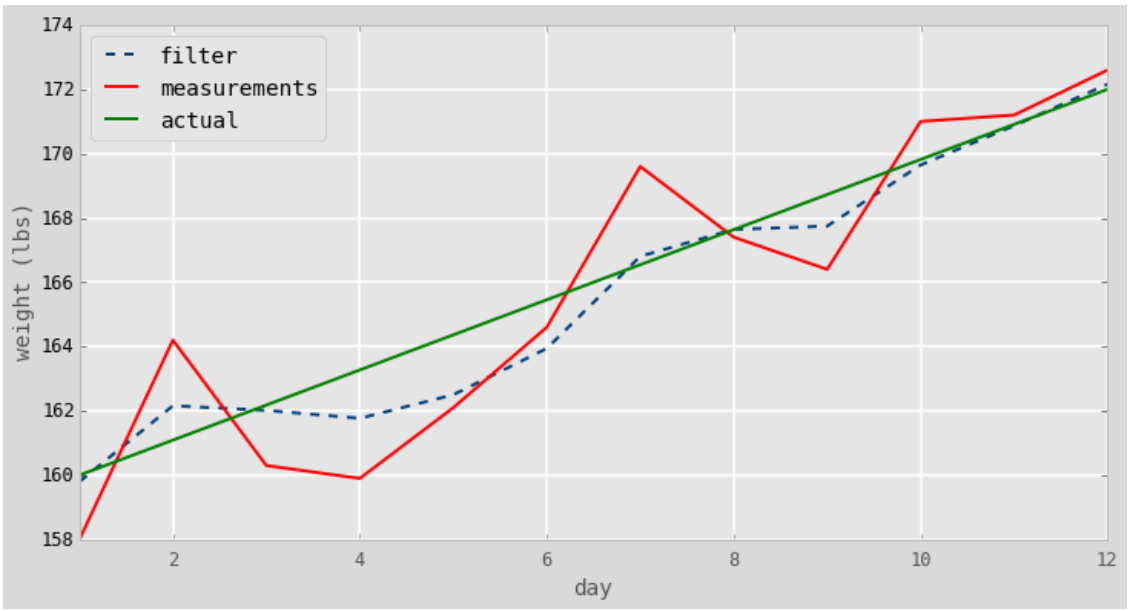
Now let's try a randomly chosen number: $\frac{4}{10}$. Our estimate will be four tenths the measurement and the rest will be from the prediction. In other words, we are expressing a belief here, a belief that the prediction is somewhat more likely to be correct than the measurement. We compute that as

$$\texttt{new estimate} = \texttt{prediction} + \frac{4}{10}(\texttt{measurement} - \texttt{prediction})$$

The difference between the measurement and prediction is called the *residual*, which is depicted by the black vertical line in the plot above. This will become an important value to use later on, as it is an exact computation of the difference between measurements and the filter's output. Smaller residuals imply better performance.

Let's just code that up and see the result when we test it against the series of weights from above.. We have to take into account one other factor. Weight gain has units of lbs/time, so to be general we will need to add a time step t, which we will set to 1 (day).

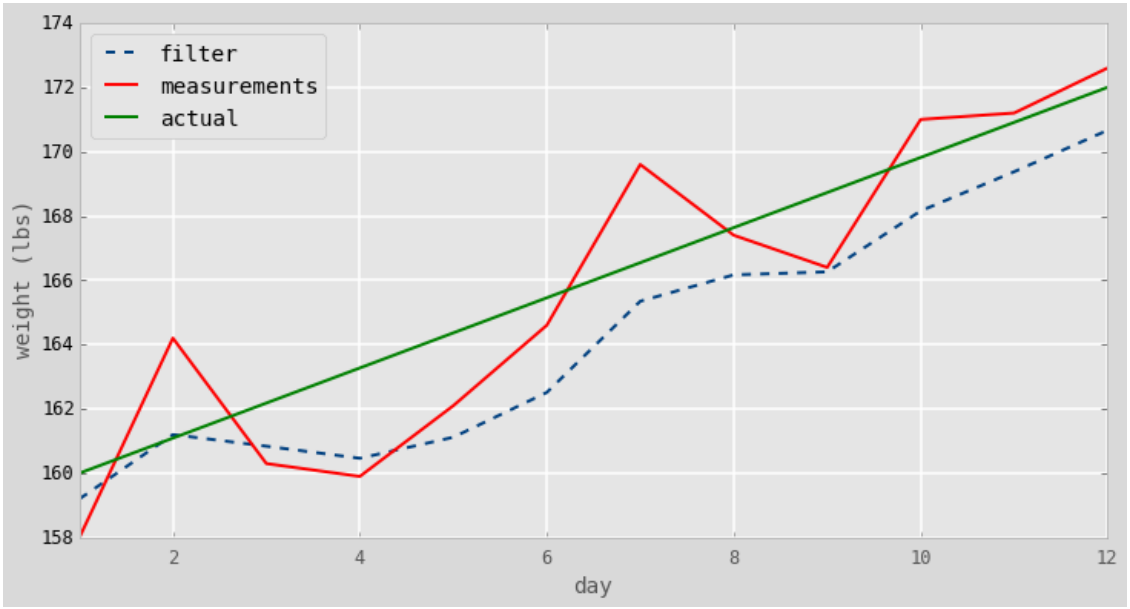
```
In [8]: weights = [158.0, 164.2, 160.3, 159.9, 162.1, 164.6,
                  169.6, 167.4, 166.4, 171.0, 171.2, 172.6]

        time_step = 1 # day
        scale_factor = 4/10

        def predict_using_gain_guess(weight, gain_rate):
            # store the filtered results
            estimates = []

            # most filter literature uses 'z' for measurements
            for z in weights:
                # predict new position
                prediction = weight + gain_rate * time_step

                # update filter
                weight = prediction + scale_factor * (z - prediction)

                # save for plotting
                estimates.append(weight)


            # plot results
            n = len(weights)
            plt.xlim([1, n])

            plt.plot (range(1, n+1), estimates, '--', label='filter')
            plt.plot(range(1, n+1), weights, c='r', label='measurements')
            plt.plot([1, n],[160, 160+n],c='g', label='actual')
            plt.legend(loc=2)
            plt.xlabel('day')
            plt.ylabel('weight (lbs)')
            plt.show()

        predict_using_gain_guess (weight=160, gain_rate=1)
```



That is pretty good! The blue dots, showing our estimates, are not a straight line, but they are straighter than the measurements and somewhat close to the trend line we created. Also, it seems to get better over time.

This may strike you as quite silly; of course the data will look good if we assume the conclusion, that our weight gain is around 1 lb/day! Let's see what the filter does if our initial guess is bad. Let's see what happens if I predict that there is no weight gain.

```
In [9]: predict_using_gain_guess (weight=160, gain_rate=0)
```



Clearly a filter that requires us to correctly guess a rate of change is not very useful. Even if our initial guess was useful, the filter will fail as soon as that rate of change changes. If I stop overeating the filter will have extremely difficulty in adjusting to that change.

But, 'what if'? What if instead of just leaving the weight gain at the initial guess of 1 lb (or whatever), we compute it from the existing measurements and estimates. On day one our estimate for the weight is:

$$(160 + 1) + \frac{4}{10}(158 - 161) = 159.8$$

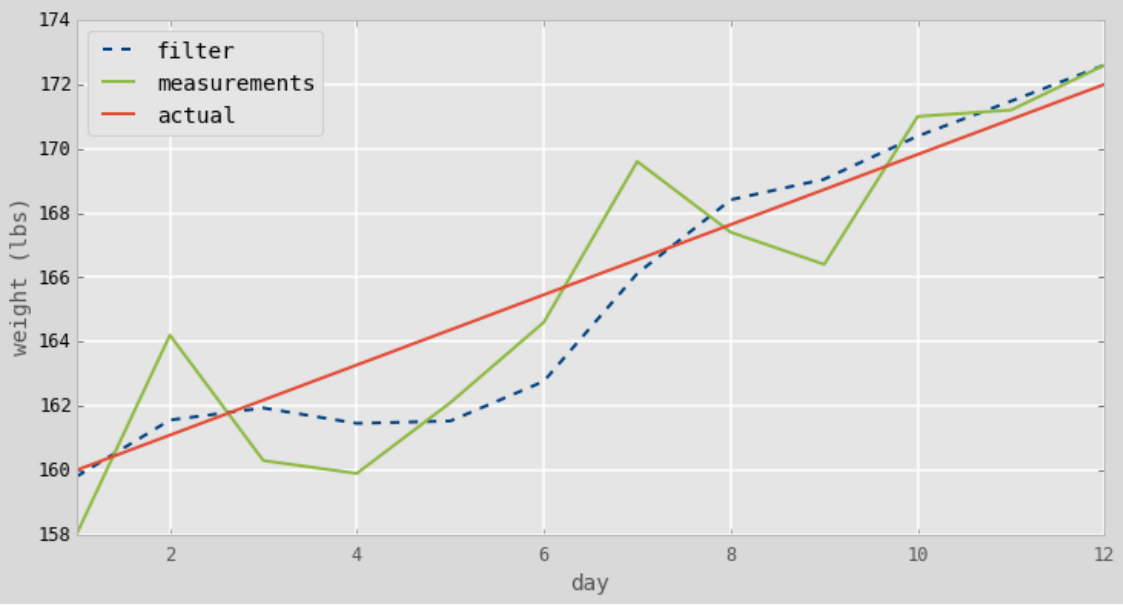
On the next day we measure 164.2, which implies a weight gain of 4.4 lbs (since 164.2 - 159.8 = 4.4), not 1. Can we use this information somehow? It seems plausible. After all, the weight measurement itself is based on a real world measurement of our weight, so there is useful information. Our estimate of our weight gain may not be perfect, but it is surely better than just guessing our gain is 1 lb. Data is better than a guess, even if it is noisy.

So, should we just set the new gain/day to 4.4 lbs? Hmm, sounds like our same problem again. Yesterday we though the weight gain was 1 lb, today we think it is 4.4 lbs. We have two numbers, and want to combine them somehow. Let's use our same tool, and the only tool we have so far - pick a value part way between the two. This time I will use another arbitrarily chosen number, $\frac{1}{3}$. The equation is identical as for the weight estimate except we have to incorporate time because this is a rate (gain/day):

$$\texttt{new gain} = \texttt{old gain} + \frac{1}{3}\frac{\mathit{measurement} - \mathit{predicted\ weight}}{1\ \mathit{day}}$$

```
In [10]: weight = 160  # initial guess
         gain_rate = 1.0 # initial guess

         time_step = 1
         weight_scale = 4/10
         gain_scale = 1/3
         estimates = []

         for z in weights:
             # prediction step
             weight = weight + gain_rate*time_step
             gain_rate = gain_rate

             # update step
             residual = z - weight

             gain_rate = gain_rate + gain_scale   * (residual/time_step)
             weight    = weight    + weight_scale * residual

             estimates.append(weight)

         # plot results
```

```
n = len(weights)
plt.xlim([1, n])

plt.plot (range(1, n+1), estimates, '--', label='filter')
plt.plot(range(1, n+1), weights, label='measurements')
plt.plot([1 ,n], [160,160+n], label='actual')
plt.legend(loc=2)
plt.xlabel('day')
plt.ylabel('weight (lbs)')
plt.show()
```



I think this is starting to look really good. We used no methodology for choosing our scaling factors of $\frac{4}{10}$ and $\frac{1}{3}$ (actually, they are poor choices for this problem), and we 'luckily' choose 1 lb/day as our initial guess for the weight gain, but otherwise all of the reasoning followed from very reasonable assumptions.

One final point before we go on. In the prediction step I wrote the line

```
gain_rate = gain_rate
```

This obviously has no effect, and can be removed. I wrote this to emphasize that in the prediction step you need to predict next value for **all** variables, both *weight* and *gain_rate*. In this case we are assuming that the the gain does not vary, but when we generalize this algorithm we will remove that assumption.

2.2 The g-h Filter

This algorithm is known as the g-h filter. g and h refer to the two scaling factors that we used in our example. g is the scaling we used for the measurement (weight in our example), and h is the scaling for the change in measurement over time (lbs/day in our example).

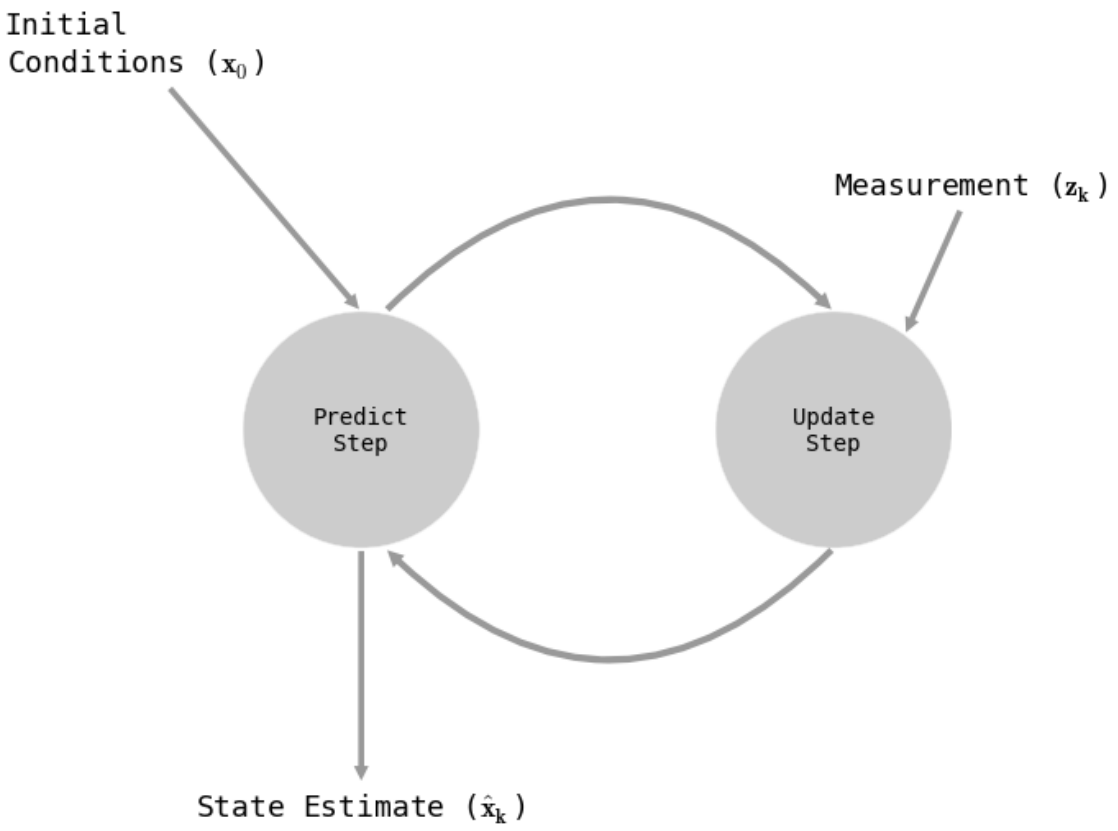
This filter is the basis for a huge number of filters, including the Kalman filter. In other words, the Kalman filter is a form of the g-h filter. So is the Least Squares filter, which you may have heard of, and so is the Benedict-Bordner filter, which you probably have not. Each filter has a different way of assigning values to g and h, but otherwise the algorithms are identical. For example, the α-β filter just assigns a constant to g and h, constrained to a certain range of values. Other filters will vary g and h dynamically, and filters like the Kalman filter will vary them based on the number of dimensions in the problem.

Let me repeat the key insights as they are so important. If you do not understand these you will not understand the rest of the book. If you do understand them, then the rest of the book will unfold naturally for you as mathematically elaborations to various 'what if' questions we will ask about g and h.

- Multiple measurements are more accurate than one measurement
- Always choose a number part way between two measurements to create a more accurate estimate
- Predict the next measurement based on the current estimate and how much we think it will change
- The new estimate is then chosen as part way between the prediction and next measurement

Let's look at a visual depiction of the algorithm.

```
In [11]: gh_internal.create_predict_update_chart()
```



I'll begin to introduce the nomenclature and variable names used in the literature. Measurement is typically denoted z, and that is what we will use in this book (some literature uses y). Subscript k indicates the time step, so $\mathbf{z_k}$ is the data for this time step. A bold font denotes a vector. So far we have only considered having one sensor, and hence one sensor measurement, but in general we may have n sensors and n measurements. $\mathbf{x}$ denotes our data, and is bold to denote that it is a vector. For example, for our scale example, it represents both the initial weight and initial weight gain rate, like so:

$$\mathbf{x} = \begin{bmatrix} x \\ \dot{x} \end{bmatrix}$$

Finally, a hat "$\hat{}$" indicates an *estimate*. So the output of the predict step time k at is the *estimate* of our state $\hat{\mathbf{x}}_\mathbf{k}$, and again this is a vector of all the state variables. So for our scale example it contains the estimate of both the weight and the gain rate.

So, the algorithm is simple. The state is initialized with $\mathbf{x_0}$. We then enter a loop, predicting the state for time k from the values from time $k-1$. We then get the measurement z_k and choose some intermediate point between the measurements and prediction, creating the estimate $\hat{\mathbf{x}}_\mathbf{k}$.

2.3 Exercise: Write Generic Algorithm

In the example above, I explicitly coded this to solve the weighing problem that we've been discussing throughout the chapter. For example, the variables are named "weight_scale", "gain", and so on. I did this to make the algorithm easy to follow - you can easily see that we correctly implemented each step. But, this is specialized code. Rewrite it to work with any data. Use this function signature:

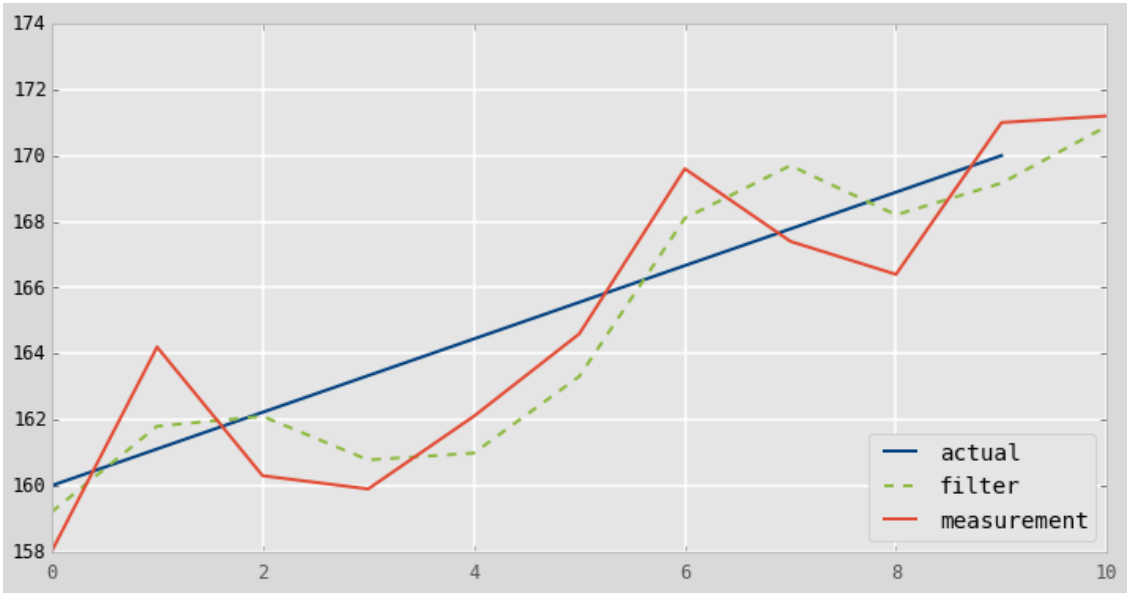
```
def g_h_filter (data, x0, dx, g, h)
    """
    Performs g-h filter on 1 state variable with a fixed g and h.

    'data' contains the data to be filtered.
    'x0' is the initial value for our state variable
    'dx' is the initial change rate for our state variable
    'g' is the g-h's g scale factor
    'h' is the g-h's h scale factor
    'dt' is the length of the time step
    """
```

Test it by passing in the same weight data as before, plot the results, and visually determine that it works.

2.3.1 Solution and Discussion

```
In [12]: def g_h_filter (data, x0, dx, g, h, dt=1., pred=None):
             """
             Performs g-h filter on 1 state variable with a fixed g and h.

             'data' contains the data to be filtered.
             'x0' is the initial value for our state variable
             'dx' is the initial change rate for our state variable
             'g' is the g-h's g scale factor
             'h' is the g-h's h scale factor
             'dt' is the length of the time step
             'pred' is an optional list. If provided, each prediction will
             be stored in it
             """

             x = x0
             results = []
             for z in data:
                 #prediction step
                 x_est = x + (dx*dt)
                 dx = dx
```

```
            if pred is not None:
                pred.append(x_est)

            # update step
            residual = z - x_est
            dx = dx    + h * (residual) / dt
            x  = x_est + g * residual

            results.append(x)

        return results

    def plot_g_h_results (measurements, filtered_data, title=''):
        plt.plot (filtered_data, '--',label='filter')
        plt.plot(measurements,label='measurement')
        plt.legend(loc=4)
        plt.title(title)
        plt.show()


    plt.xlim([0,10])
    plt.plot([0,9],[160,170],label='actual')
    data = g_h_filter (data=weights, x0=160, dx=1, g=6./10, h = 2./3, dt=1.)
    plot_g_h_results (weights, data)
```



2.4 Choice of g and h

The g-h filter is not one filter - it is a classification for a family of filters. Eli Brookner in *Tracking and Kalman Filtering Made Easy* lists 11, and I am sure there are more. Not only that, but each type of filter has numerous subtypes. Each filter is differentiated by how g and h are chosen. So there is no 'one fits all' advice that I can give here. Some filters set g and h as constants, others vary them dynamically. The Kalman filter varies them dynamically at each step k. Some filters allow g and h to take any value within a range, others constrain one to be dependent on the other by some function $f()$, where $g = f(h)$.

The topic of this book is not the entire family of g-h filters; more importantly, we are interested in the *Bayesian* aspect of these filters, which I have not addressed yet. Therefore I will not cover selection of g and h in depth. Eli Brookner's book *Tracking and Kalman Filtering Made Easy* is an excellent resource for that topic, if it interests you. If this strikes you as an odd position for me to take, recognize that the typical formulation of the Kalman filter does not use g and h at all; the Kalman filter is a g-h filter because it mathematically reduces to this algorithm. When we design the Kalman filter we will be making a number of carefully considered choices to optimize it's performance, and those choices indirectly affect g and h. Don't worry if this is not too clear right now, it will be much clearer later after we develop the Kalman filter theory.

However, it is worth seeing how varying g and h affects the results, so we will work through some examples. This will give us strong insight into the fundamental strengths and limitations of this type of filter, and help us understand the behavior of the rather more sophisticated Kalman filter.

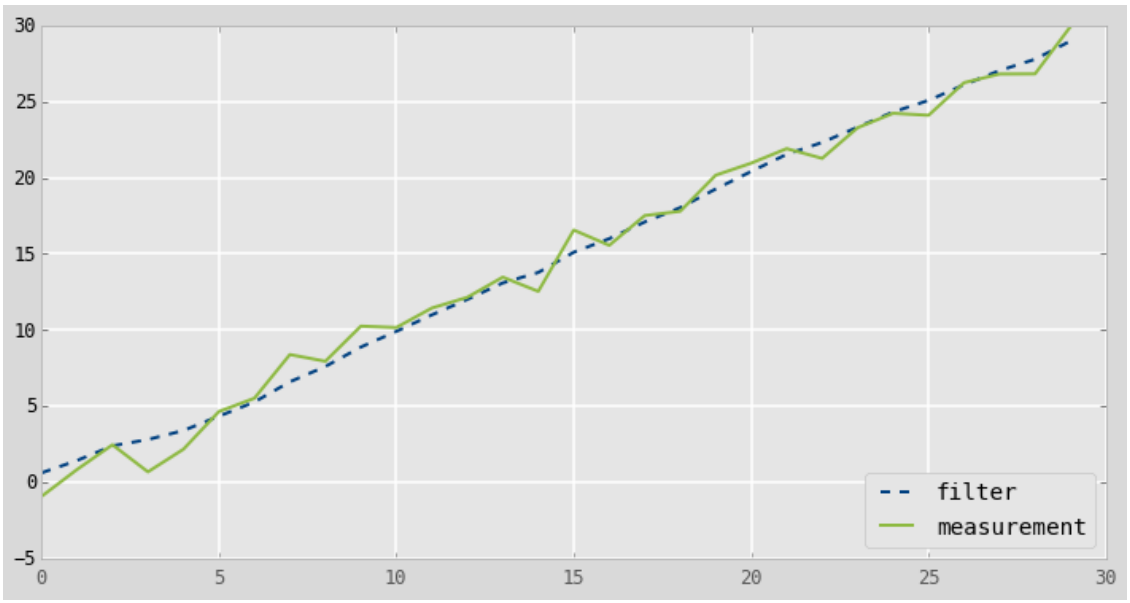
2.5 Exercise: create measurement function

Now let's write a function that generates noisy data for us. Recall from chapter 0 that we model a noisy signal as the signal plus white noise generated by `numpy.random.randn()`. We want a function that we call with the starting value, the amount of change per step, the number of steps, and the amount of noise we want to add. It should return a list of the data. Test it by creating 30 points, filtering it with `g_h_filter()`, and plot the results with `plot_g_h_results()`.

```
In [13]: # your code here
```

2.5.1 Solution

```
In [14]: import numpy.random as random
         def gen_data (x0, dx, count, noise_factor):
             return [x0 + dx*i + random.randn()*noise_factor for i in range (count)]

         measurements = gen_data (0, 1, 30, 1)
         data = g_h_filter (data=measurements, x0=0, dx=1, dt=1, g=.2, h=0.02)
         plot_g_h_results (measurements, data)
```



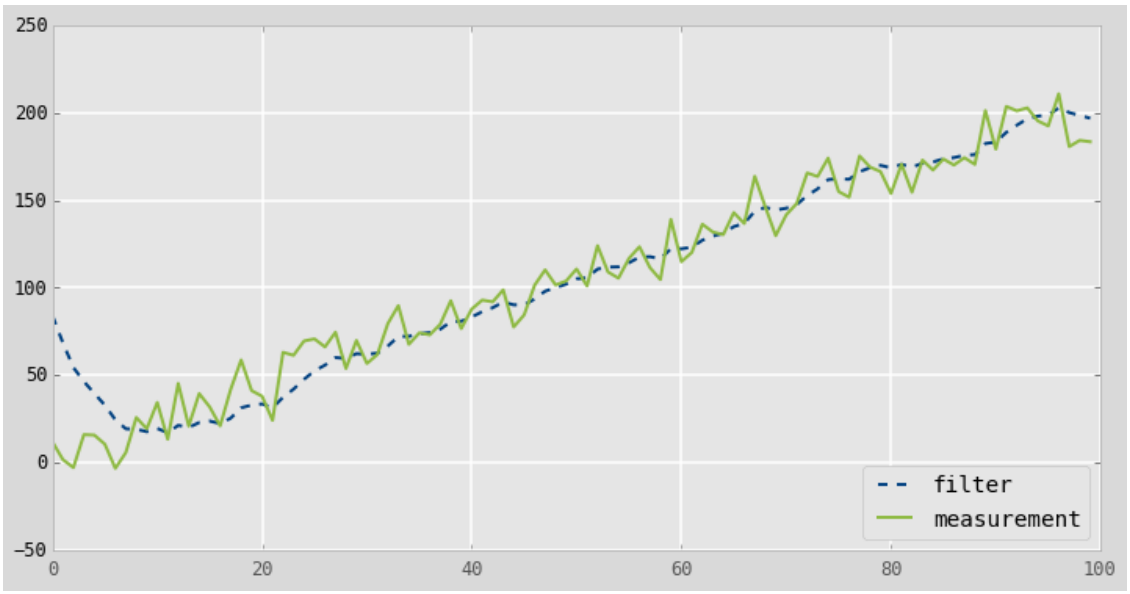
2.6 Exercise: Bad Initial Conditions

Now write code that uses `gen_data` and `g_h_filter` to filter 100 data points that starts at 5, has a derivative of 2, a noise scaling factor of 10, and uses g=0.2 and h=0.02. Set you initial guess for x to be 100.

```
In [15]: # your code here
```

2.6.1 Solution and Discussion

```
In [16]: zs = gen_data (x0=5, dx=2, count=100, noise_factor=10)
         data = g_h_filter (data=zs, x0=100., dx=2., dt=1.,g=0.2, h=0.01)
         plot_g_h_results  (measurements=zs, filtered_data=data)
```



The filter starts out with estimates that are far from the measured data due to the bad initial guess of 100. You can see that it 'rings' before settling in on the measured data. 'Ringing' means that the signal overshoots and undershoots the data in a sinusodial type pattern. This is a very common phenomena in filters, and a lot of work in filter design is devoted to minimizing ringing. That is a topic that we are not yet prepared to address, but I wanted to show you the phenomenon.

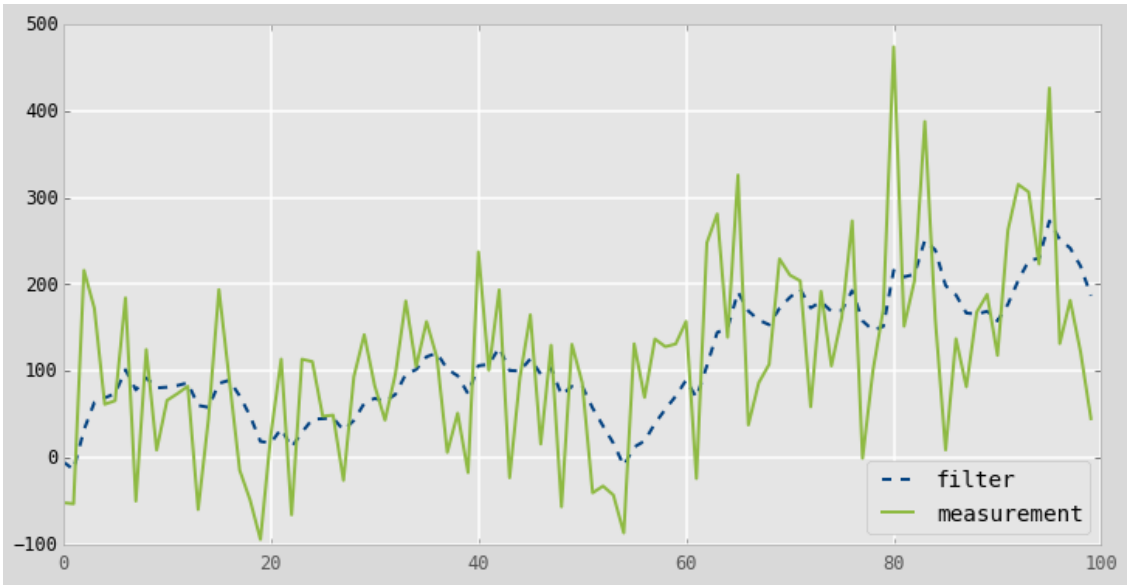
2.7 Exercise: Extreme Noise

Rerun the same test, but this time use a noise factor of 100. Remove the initial condition ringing by changing the initial condition from 100 down to 5.

```
In [17]: # your code here
```

2.7.1 Solution and Discussion

```
In [18]: zs = gen_data (x0=5, dx=2, count=100, noise_factor=100)
         data = g_h_filter (data=zs, x0=5., dx=2., g=0.2, h=0.02)
         plot_g_h_results  (measurements=zs, filtered_data=data)
```



This doesn't look so wonderful to me. We can see that perhaps the filtered signal varies less than the noisy signal, but it is far from the straight line. If we were to plot just the filtered result no one would guess that the signal with no noise starts at 5 and increments by 2 at each time step. And while in locations the filter does seem to reduce the noise, in other places it seems to overshoot and undershoot.

At this point we don't know enough to really judge this. We added **a lot** of noise; maybe this is as good as filtering can get. However, the existence of the multitude of chapters beyond this one should suggest that we can do much better than this suggests.

2.8 Exercise: The Effect of Acceleration

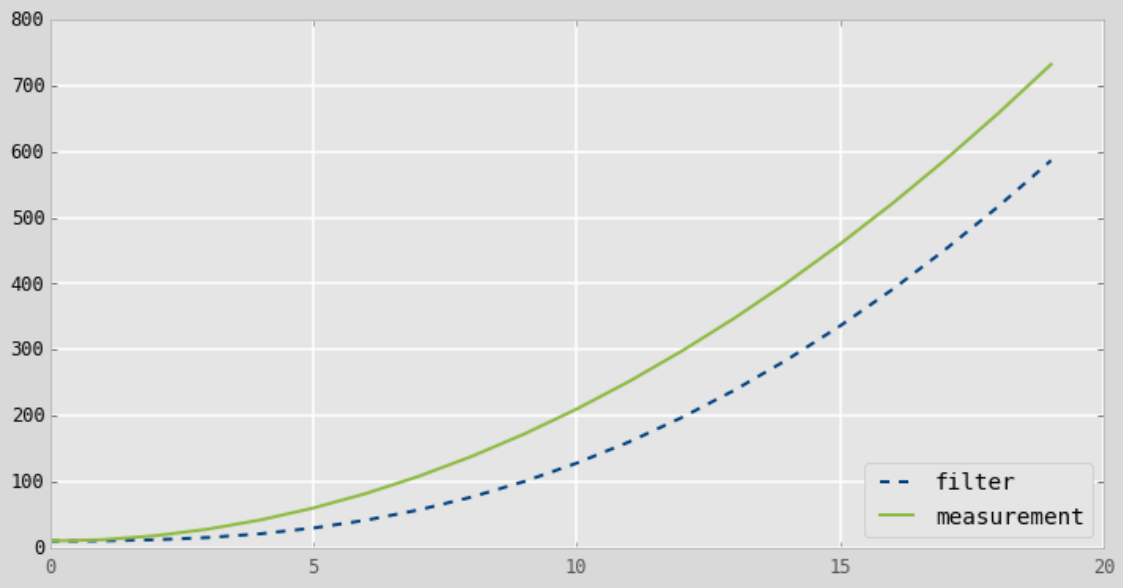
Write a new data generation function that adds in a constant acceleration factor to each data point. In other words, increment dx as you compute each data point so that the velocity (dx) is ever increasing. Set the noise to 0, $g = 0.2$ and $h = 0.02$ and plot the results. Explain what you see.

```
In [19]: # your code here
```

2.8.1 Solution and Discussion

```
In [20]: def gen_data (x0, dx, count, noise_factor, accel=0):
             zs = []
             for i in range (count):
                 zs.append (x0 + dx*i + random.randn()*noise_factor)
                 dx += accel
             return zs
```

```
predictions = []
zs = gen_data (x0=10, dx=0, count=20, noise_factor=0, accel = 2)
data = g_h_filter (data=zs, x0=10, dx=0, g=0.2, h=0.02, pred=predictions)
plt.xlim([0,20])
plot_g_h_results  (measurements=zs, filtered_data=data)
```



Each prediction lags behind the signal. If you think about what is happening this makes sense. Our model assumes that velocity is constant. The g-h filter computes the first derivative of x (we use $\dot{x}$ to denote the derivative) but not the second derivative $\ddot{x}$. So we are assuming that $\ddot{x} = 0$. At each prediction step we predict the new value of x as $x + \dot{x} * t$. But because of the acceleration the prediction must necessarily fall behind the actual value. We then try to compute a new value for $\dot{x}$, but because of the h factor we only partially adjust $\dot{x}$ to the new velocity. On the next iteration we will again fall short.

Note that there is no adjustment to g or h that we can make to correct this problem. This is called the *lag error* or *systemic error* of the system. It is a fundamental property of g-h filters. Perhaps your mind is already suggesting solutions or workarounds to this problem. As you might expect, a lot of research has been devoted to this problem, and we will be presenting various solutions to this problem in this book. > The 'take home' point is that the filter is only as good as the mathematical model used to express the system.

2.9 Exercise: Varying g

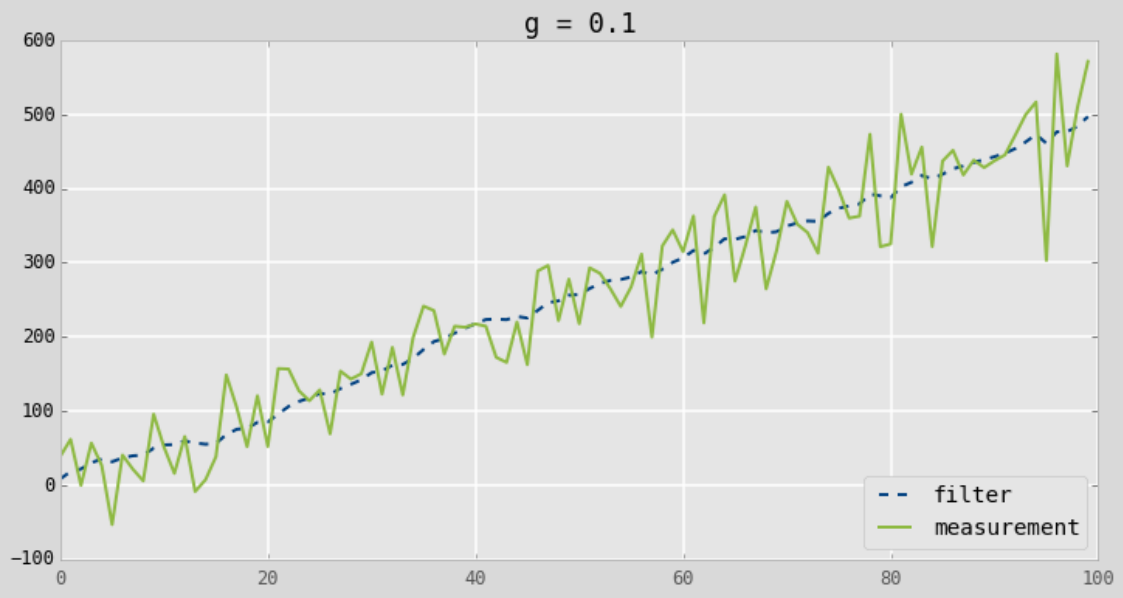
Now let's look at the effect of varying g. Before you perform this exercise, recall that g is the scale factor for choosing between the measurement and prediction. What do you think of a large value of g will be? A small value?

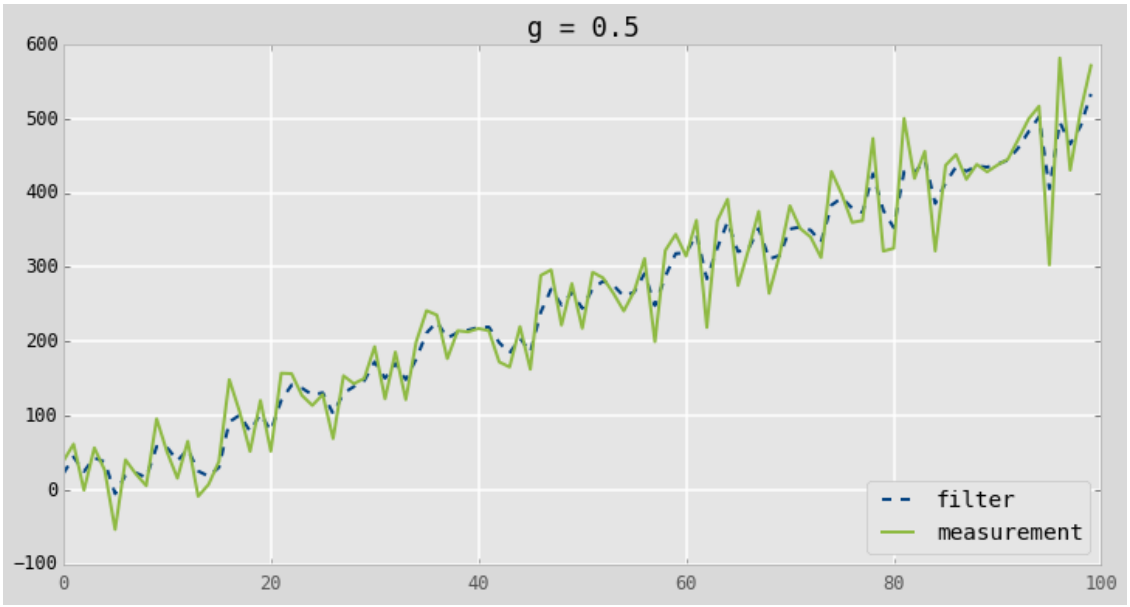
Now, let the `noise_factor=50` and `dx=5`. Plot the results of $g = 0.1,\ 0.5,$ and 0.9.

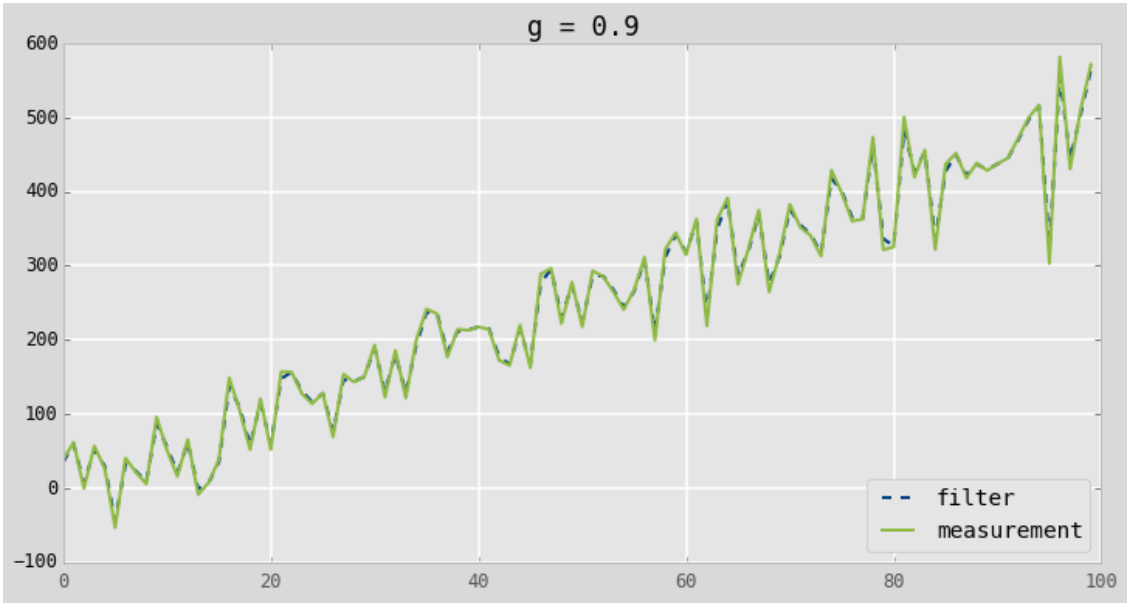
In [21]: # your code here

2.9.1 Solution and Discussion

In [22]:
```
zs = gen_data (x0=5, dx=5, count=100, noise_factor=50)

data = g_h_filter (data=zs, x0=0., dx=5., dt=1.,g=0.1, h=0.01)
plot_g_h_results  (zs, data, 'g = 0.1')

data = g_h_filter (data=zs, x0=0., dx=5., dt=1.,g=0.5, h=0.01)
plot_g_h_results  (zs, data, 'g = 0.5')

data = g_h_filter (data=zs, x0=0., dx=5., dt=1.,g=0.9, h=0.01)
plot_g_h_results  (zs, data, 'g = 0.9')
```

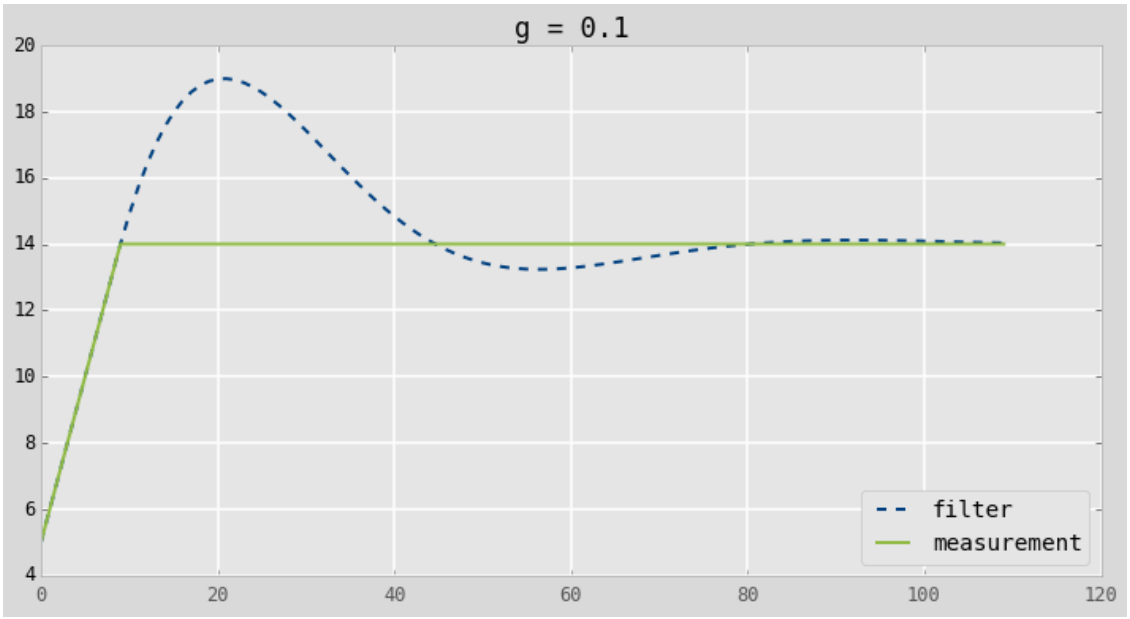


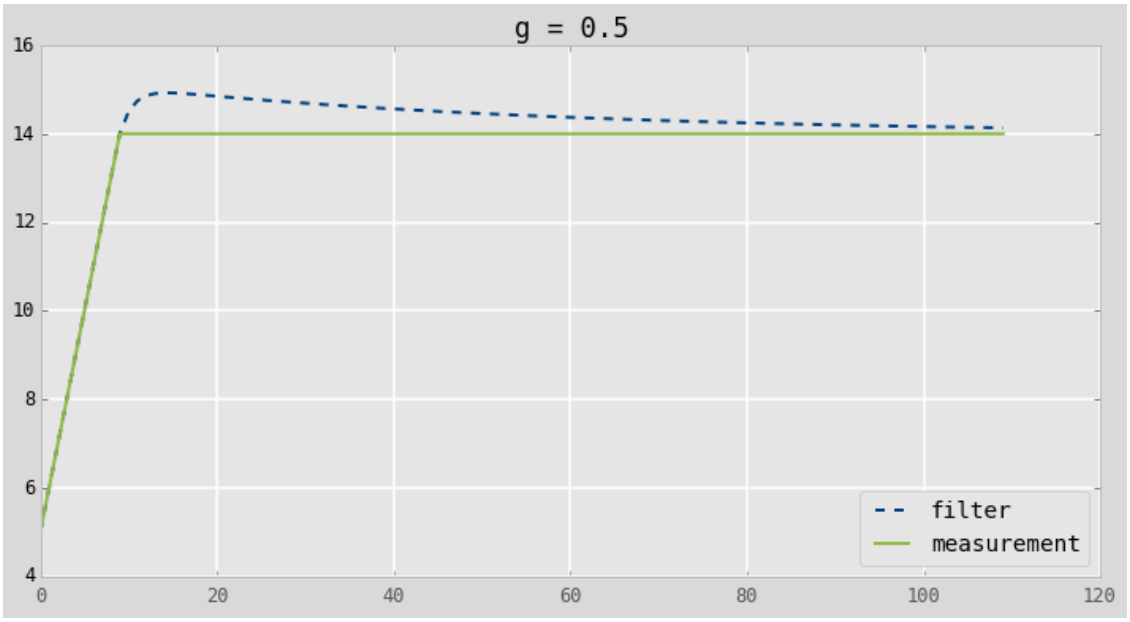


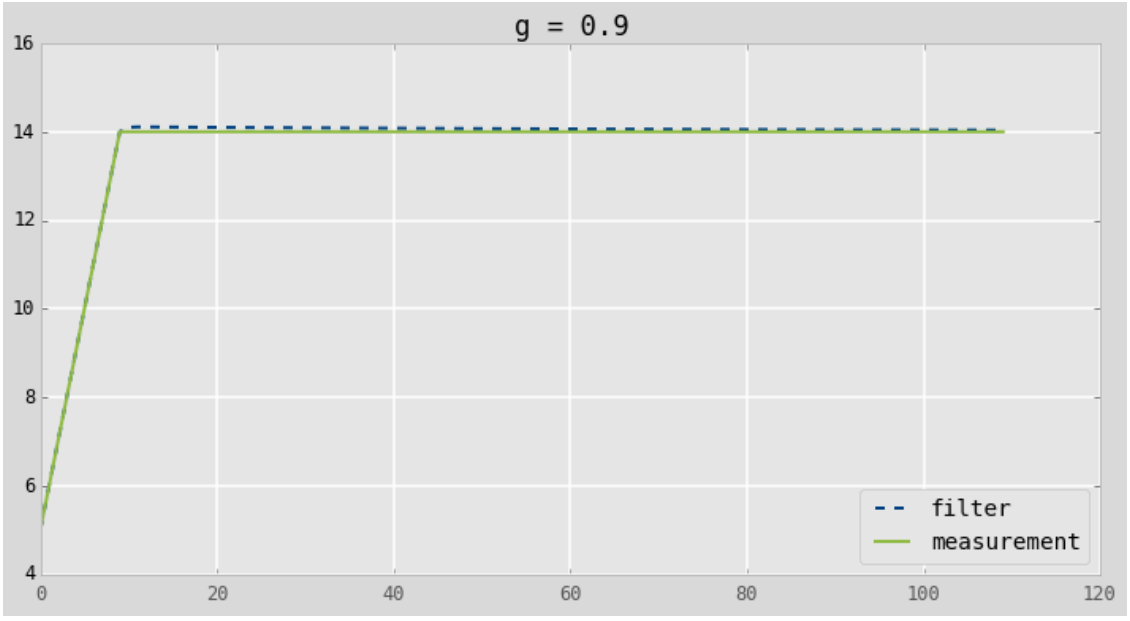


It is clear that as g is larger we more closely follow the measurement instead of the prediction. When $g = 0.9$ we follow the signal almost exactly, and reject almost none of the noise. One might naively conclude that g should always be very small to maximize noise rejection. However, that means that we are mostly ignoring the measurements in favor of our prediction. What happens when the signal changes not due to noise, but an actual state change? Let's look. I will create data that has $\dot{x} = 1$ for 9 steps before changing to $\dot{x} = 0$.

In [23]:
```
zs = [5,6,7,8,9,10,11,12,13,14]

for i in range(100):
    zs.append(14)

data = g_h_filter (data=zs, x0=4., dx=1., dt=1.,g=0.1, h=0.01)
plot_g_h_results  (zs, data, 'g = 0.1')

data = g_h_filter (data=zs, x0=4., dx=1., dt=1.,g=0.5, h=0.01)
plot_g_h_results  (zs, data, 'g = 0.5')

data = g_h_filter (data=zs, x0=4., dx=1., dt=1.,g=0.9, h=0.01)
plot_g_h_results  (zs, data, 'g = 0.9')
```





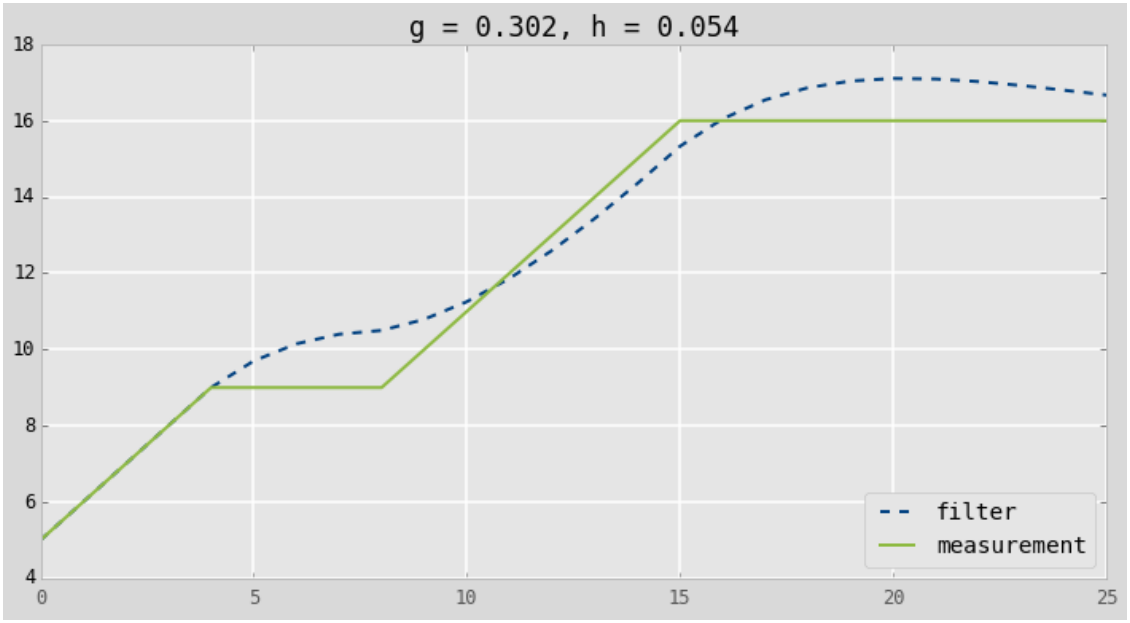


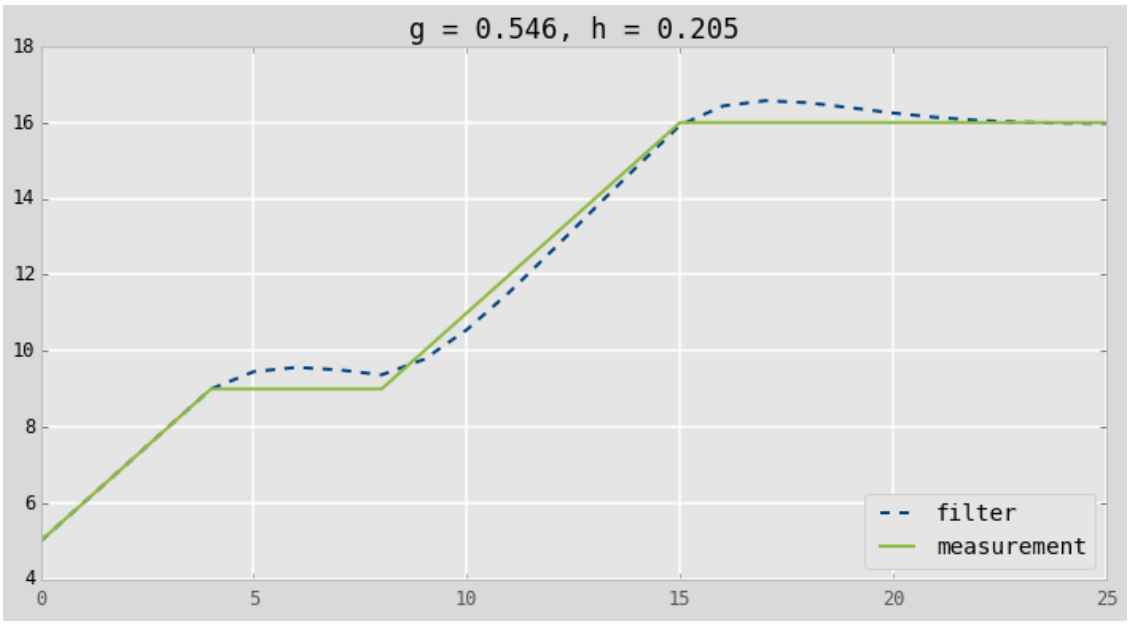
Here we can see the effects of ignoring the signal. We not only filter out noise, but legitimate changes in the signal as well.

Maybe we need a 'Godilocks' filter, where is not too large, not too small, but just right? Well, not exactly. As alluded to earlier, different filters choose g and h in different ways depending on the mathematical properties of the problem. For example, the Benedict-Bordner filter was invented to minimize the transient error in this example, where $\dot{x}$ makes

a step jump. We will not discuss this filter in this book, but here are two plots chosen with different allowable pairs of g and h. This filter design minimizes transient errors for step jumps in $\dot{x}$ at the cost of not being optimal for other types of changes in $\dot{x}$.

In [24]:
```
zs = [5,6,7,8,9,9,9,9,9,10,11,12,13,14,15,16,16,16,16,16,16,16,16,16,16,16]

data = g_h_filter (data=zs, x0=4., dx=1., dt=1.,g=.302, h=0.054)
plot_g_h_results  (zs, data, 'g = 0.302, h = 0.054')

data = g_h_filter (data=zs, x0=4., dx=1., dt=1.,g=.546, h=0.205)
plot_g_h_results  (zs, data, 'g = 0.546, h = 0.205')
```





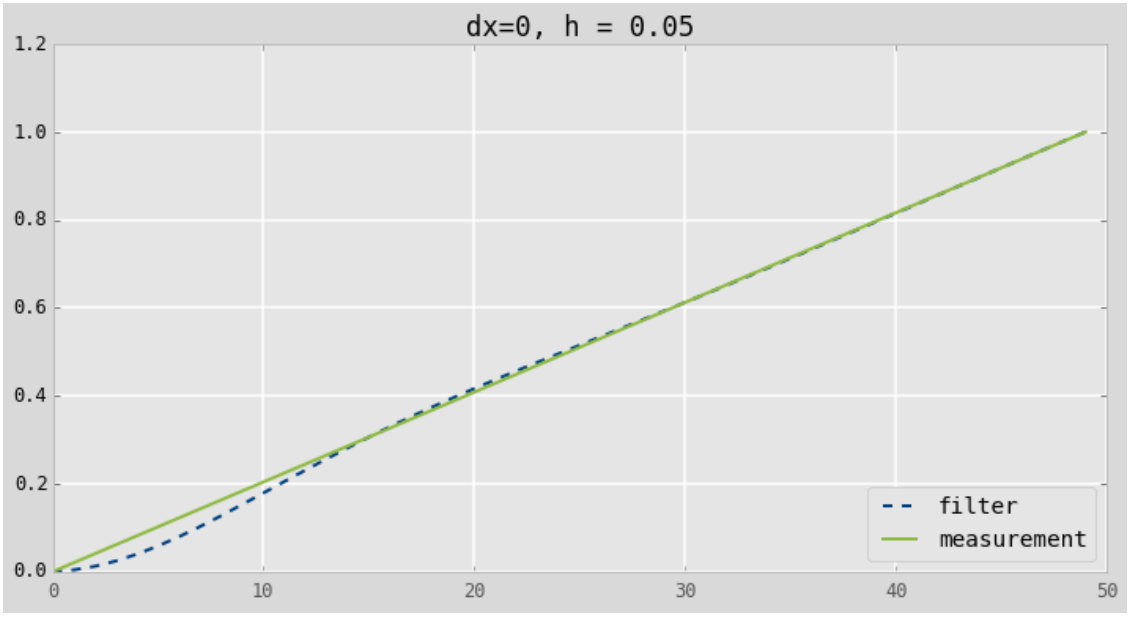
2.10 Varying h

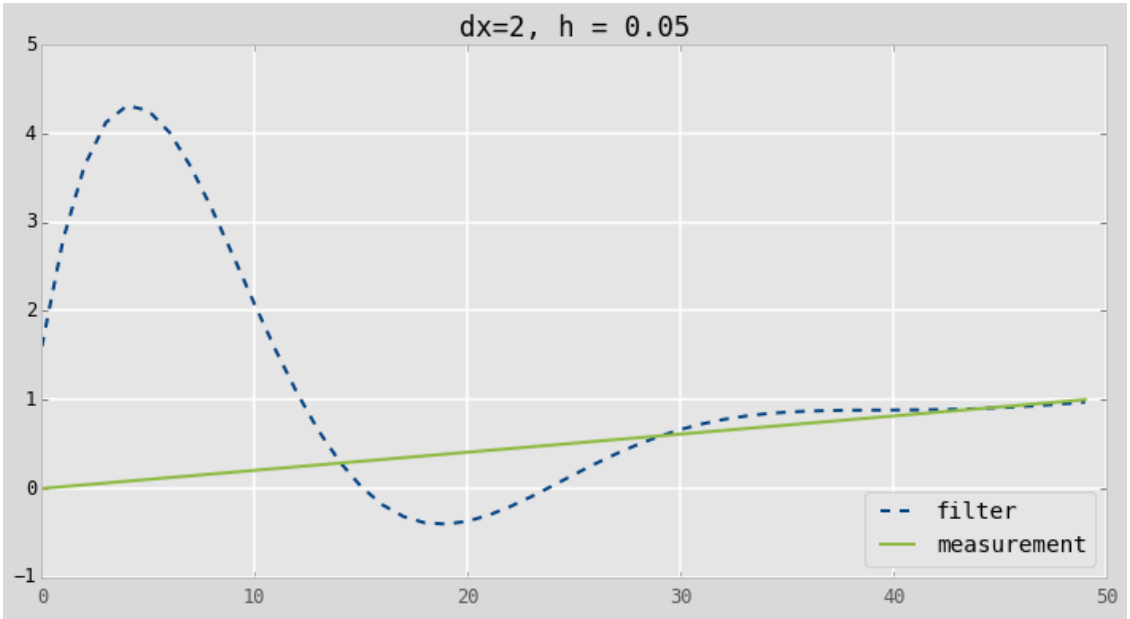
Now let's leave g unchanged and investigate the effect of modifying h. We know that h affects how much of we favor the measurement of $\dot{x}$ vs our prediction. But what does this *mean*? If our signal is changing a lot (quickly relative to the time step of our filter), then a large h will cause us to react to those transient changes rapidly. A smaller h will cause us to react more slowly.

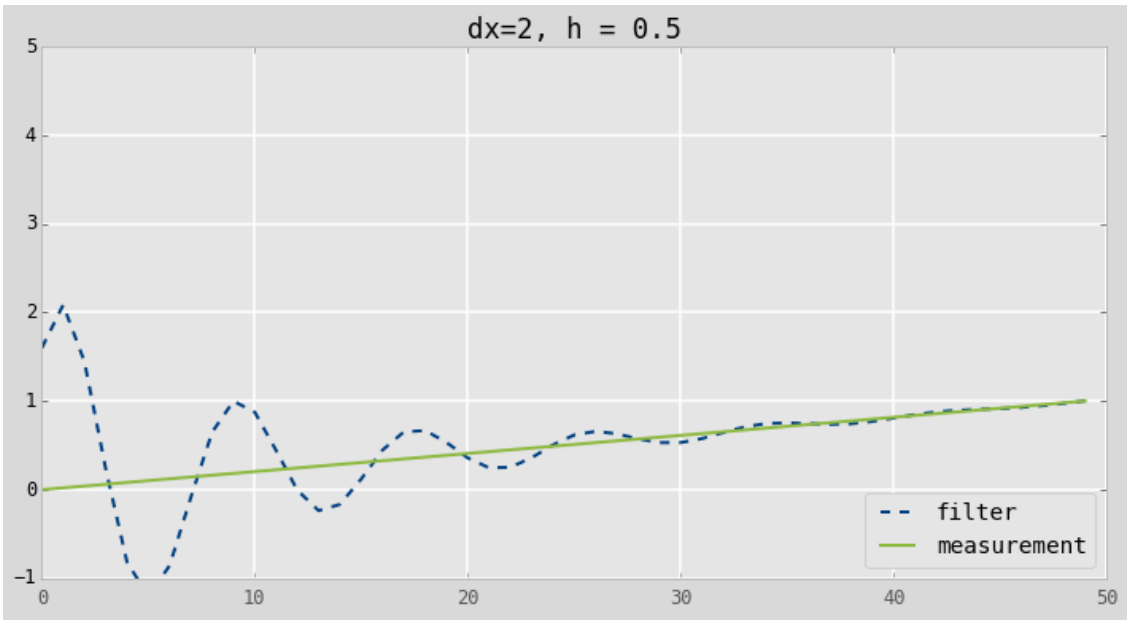
We will look at three examples. We have a noiseless measurement that slowly goes from 0 to 1 in 50 steps. Our first filter uses a nearly correct initial value for $\dot{x}$ and a small h. You can see from the output that the filter output is very close to the signal. The second filter uses the very incorrect guess of $\dot{x} = 2$. Here we see the filter 'ringing' until it settles down and finds the signal. The third filter uses the same conditions but it now sets $h = 0.5$. If you look at the amplitude of the ringing you can see that it is much smaller than in the second chart, but the frequency is greater. It also settles down a bit quicker than the second filter, though not by much.

```
In [25]: zs = np.linspace(0,1,50)

         data = g_h_filter (data=zs, x0=0, dx=0., dt=1.,g=.2, h=0.05)
         plot_g_h_results  (zs, data, 'dx=0, h = 0.05')

         data = g_h_filter (data=zs, x0=0, dx=2., dt=1.,g=.2, h=0.05)
         plt.ylim([-1,5])
         plot_g_h_results  (zs, data, 'dx=2, h = 0.05')
```

```
data = g_h_filter (data=zs, x0=0, dx=2., dt=1.,g=.2, h=0.5)
plt.ylim([-1,5])
plot_g_h_results  (zs, data, 'dx=2, h = 0.5')
```







2.11 Final Thoughts

Near the beginning of the chapter I used `numpy.polyfit()` to fit a straight line to the weight measurements. It fits a n-th degree polynomial to the data using a 'least squared fit'. How does this differ from the g-h filter?

Well, it depends. We will eventually learn that the Kalman filter is optimal from a least squared fit perspective. However, `polyfit()` fits a polynomial to the data, not an arbitrary curve, by minimizing the value of this formula:

$$E = \sum_{j=0}^{k} |p(x_j) - y_j|^2$$

I assumed that my weight gain was constant at 1 lb/day, and so when I tried to fit a polynomial of $n = 1$, which is a line, the result very closely matched the actual weight gain. But, of course, no one consistently only gains or loses weight. We fluctuate. Using 'polyfit()' for a longer series of data would yield poor results. In contrast, the g-h filter reacts to changes in the rate - the h term controls how quickly the filter reacts to these changes. If we gain weight, hold steady for awhile, then lose weight, the filter will track that change automatically. 'polyfit()' would not be able to do that unless the gain and loss could be well represented by a polynomial.

Another advantage of this form of filter, even if the data fits a n-degree polynomial, is that it is *recursive*. That is, we can compute the estimate for this time period knowing nothing more than the estimate and rate from the last time period. In contrast, if you dig into the implementation for `polyfit()` you will see that it needs all of the data before it

can produce an answer. Therefore algorithms like `polyfit()` are not well suited for real-time data filtering. In the 60's when the Kalman filter was developed computers were very slow and had extremely limited memory. They were utterly unable to store, for example, thousands of readings from an aircraft's inertial navigation system, nor could they process all of that data in the short period of time needed to provide accurate and up-to-date navigation information.

Up until the mid 20th century various forms of Least Squares Estimation was used for this type of filtering. For example, for NASA's Apollo program had a ground network for tracking the Command and Service Model (CSM) and the Lunar Module (LM). They took measurements over many minutes, batched the data together, and slowly computed an answer. In 1960 Stanley Schmidt at NASA Ames recognized the utility of Rudolf Kalman's seminal paper and invited him to Ames. Schmidt applied Kalman's work to the onboard navigation systems on the CSM and LM, and called it the "Kalman filter".[1] Soon after, the world moved to this faster, recursive filter.

The Kalman filter only needs to store the last estimate and a few related parameters, and requires only a relatively small number of computations to generate the next estimate. Today we have so much memory and processing power that this advantage is somewhat less important, but at the time the Kalman filter was a major breakthrough not just because of the mathematical properties, but because it could (barely) run on the hardware of the day.

This subject is much deeper than this short discussion suggests. We will consider these topics many more times throughout the book.

2.12 Summary

I encourage you to experiment with this filter to develop your understanding of how it reacts. It shouldn't take too many attempts to come to the realization that ad-hoc choices for g and h do not perform very well. A particular choice might perform well in one situation, but very poorly in another. Even when you understand the effect of g and h it can be difficult to choose proper values. In fact, it is extremely unlikely that you will choose values for g and h that is optimal for any given problem. Filters are *designed*, not selected *ad hoc*.

In some ways I do not want to end the chapter here, as there is a significant amount that we can say about selecting g and h. But the g-h filter in this form is not the purpose of this book. Designing the Kalman filter requires you to specify a number of parameters - indirectly they do relate to choosing g and h, but you will never refer to them direcly when designing Kalman filters. Furthermore, g and h will vary at every time step in a very non-obvious manner.

There is another feature of these filters we have barely touched upon - Bayesian statistics. You will note that the term 'Bayesian' is in the title of this book; this is not a coincidence! For the time being we will leave g and h behind, largely unexplored, and develop a very powerful form of probabilistic reasoning about filtering. Yet suddenly this same g-h filter algorithm will appear, this time with a formal mathematical edifice that allows us to create filters from multiple sensors, to accurately estimate the amount of error in our solution, and to control robots.

2.13 References

- [1] [NASA Kalman Filtering Presentation](http://nescacademy.nasa.gov/review/downloadfile.php?fil

Chapter 3

Discrete Bayes Filter

The Kalman filter belongs to a family of filters called *bayesian filters*. Without going into
blah blah

3.1 Tracking a Dog

Let us begin with a simple problem. We have a dog friendly workspace, and so people bring their dogs to work. However, occasionally the dogs wander out of your office and down the halls. We want to be able to track them. So during a hackathon somebody created a little sonar sensor to attach to the dog's collar. It emits a signal, listens for the echo, and based on how quickly an echo comes back we can tell whether the dog is in front of an open doorway or not. It also senses when the dog walks, and reports in which direction the dog has moved. It connects to our network via wifi and sends an update once a second.

I want to track my dog Simon, so I attach the device to his collar and then fire up Python, ready to try to write code to track him through the building. At first blush this may appear impossible. If I start listening to the sensor of Simon's collar I might read 'door', 'hall', 'hall', and so on. How can I use that information to determine where Simon is?

To keep the problem small, we will assume that there are only 10 positions in a single hallway to consider, which we will number 0 to 9, where 1 is to the right of 0, 2 is to the right of 1, and so on. For reasons that will be clear later, we will also assume that the hallway is circular or rectangular. If you move right from position 9, you will be at position 0.

When I begin listening to the sensor I have no reason to believe that Simon is at any particular position in the hallway. He is equally likely to be in any position. The probability that he is in each position is therefore 1/10.

Let us represent our belief of his position at any time in a numpy array.

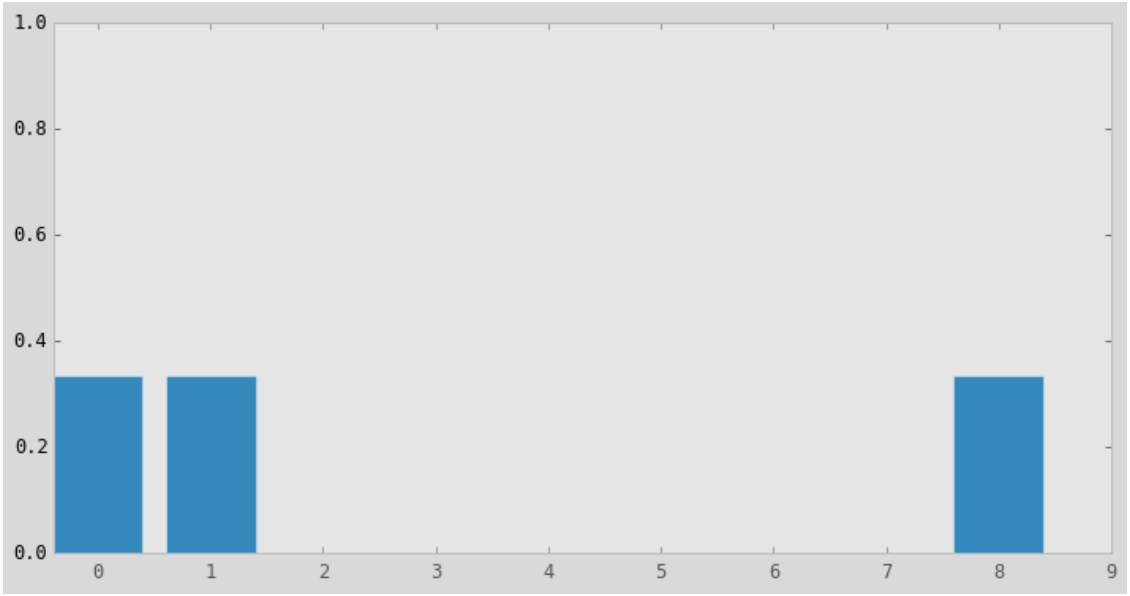
```
In [2]: import numpy as np

        pos = np.array([.1, .1, .1, .1, .1, .1, .1, .1, .1, .1])
```

Now let's create a map of the hallway in another list. Suppose there are first two doors close together, and then another door quite a bit further down the hallway. We will use 1 to denote a door, and 0 to denote a wall:

```
In [3]: hallway = np.array([1, 1, 0, 0, 0, 0, 0, 0, 1, 0])
```

So I start listening to Simon's transmissions on the network, and the first data I get from the sesnor is "door". From this I conclude that he is in front of a door, but which one? I have no idea. I have no reason to believe is in front of the first, second, or third door. But what I can do is assign a probability to each door. All doors are equally likely, so I assign a probability of 1/3 to each door.

```
In [4]: from __future__ import print_function, division
        import matplotlib.pyplot as plt
        import bar_plot
        import numpy as np

        pos = np.array([0.333, 0.333, 0., 0., 0., 0., 0., 0., 0.333, 0.])
        bar_plot.plot (pos)
```



We call this a multimodal distribution because we have multiple beliefs about the position of our dog. Of course we are not saying that we think he is simultaneously in three different locations, merely that so far we have narrowed down our knowledge in his position to these locations.

I hand coded the pos array in the code above. How would we implement this in code? Well, hallway represents each door as a 1, and wall as 0, so we will multiply the hallway variable by the percentage, like so;

```
In [5]: pos = hallway * 0.3
        print('pos =', pos)
```

```
pos = [ 0.3  0.3  0.   0.   0.   0.   0.   0.   0.3  0. ]
```

3.2 Extracting Information from Multiple Sensor Readings

Let's put Python aside and think about the problem a bit. Suppose we were to read the following from Simon's sensor:

- door
- move right
- door

Can we deduce where Simon is at the end of that sequence? Of course! Given the hallway's layout there is only one place where you can be in front of a door, move once to the right, and be in front of another door, and that is at the left end. Therefore we can confidently state that Simon is in front of the second doorway. If this is not clear, suppose Simon had started at the second or third door. After moving to the right, his sensor would have returned 'wall'. Therefore the only possibility is that he is now in front of the second door. We denote this in Python with:

```
In [6]: pos = np.array([0,1,0,0,0,0,0,0,0,0])
        print(pos)
```

```
[0 1 0 0 0 0 0 0 0 0]
```

Obviously I carefully constructed the hallway layout and sensor readings to give us an exact answer quickly. Real problems will not be so clear cut. But this should trigger your intuition - the first sensor reading only gave us very low probabilities (0.333) for Simon's location, but after a position update and another sensor reading we knew much more about where he is. You might suspect, correctly, that if you had a very long hallway with a large number of doors that after several sensor readings and positions updates we would either be able to know where Simon was, or have the possibilities narrowed down to a small number of possibilities. For example, suppose we had a long sequence of "door, right, door, right, wall, right, wall, right, door, right, door, right, wall, right, wall, right, wall, right, wall, right, door". Simon could only be located where we had a sequence of [1,1,0,0,1,1,0,0,0,0,1] in the hallway. There might be only one match for that, or at most a few. Either way we will be far more certain about his position then when we started.

We could work through the code to implement this solution, but instead let us consider a real world complication to the problem.

3.3 Noisy Sensors

Unfortunately I have yet to come across a perfect sensor. Perhaps the sensor would not detect a door if Simon sat in front of it while scratching himself, or it might report there is a door if he is facing towards the wall, not down the hallway. So in practice when I get a report 'door' I cannot assign 1/3 as the probability for each door. I have to assign something

less than 1/3 to each door, and then assign a small probability to each blank wall position. At this point it doesn't matter exactly what numbers we assign; let us say that the probably of 'door' being correct is 0.6, and the probability of being incorrect is 0.2, which is another way of saying it is about 3 times more likely to be right than wrong. How would we do this?

At first this may seem like an insurmountable problem. If the sensor is noisy it casts doubt on every piece of data. How can we conclude anything if we are always unsure?

The key, as with the problem above, is probabilities. We are already comfortable with assigning a probabilistic belief about the location of the dog; now we just have to incorporate the additional uncertainty caused by the sensor noise. Say we think there is a 50% chance that our dog is in front of a specific door and we get a reading of 'door'. Well, we think that is only likely to be true 0.6 of the time, so we multiply: $0.5 * 0.6 = 0.3$. Likewise, if we think the chances that our dog is in front of a wall is 0.1, and the reading is 'door', we would multiply the probability by the chances of a miss: $0.1 * 0.2 = 0.02$.

However, we more or less chose 0.6 and 0.2 at random; if we multiply the pos array by these values the end result will no longer represent a true probability distribution.

```
In [7]: def update (pos, measure, p_hit, p_miss):
            q = np.array(pos, dtype=float)
            for i in range(len(hallway)):
                if hallway[i] == measure:
                    q[i] = pos[i] * p_hit
                else:
                    q[i] = pos[i] * p_miss
            return q

        pos = np.array([0.2]*10)
        reading = 1 # 1 is 'door'
        pos = update (pos, 1, .6, .2)

        print(pos)
        print('sum =', sum(pos))
```

```
[ 0.12  0.12  0.04  0.04  0.04  0.04  0.04  0.04  0.12  0.04]
sum = 0.64
```

We can see that this is not a probability distribution because it does not sum to 1.0. But we can see that the code is doing mostly the right thing - the doors are assigned a number (0.12) that is 3 times higher than the walls (0.04). So we can write a bit of code to normalize the result so that the probabilities correctly sum to 1.0.

```
In [8]: def normalize(p):
            s = sum(p)
            for i in range (len(p)):
                p[i] = p[i] / s
```

```
        def update(pos, measure, p_hit, p_miss):
            q = np.array(pos, dtype=float)
            for i in range(len(hallway)):
                if hallway[i] == measure:
                    q[i] = pos[i] * p_hit
                else:
                    q[i] = pos[i] * p_miss
            normalize(q)
            return q


        pos = np.array([0.2]*10)
        reading = 1 # 1 is 'door'
        pos = update(pos, 1, .6, .2)

        print('sum =', sum(pos))
        print('probability of door =', pos[0])
        print('probability of wall =', pos[2])
```

```
sum = 1.0
probability of door = 0.1875
probability of wall = 0.0625
```

Normalization is done by dividing each element by the sum of all elements in the list. If this is not clear you should spend a few minutes proving it to yourself algebraically. We can see from the output that the sum is now 1.0, and that the probability of a door vs wall is still three times larger. The result also fits our intuitiion that the probability of a door must be less than 0.333, and that the probability of a wall must be greater than 0.0. Finally, it should fit our intuition that we have not yet been given any information that would allow us to distinguish between any given door or wall position, so all door positions should have the same value, and the same should be true for wall positions.

3.4 Incorporating Movement Data

Recall how quickly we were able to find an exact solution to our dog's position when we incorporated a series of measurements and movement updates. However, that occured in a fictional world of perfect sensors. Might we be able to find an exact solution even in the presense of noisy sensors?

Unfortunately, the answer is no. Even if the sensor readings perfectly match an extremely complicated hallway map we could not say that we are 100% sure that the dog is in a specific position - there is, after all, the possibility that every sensor reading was wrong! Naturally, in a more typical situation most sensor readings will be correct, and we might be close to 100% sure of our answer, but never 100% sure. This may seem head-spinningly complicated, but lets just go ahead and program the math, which as we have seen is quite simple.

First let's deal with the simple case - assume the movement sensor is perfect, and it reports that the dog has moved one space to the right. How would we alter our pos array?

I hope after a moment's thought it is clear that we should just shift all the values one space to the right. If we previously thought there was a 50% chance of simon being at position 3, then after the move to the right we should believe that there is a 50% chance he is at position 4. So let's implement that. Recall that the hallway is circular, so we will use modulo arithmetic to perform the shift correctly

```
In [9]: import numpy
        def perfect_predict(pos, move):
            """ move the position by 'move' spaces, where positive is to the right, an
            is to the left
            """
            n = len(pos)
            result = np.array(pos, dtype=float)
            for i in range(n):
                result[i] = pos[(i-move) % n]
            return result

        pos = np.array([.4, .1, .2, .3])
        print('pos before predict =', pos)
        pos = perfect_predict(pos, 1)
        print('pos after predict =', pos)
```

```
pos before predict = [ 0.4  0.1  0.2  0.3]
pos after predict = [ 0.3  0.4  0.1  0.2]
```

We can see that we correctly shifted all values one position to the right, wrapping from the end of the array back to the beginning.

3.5 Adding Noise to the Prediction

We want to solve real world problems, and we have already stated that all sensors have noise. Therefore the code above must be wrong. What if the sensor reported that our dog moved one space, but he actually moved two spaces, or zero? Once again this may initially sound like an insummountable problem, but let's just model it in math. Since this is just an example, we will create a pretty simple noise model for the sensor - later in the book we will handle far more sophisticated errors.

We will say that when the sensor sends a movement update, it is 80% likely to be right, and it is 10% likely to overshoot one position to the right, and 10% likely to undershoot to the left. That is, if we say the movement was 4 (meaning 4 spaces to the right), the dog is 80% likely to have moved 4 spaces to the right, 10% to have moved 3 spaces, and 10% to have moved 5 spaces.

This is slightly harder than the math we have done so far, but it is still tractable. Each result in the array now needs to incorporate probabilities for 3 different situations. For

example, consider position 9 for the case where the reported movement is 2. It should be clear that after the move we need to incorporate the probability that was at position 7 (9-2). However, there is a small chance that our dog actually moved from either 1 or 3 spaces away due to the sensor noise, so we also need to use positions 6 and 8. How much? Well, we have the probabilities, so we can just multiply and add. It would be 80% of position 7 plus 10% of position 6 and 10% of position 8! Let's try coding that:

```
In [10]: def predict(pos, move, p_correct, p_under, p_over):
             n = len(pos)
             result = np.array(pos, dtype=float)
             for i in range(n):
                         result[i] =  \
                     pos[(i-move) % n]   * p_correct + \
                     pos[(i-move-1) % n] * p_over + \
                     pos[(i-move+1) % n] * p_under
             return result

         p = np.array([0,0,0,1,0,0,0,0])
         res = predict(p, 2, .8, .1, .1)
         print(res)
```

```
[ 0.   0.   0.   0.   0.1  0.8  0.1  0. ]
```

The simple test case that we ran appears to work correctly. We initially believed that the dog was in position 3 with 100% certainty; after the movement update we now give an 80% probability to the dog being in position 5, and a 10% chance to undershooting to position 4, and a 10% chance of overshooting to position 6. Let us look at a case where we have multiple beliefs:

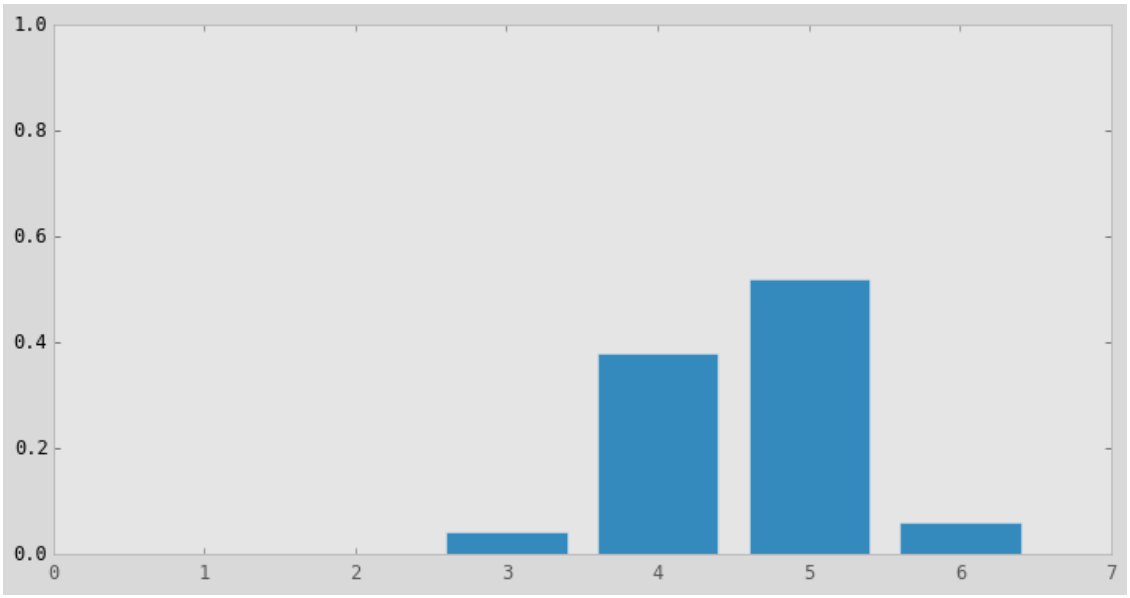
```
In [11]: p = np.array([0, 0, .4, .6, 0, 0, 0, 0])
         res = predict (p, 2, .8, .1, .1)
         print(res)
```

```
[ 0.    0.    0.    0.04  0.38  0.52  0.06  0.  ]
```

Here the results are more complicated, but you should still be able to work it out in your head. The 0.04 is due to the possibility that the 0.4 belief undershot by 1. The 0.38 is due to the following: the 80% chance that we moved 2 positions ($.4 * .8$) and the 10% chance that we undershot ($.6 * .1$). Overshooting plays no role here because if we overshot both .4 and .6 would be past this position. **I strongly suggest working some examples until all of this is very clear, as so much of what follows depends on understanding this step.**

If you look at the probabilities after performing the update you probably feel dismay. In the example above we started with probabilitys of .4 and .6 in two fields; after performing the update the probabilities are not only lowered, but they are strewn out across the map.

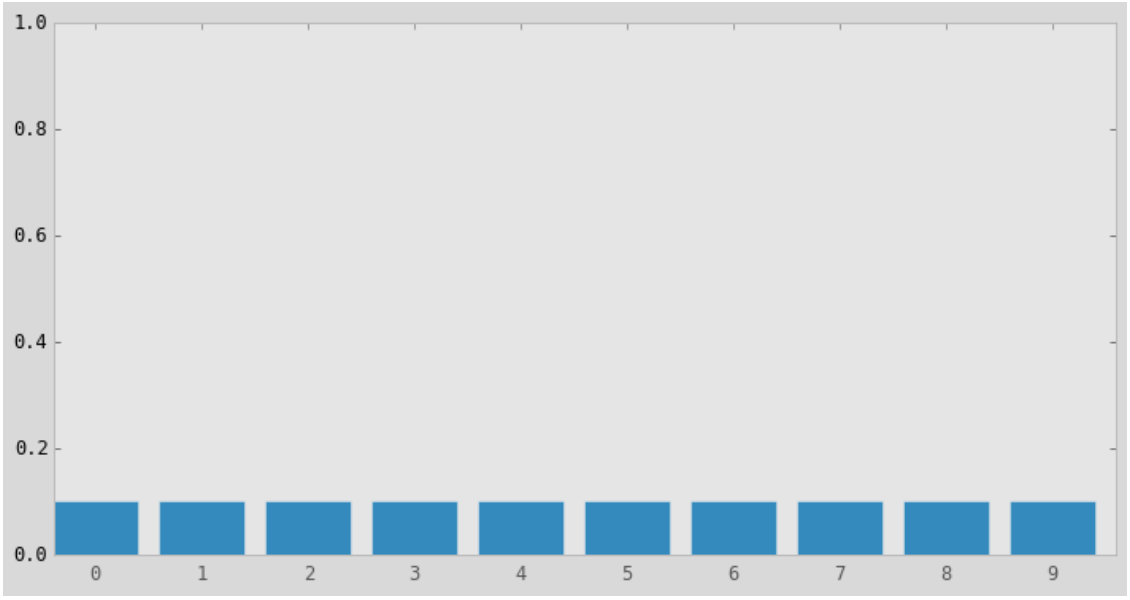
```
In [12]: bar_plot.plot (res)
```



This is not a coincidence, or the result of a carefully chosen example - it is always true of the update step. This is inevitable; if our sensor is noisy we will lose a bit of information on every update. Suppose we were to perform the update an infinite number of times - what would the result be? If we lose information on every step, we must eventually end up with no information at all, and our probabilities will be equally distributed across the pos array. Let's try this with say 500 iterations.

```
In [13]: pos = [1.0,0,0,0,0,0,0,0,0,0]
         for i in range (500):
             pos = predict(pos, 1, .8, .1, .1)
         print(pos)
         bar_plot.plot(pos)
```

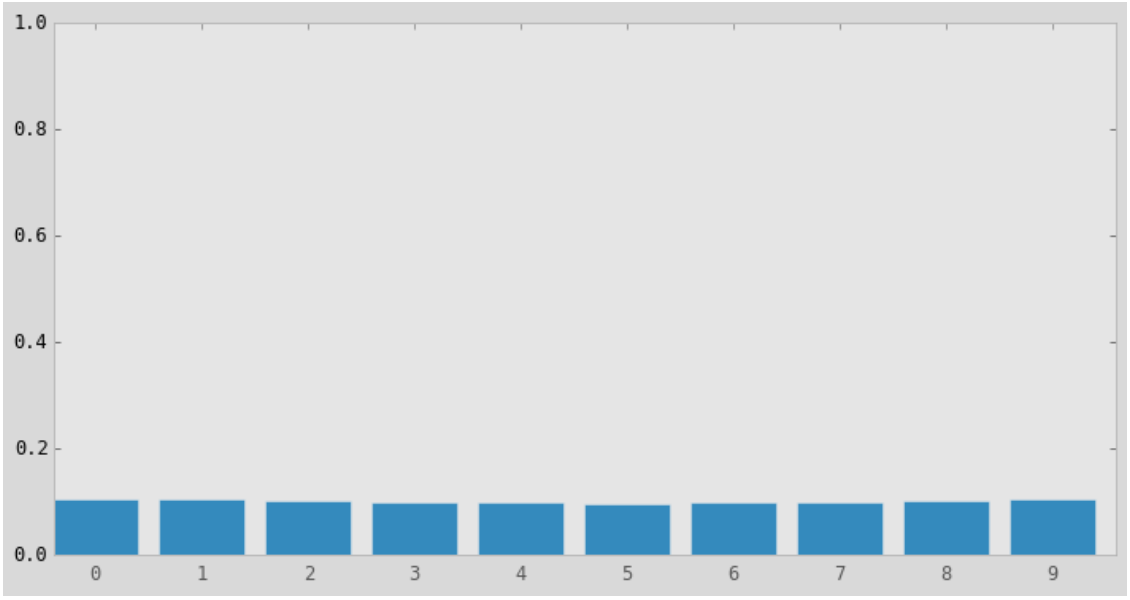
```
[ 0.1  0.1  0.1  0.1  0.1  0.1  0.1  0.1  0.1  0.1]
```



After 500 iterations we have lost all information, even though we were 100% sure that we started in position 1. Feel free to play with the numbers to see the effect of different number of updates. For example, after 100 updates we have a small amount of information left.

```
In [14]: pos = [1.0,0,0,0,0,0,0,0,0,0]
         for i in range(100):
             pos = predict(pos, 1, .8, .1, .1)
         print(pos)
         bar_plot.plot(pos)
```

```
[ 0.10407069  0.10329322  0.10125784  0.09874205  0.09670682  0.09592945
  0.09670682  0.09874205  0.10125784  0.10329322]
```



3.6 Integrating Measurements and Movement Updates

The problem of loosing information during an update may make it seem as if our system would quickly devolve into no knowledge. However, recall that our process is not an endless series of updates, but of *measure->update->measure->update->measure->update...* The output of the measure step is fed into the update. The update step, with a degraded certainty, is then fed into the measure step.

Let's think about this intuitively. After the first measure->update round we have degraded the knowledge we gained by the measurement by a small amount. But now we take another measurement. When we try to incorporate that new measurement into our belief, do we become more certain, less certain, or equally certain. Consider a simple case - you are sitting in your office. A co-worker asks another co-worker where you are, and they report "in his office". You keep sitting there while they ask and answer "has he moved"? "No" "Where is he" "In his office". Eventually you get up and move, and lets say the person didn't see you move. At that time the questions will go "Has he moved" "no" (but you have!) "Where is he" "In the kitchen". Wow! At that moment the statement that you haven't moved conflicts strongly with the next measurement that you are in the kitchen. If we were modelling these with probabilities the probability that you are in your office would lowever, and the probability that you are in the kitchen would go up a little bit. But now imagine the subsequent conversation: "has he moved" "no" "where is he" "in the kitchen". Pretty quickly the belief that you are in your office would fade away, and the belief that you are in the kitchen would increase to near certainty. The belief that you are in the office will never go to zero, nor will the belief that you are in the kitchen ever go to 1.0 because of the chances of error, but in practice your co-workers would be correct to be quite confident in their system.

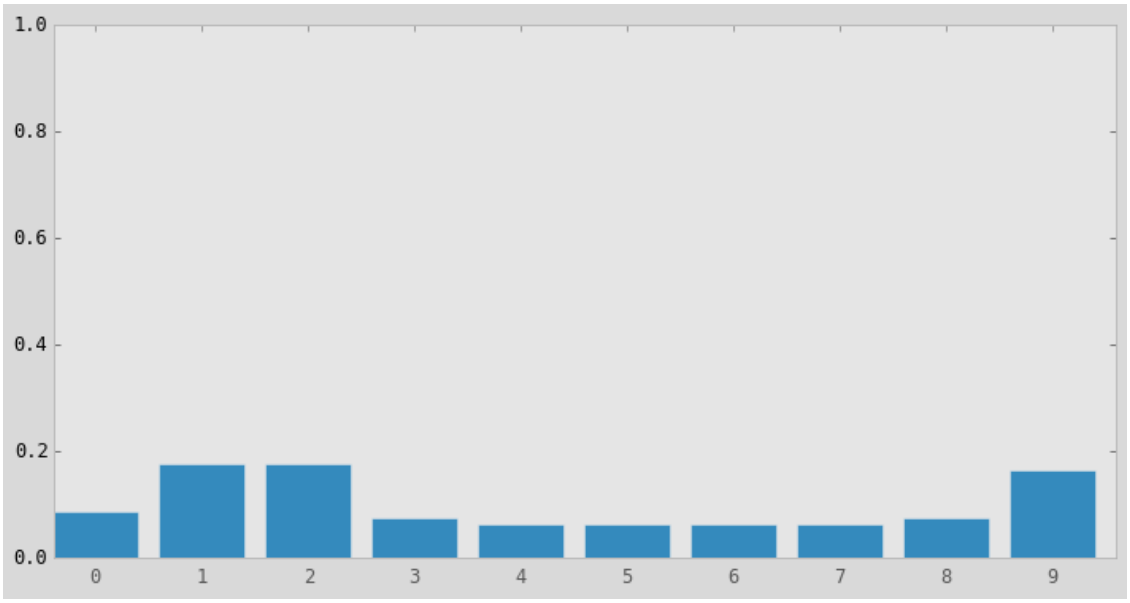
That is what intuition tells us. What does the math tell us?

Well, we have already programmed the measure step, and we have programmed the update step. All we need to do is feed the result of one into the other, and we will have programmed our dog tracker!!! Let's see how it performs. We will input data as if the dog started at position 0 and moved right at each update. However, as in a real world application, we will start with no knowledge and assign equal probability to all positions.

```
In [15]: p = np.array([.1]*10)
         p = update(p, 1, .6, .2)
         print(p)
         p = predict(p, 1, .8, .1, .1)
         print(p)
         bar_plot.plot(p)
```

```
[ 0.1875  0.1875  0.0625  0.0625  0.0625  0.0625  0.0625  0.0625  0.1875
  0.0625]
```

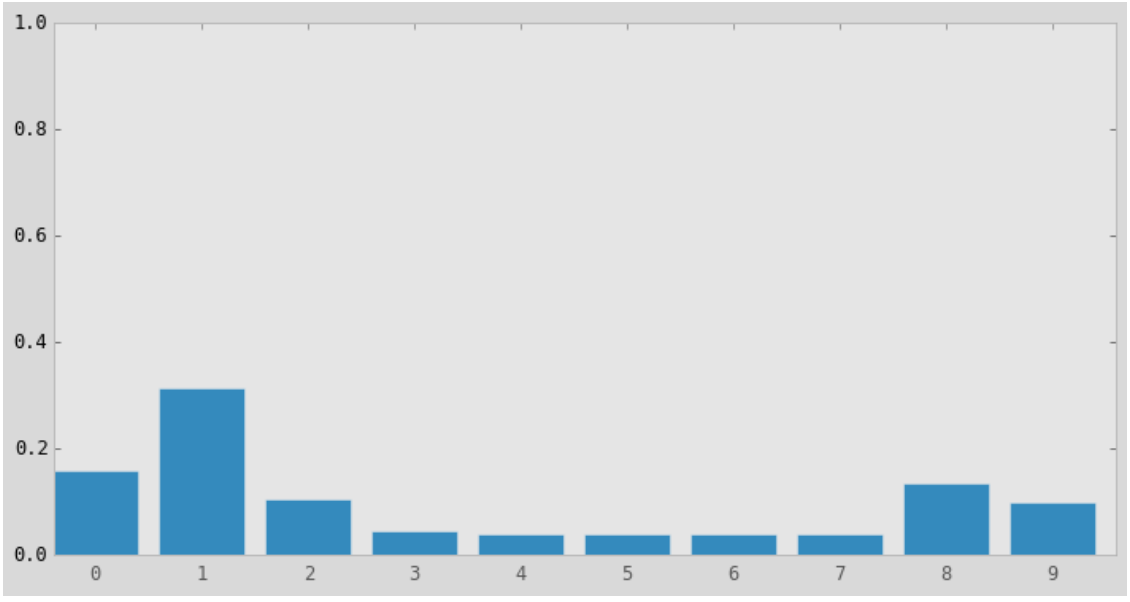
```
[ 0.0875  0.175   0.175   0.075   0.0625  0.0625  0.0625  0.0625  0.075
  0.1625]
```



So after the first sense we have assigned a high probability to each door position, and a low probability to each wall position. The update step shifted these probabilities to the right, smearing them about a bit. Now lets look at what happens at the next sense.

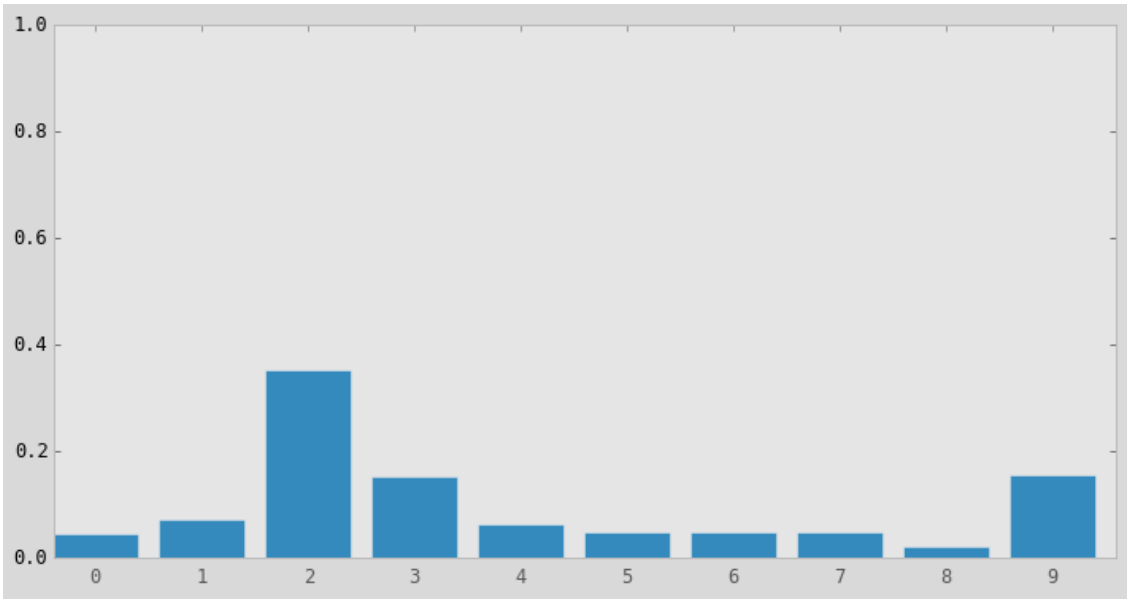
```
In [16]: p = update(p, 1, .6, .2)
         print(p)
         bar_plot.plot(p)
```

```
[ 0.15671642  0.31343284  0.10447761  0.04477612  0.03731343  0.03731343
  0.03731343  0.03731343  0.13432836  0.09701493]
```



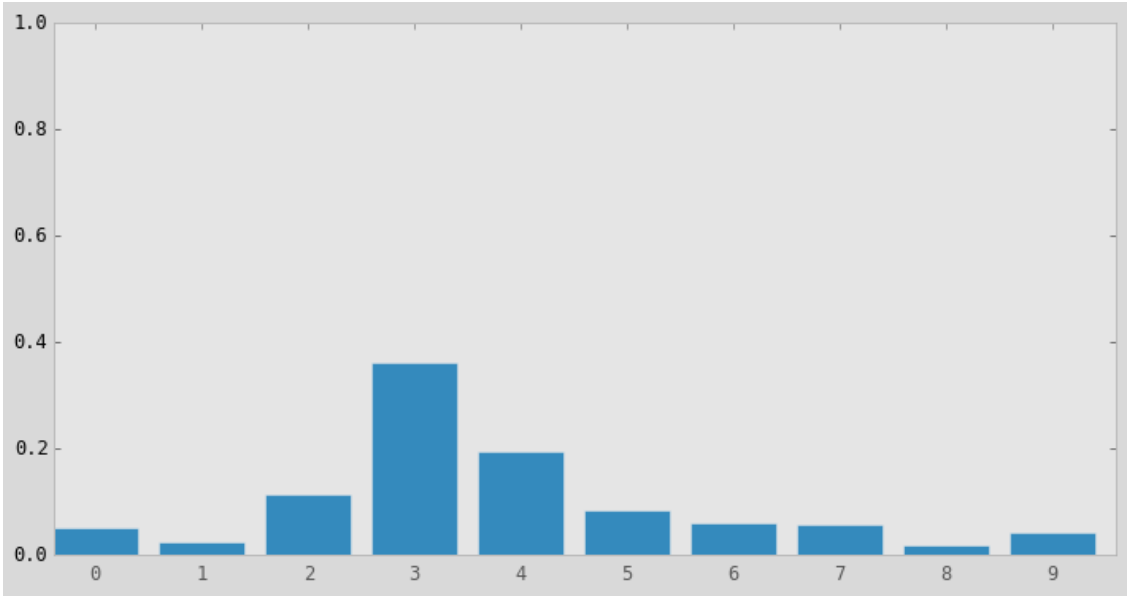
Notice the tall bar at position 1. This corresponds with the (correct) case of starting at position 0, sensing a door, shifting 1 to the right, and sensing another door. No other positions make this set of observations as likely. Now lets add an update and then sense the wall.

```
In [17]: p = predict(p, 1, .8, .1, .1)
         p = update(p, 0, .6, .2)
         bar_plot.plot(p)
```



This is exciting! We have a very prominent bar at position 2 with a value of around 35%. It is over twice the value of any other bar in the plot, and is about 4% larger than our last plot, where the tallest bar was around 31%. Let's see one more sense->update cycle.

```
In [18]: p = predict(p, 1, .8, .1, .1)
         p = update(p, 0, .6, .2)
         bar_plot.plot(p)
```



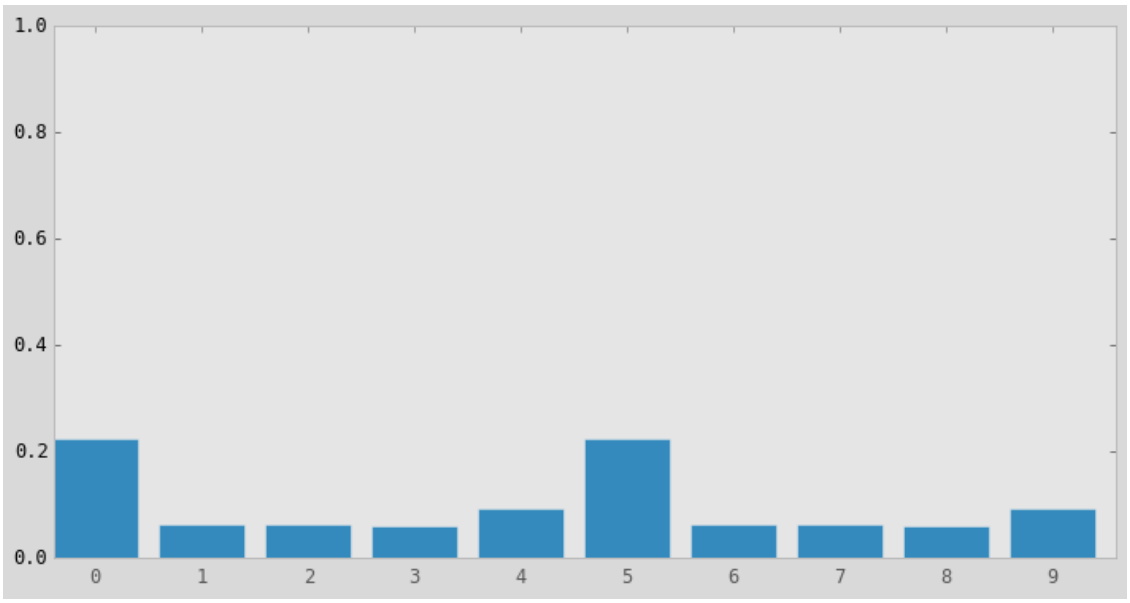
Here things have degraded a bit due to the long string of wall positions in the map. We cannot be as sure where we are when there is an undifferentiated line of wall positions, so naturally our probabilities spread out a bit.

3.7 The Effect of Bad Sensor Data

You may be suspicious of the results above because I always passed correct sensor data into the functions. However, we are claiming that this code implements a *filter* - it should filter out bad sensor measurements. Does it do that?

To make this easy to program and visualize I will change the layout of the hallway to mostly alternating doors and hallways:

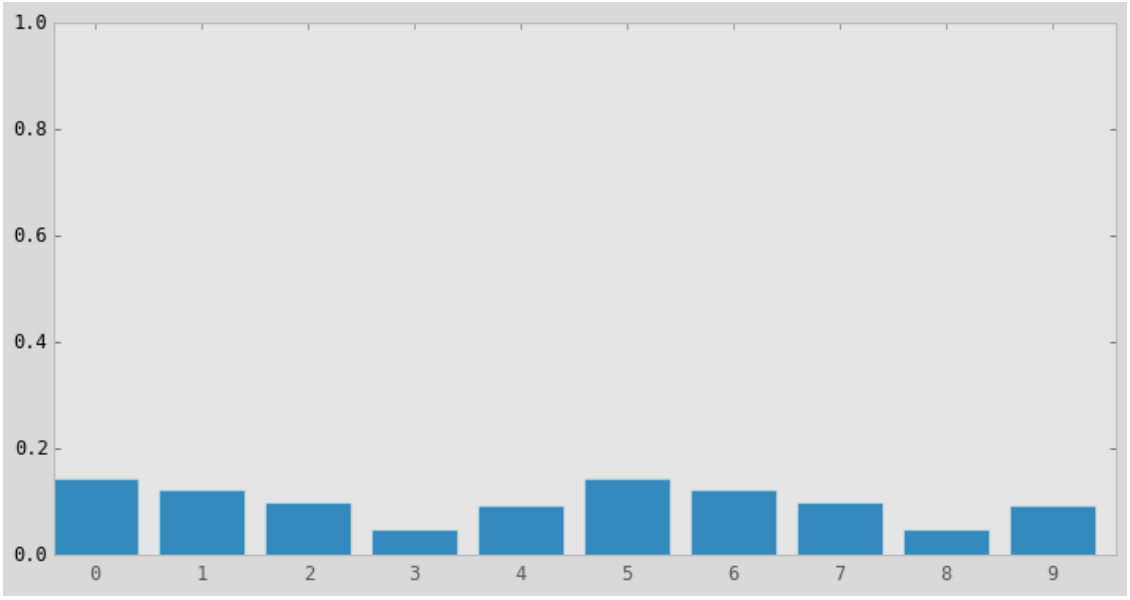
```
In [19]: hallway = [1,0,1,0,0,1,0,1,0,0]
         pos = np.array([.1]*10)
         measurements = [1,0,1,0,0]

         for m in measurements:
             pos = update(pos, m, .6, .2)
             pos = predict(pos, 1, .8, .1, .1)
         bar_plot.plot(pos)
         print(pos)
```




```
[ 0.2245871   0.06288015  0.06109133  0.0581008   0.09334062  0.2245871
  0.06288015  0.06109133  0.0581008   0.09334062]
```

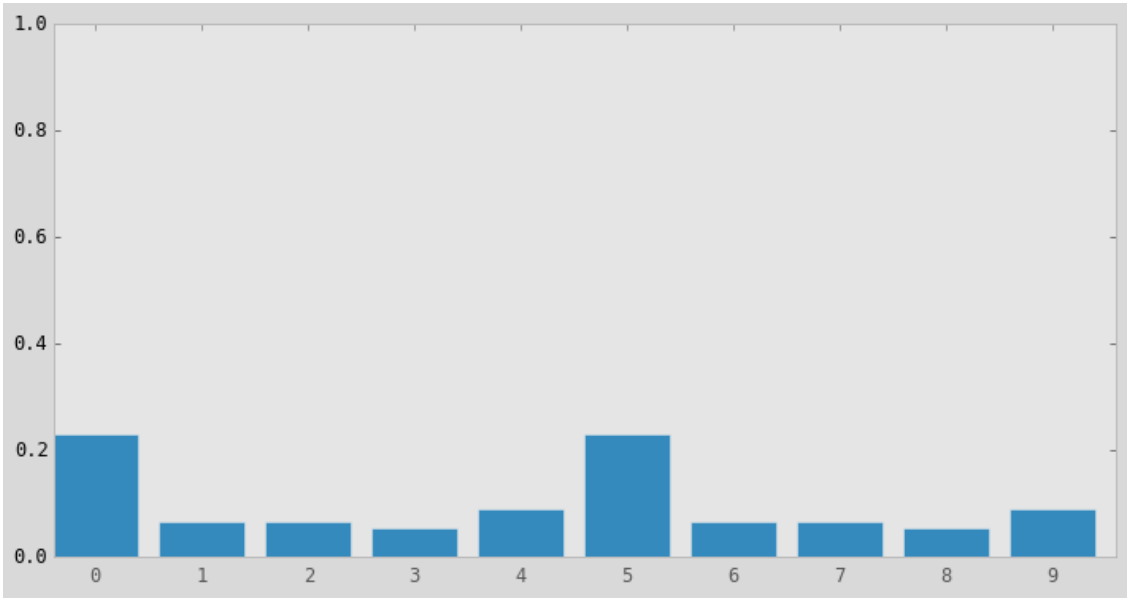
At this point we have correctly identified the likely cases, we either started at position 0 or 5, because we saw the following sequence of doors and walls 1,0,1,0,0. But now lets inject a bad measurement, and see what happens:

```
In [20]: pos = update(pos, m, .6, .2)
         pos = predict(pos, 1, .8, .1, .1)
         bar_plot.plot(pos)
```



That one bad measurment appears to have significantly eroded our knowledge. However, note that our highest probabilities are still at 0 and 5, which is correct. Now let's continue with a series of correct measurements

```
In [21]: measurements = [0,1,0,1,0,0]

         for m in measurements:
             pos = update(pos, m, .6, .2)
             pos = predict(pos, 1, .8, .1, .1)
         bar_plot.plot(pos)
```



As you can see we quickly filtered out the bad sensor reading and converged on the most likely positions for our dog.

3.8 Drawbacks and Limitations

Do not be mislead by the simplicity of the examples I chose. This is a robust and complete implementation of a histogram filter, and you may use the code in real world solutions. If you need a multimodal, discrete filter, this filter works.

With that said, while this filter is used in industry, it is not used often because it has several limitations. Getting around those limitations is the motivation behind the chapters in the rest of this book.

The first problem is scaling. Our dog tracking problem used only one variable, *pos*, to denote the dog's position. Most interesting problems will want to track several things in a

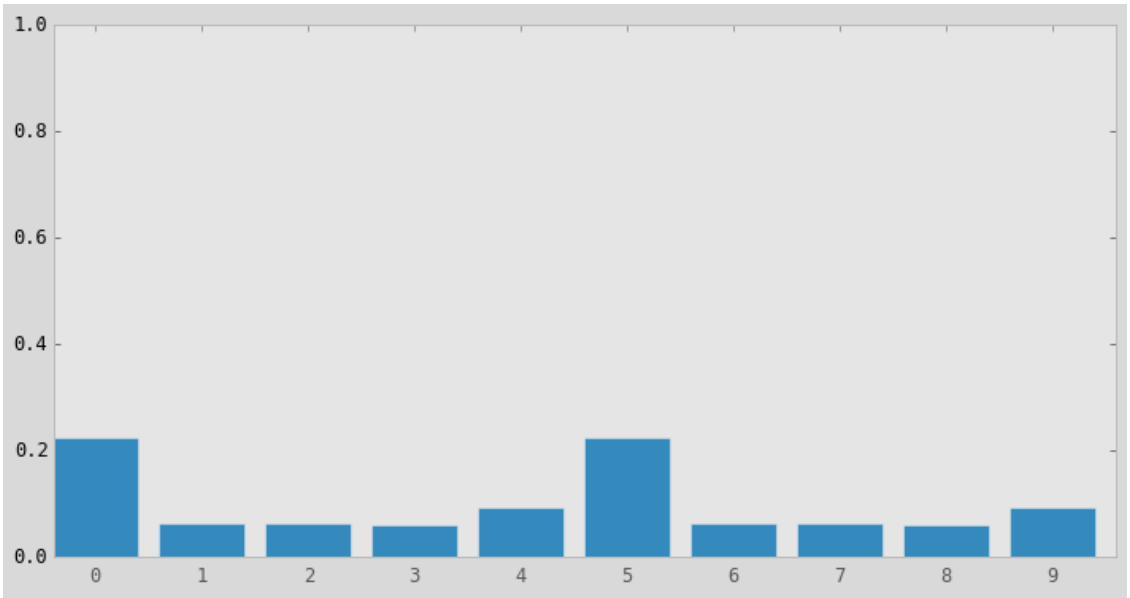
large space. Realistically, at a minimum we would want to track our dogs (x, y) coordinate, and probably his velocity $(\dot{x}, \dot{y})$ as well. We have not covered the multidimensional case, but instead of a histogram we use a multidimensional grid to store the probabilities at each discrete location. Each *sense()* and *update()* step requires updating all values in the grid, so a simple four variable problem would require $O(n^4)$ running time *per time step*. Realistic filters have 10 or more variables to track, leading to exhorbinant computation requirements.

The second problem is that the histogram is discrete, but we live in a continuous world. The histogram requires that you model the output of your filter as a set of discrete points. In our dog in the hallway example, we used 10 positions, which is obviously far too few positions for anything but a toy problem. For example, for a 100 meter hallway you would need 10,000 positions to model the hallway to 1cm accuracy. So each sense and update operation would entail performing calculations for 10,000 different probabilities. It gets exponentially worse as we add dimensions. If our dog was roaming in a $100x100m^2$ courtyard, we would need 100,000,000 bins $(10,000^2)$ to get 1cm accuracy.

A third problem is that the histogram is multimodal. This is not always a problem - an entire class of filters, the particle filters, are multimodal and are often used because of this property. But imagine if the GPS in your car reported to you that it is 40% sure that you are on D street, but 30% sure you are on Willow Avenue. I doubt that you would find that useful. Also, GPSs report their error - they might report that you are at $(109.878W, 38.326N)$ with an error of $9m$. There is no clear mathematical way to extract error information from a histogram. Heuristics suggest themselves to be sure, but there is no exact determination. You may or may not care about that while driving, but you surely do care if you are trying to send a rocket to Mars or track and hit an oncoming missle.

This difficulty is related to the fact that the filter often does not represent what is physically occuring in the world. Consider this distribution for our dog:

```
In [22]: p = [0.2245871, 0.06288015, 0.06109133, 0.0581008, 0.09334062, 0.2245871,
              0.06288015, 0.06109133, 0.0581008,  0.09334062]
         bar_plot.plot(p)
```



The largest probabilities are in position 0 and position 5. This does not fit our physical intuition at all. A dog cannot be in two places at once (my dog Simon certainly tries - his food bowl and my lap often have equal allure to him). We would have to use heuristics to decide how to interpret this distribution, and there is usually no satisfactory answer. This is not always a weakness - a considerable amount of literature has been written on *Multi-Hypothesis Tracking (MHT)*. We cannot always distill our knowledge to one conclusion, and MHT uses various techniques to maintain multiple story lines at once, using backtracking schemes to go *back in time* to correct hypothesis once more information is known. This will be the subject of later chapters. In other cases we truly have a multimodal situation - we may be optically tracking pedistrians on the street and need to represent all of their positions.

In practice it is the exponential increase in computation time that leads to this filter being the least frequently used of all filters in this book. Many problems are best formulated as discrete or multimodal, but we have other filter choices with better performance. With that said, if I had a small problem that this technique could handle I would choose to use it; it is trivial to implement, debug, and understand, all virtues in my book.

3.9 Generalizing to Multiple Dimensions

3.10 Summary

The code is very small, but the result is huge! We will go into the math more later, but we have implemented a form of a Bayesian filter. It is commonly called a Histogram filter. The Kalman filter is also a Bayesian filter, and uses this same logic to produce it's results. The math is a bit more complicated, but not by much. For now, we will just explain that Bayesian statistics compute the liklihood of the present based on the past. If we know there are two doors in a row, and the sensor reported two doors in a row, it is likely that we are positioned near those doors. Bayesian statistics just formalizes that example, and Bayesian filters formalize filtering data based on that math by implementing the sense->update->sense->update process.

We have learned how to start with no information and derive information from noisy sensors. Even though our sensors are very noisey (most sensors are more then 80% accurate, for example) we quickly converge on the most likely position for our dog. We have learned how the update step always degrades our knowledge, but the addition of another measurement, even when it might have noise in it, improves our knowlege, allowing us to converge on the most likely result.

If you followed the math carefully you will realize that all of this math is exact. The bar charts that we are displaying are not an *estimate* or *guess* - they are mathematically exact results that exactly represent our knowledge. The knowledge is probabilistic, to be sure, but it is exact, and correct.

However, we are a long way from tracking an airplane or a car. This code only handles the 1 dimensional case, whereas cars and planes operate in 2 or 3 dimensions. Also, our

position vector is *multimodal*. It expresses multiple beliefs at once. Imagine if your GPS told you "it's 20% likely that you are here, but 10% likely that you are on this other road, and 5% likely that you are at one of 14 other locations. That would not be very useful information. Also, the data is discrete. We split an area into 10 (or whatever) different locations, whereas in most real world applications we want to work with continuous data. We want to be able to represent moving 1 km, 1 meter, 1 mm, or any arbitrary amount, such as 2.347 cm.

Finally, the bar charts may strike you as being a bit less certain than we would want. A 25% certaintly may not give you a lot of confidence in the anwser. Of course, what is important here is the ratio of this probability to the other probabilities in your vector. If the next largest bar is 23% then we are not very knowledgable about our position, whereas if the next largest is 3% we are in fact quite certain. But this is not clear or intuitive. However, there is an extremely important insight that Kalman filters implement that will signficantly improve our accuracy from the same data.

If you can understand this chapter you will be able to understand and implement Kalman filters I cannot stress this enough. If anything is murky, go back and reread this chapter and play with the code. the rest of this book will build on the algorithms that we use here. If you don't intuitively understand why this histogram filter works, and can at least work through the math, you will have little success with the rest of the material. However, if you grasp the fundamental insight - multiplying probabilities when we measure, and shifting probabilities when we update leads to a converging solution - then you understand everything important you need to grasp the Kalman filter.

Author notes: Do I want to go to the multidimensional case? At least describe it, but why not implement it as well

Chapter 4

Least Squares Filters

4.1 Introduction

Chapter 5

Gaussian Probabilities

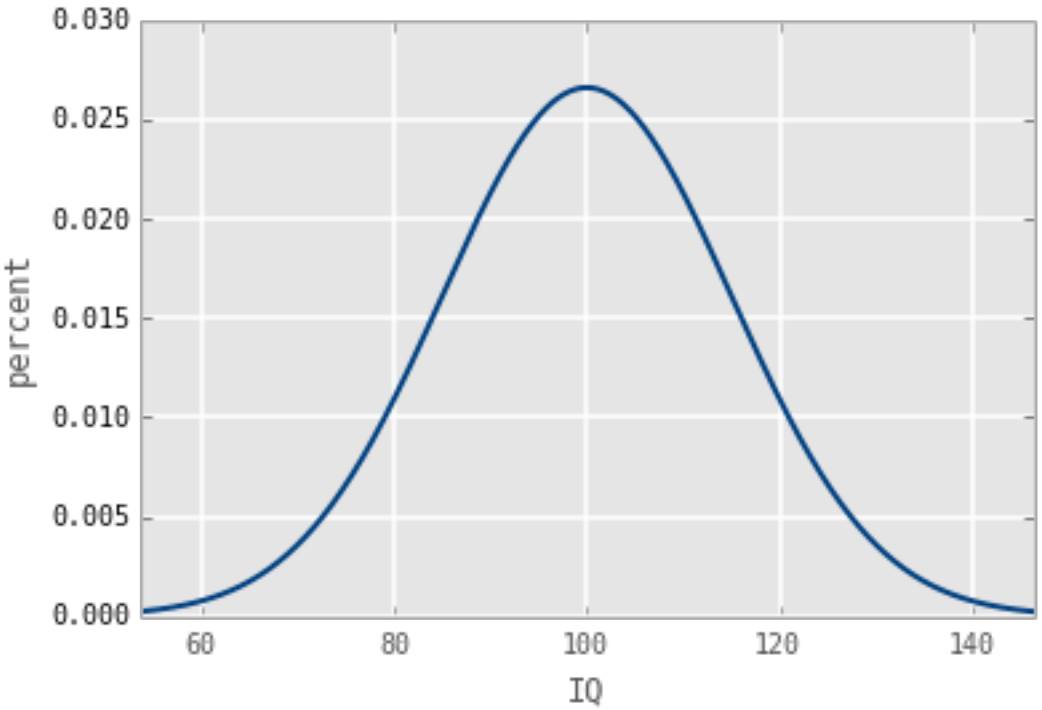
5.1 Introduction

The last chapter ended by discussing some of the drawbacks of the Discrete Bayesian filter. For many tracking and filtering problems our desire is to have a filter that is *unimodal* and *continuous*. That is, we want to model our system using floating point math (continuous) and to have only one belief represented (unimodal). For example, we want to say an aircraft is at (12.34381, -95.54321,2389.5) where that is latitude, longitude, and altitude. We do not want our filter to tell us "it might be at (1,65,78) or at (34,656,98)" That doesn't match our physical intuition of how the world works, and as we discussed, it is prohibitively expensive to compute.

> So we desire a unimodal, continuous way to represent probabilities that models how the real world works, and that is very computationally efficient to calculate. As you might guess from the chapter name, Gaussian distributions provide all of these features.

Before we go into the math, lets just look at a graph of the Gaussian distribution to get a sense of what we are talking about.

```
In [13]: from stats import plot_gaussian

         plot_gaussian(mean=100, variance=15*15, xlabel='IQ', ylabel='percent')
```



Probably this is immediately recognizable to you as a 'bell curve'. This curve is ubiquitous because under real world conditions most observations are distributed in such a manner. In fact, this is the bell curve for IQ (Intelligence Quotient). You've probably seen this before, and understand it. It tells us that the average IQ is 100, and that the number of people that have IQs higher or lower than that drops off as they get further away from 100. It's hard to see the exact number, but we can see that very few people have an IQ over 150 or under 50, but a lot have an IQ of 90 or 110.

This curve is not unique to IQ distributions - a vast amount of natural phenomena exhibits this sort of distribution, including the sensors that we use in filtering problems. As we will see, it also has all the attributes that we are looking for - it represents a unimodal belief or value as a probability, it is continuous, and it is computationally efficient. We will soon discover that it also other desirable qualities that we do not yet recognize we need.

5.2 Nomenclature

A bit of nomenclature before we continue - this chart depicts the probability of of a *random variable* having any value between $(-\infty..\infty)$. For example, for this chart the probability of the variable being 100 is roughly 2.7%, whereas the probability of it being 80 is around 1%. > *Random variable* will be precisely defined later. For now just think of it as a variable that can 'freely' and 'randomly' vary. A dog's position in a hallway, air temperature, and a drone's height above the ground are all random variables. The position of the North Pole is not, nor is a sin wave (a sin wave is anything but 'free').

You may object that human IQs cannot be less than zero, let alone $-\infty$. This is true, but this is a common limitation of mathematical modeling. "The map is not the territory" is a common expression, and it is true for Bayesian filtering and statistics. The Gaussian distribution above very closely models the distribution of IQ test results, but being a model it is necessarily imperfect. The difference between model and reality will come up again and again in these filters.

You will see these distributions called *Gaussian distributions*, *normal distributions*, and *bell curves*. Bell curve is ambiguous because there are other distributions which also look bell shaped but are not Gaussian distributions, so we will not use it further in this book. But *Gaussian* and *normal* both mean the same thing, and are used interchangeably. I will use both throughout this book as different sources will use either term, and so I want you to be used to seeing both. Finally, as in this paragraph, it is typical to shorten the name and just talk about a *Gaussian* or *normal* - these are both typical shortcut names for the *Gaussian distribution*.

5.3 Gaussian Distributions

So let us explore how Gaussians work. A Gaussian is a *continuous probability distribution* that is completely described with two parameters, the mean (μ) and the variance (σ^2). It is defined as:

$$f(x, \mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{1}{2}(x-\mu)^2/\sigma^2}$$

Don't be dissuaded by the equation if you haven't seen it before; you will not need to memorize or manipulate it. The computation of this function is stored in stats.py.

> **Optional:** Let's remind ourselves how to look at a function stored in a file by using the *%load* magic. If you type *%load -s gaussian stats.py* into a code cell and then press CTRL-Enter, the notebook will create a new input cell and load the function into it.

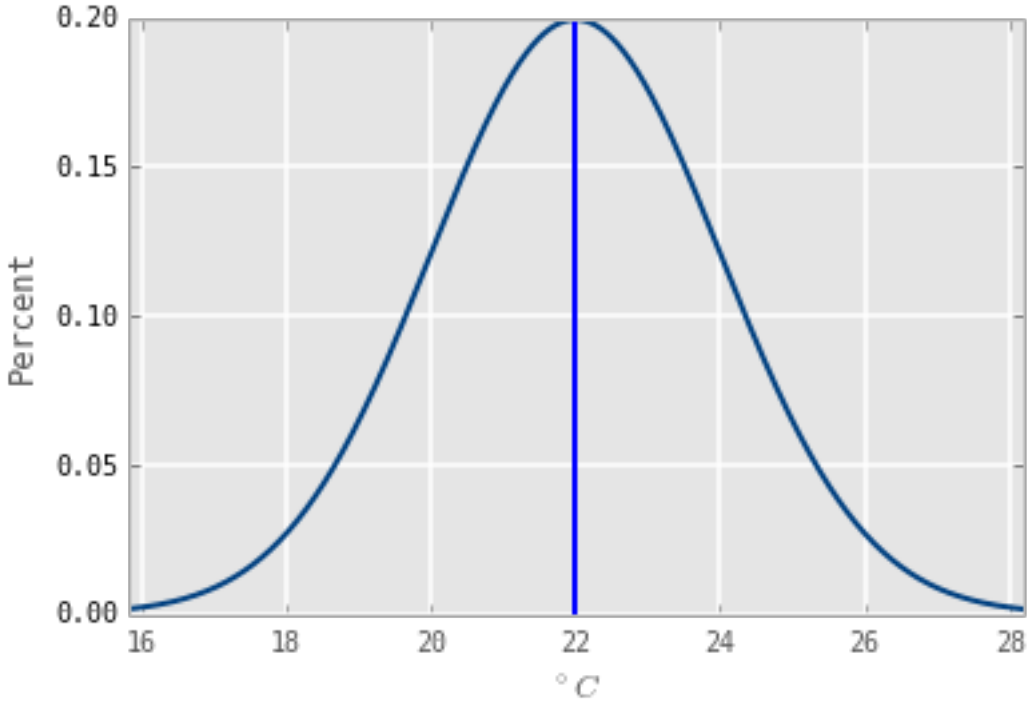
```
%load -s gaussian stats.py

def gaussian(x, mean, var):
    """returns normal distribution for x given a
    gaussian with the specified mean and variance.
    """
    return math.exp((-0.5*(x-mean)**2)/var) / \
                    math.sqrt(_two_pi*var)
```

We will plot a Gaussian with a mean of 22 ($\mu = 22$), with a variance of 4 ($\sigma^2 = 4$), and then discuss what this means.

```
In [14]: from stats import gaussian
         plot_gaussian(22,4,mean_line=True,xlabel='$^{\circ}C$',ylabel="Percent")
```

```
print('Probability of 22 is %.2f' % (gaussian(22,22,4)*100))
print('Probability of 24 is %.2f' % (gaussian(24,22,4)*100))
```

```
Probability of 22 is 19.95
Probability of 24 is 12.10
```



So what does this curve *mean*? Assume for a moment that we have a thermometer, which reads $22\,°C$. No thermometer is perfectly accurate, and so we normally expect that thermometer will read $\pm$ that temperature by some amount each time we read it. Furthermore, a theorem called **Central Limit Theorem** states that if we make many measurements that the measurements will be normally distributed. If that is true, then this chart can be interpreted as a continuous curve depicting our belief that the temperature is any given temperature. In this curve, we assign a probability of the temperature being exactly $22°C$ is 19.95%. Looking to the right, we assign the probability that the temperature is $24°C$ is 12.10%. Because of the curve's symmetry, the probability of 20°C is also 12.10%.

So the mean (μ) is what it sounds like - the average of all possible probabilities. Because of the symmetric shape of the curve it is also the tallest part of the curve. The thermometer reads $22°C$, so that is what we used for the mean.

> *Important*: I will repeat what I wrote at the top of this section: "A Gaussian. . . is completely described with two parameters"

The standard notation for a normal distribution for a random variable X is $X \sim \mathcal{N}(\mu, \sigma^2)$. This means I can express the temperature reading of our thermometer as

$$temp = \mathcal{N}(22, 4)$$

This is an **extremely important** result. Gaussians allow me to capture an infinite number of possible values with only two numbers! With the values $\mu = 22$ and $\sigma^2 = 4$ I can compute the probability of the temperature being $22\,^\circ C$, $20\,^\circ C$, $87.34\,^\circ C$, or any other arbitrary value.

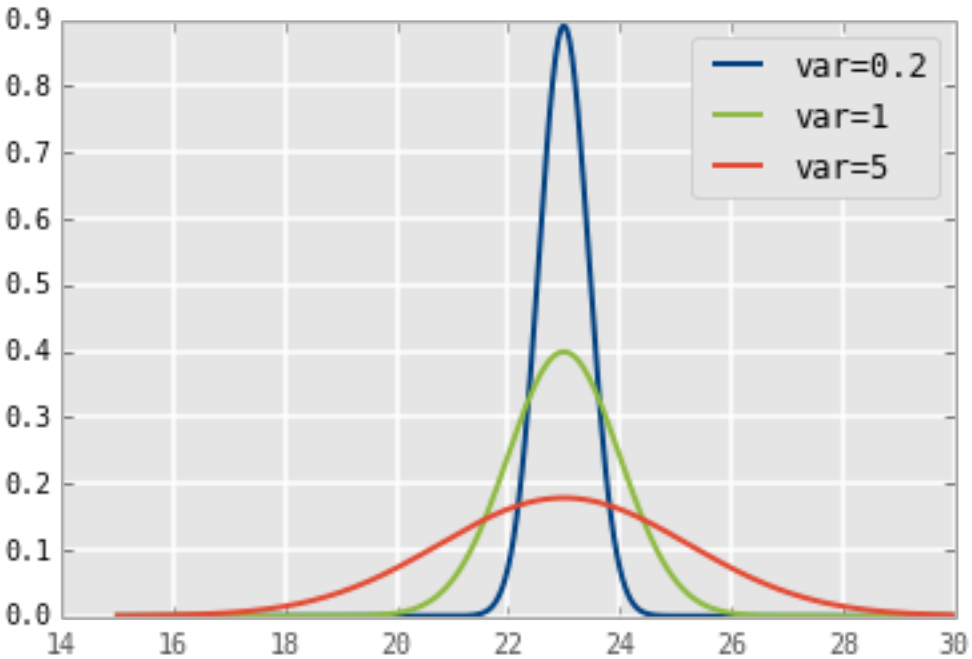
The Variance

Since this is a probability distribution it is required that the area under the curve always equals one. This should be intuitively clear - the area under the curve represents all possible occurences, which must sum to one.

This leads to an important insight. If the variance is small the curve will be narrow. To keep the area equal to 1, the curve must also be tall. On the other hand if the variance is large the curve will be wide, and thus it will also have to be short to make the area equal to 1.

Let's look at that graphically:

```
In [15]: import numpy as np
         import matplotlib.pyplot as plt

         xs = np.arange(15,30,0.05)
         p1, = plt.plot (xs,[gaussian(x, 23, .2) for x in xs], label='var=0.2')
         p2, = plt.plot (xs,[gaussian(x, 23, 1) for x in xs], label='var=1')
         p3, = plt.plot (xs,[gaussian(x, 23, 5) for x in xs], label='var=5')
         plt.legend()
         plt.show()
```



So what is this telling us? The blue gaussian is very narrow. It is saying that we believe $x = 23$, and that we are very sure about that ($90 are much less sure about that (18$ and so our belief about the likely possible values for x is spread out - we think it is quite likely that $x = 20$ or $x = 26$, for example. The blue gaussian has almost completely eliminated 22 or 24 as possible value - their probability is almost 0%, whereas the red curve considers them nearly as likely as 23.

If we think back to the thermometer, we can consider these three curves as representing the readings from three different thermometers. The blue curve represents a very accurate thermometer, and the red one represents a fairly inaccurate one. Green of course represents one in between the two others. Note the very powerful property the Gaussian distribution affords us - we can entirely represent both the reading and the error of a thermometer with only two numbers - the mean and the variance.

The standard notation for a normal distribution for a random variable X is just $X \sim \mathcal{N}(\mu, \sigma^2)$ where μ is the mean and σ^2 is the variance. It may seem odd to use σ squared - why not just σ? We will not go into great detail about the math at this point, but in statistics σ is the *standard deviation* of a normal distribution. *Variance* is defined as the square of the standard deviation, hence σ^2.

It is worth spending a few words on standard deviation now. The standard deviation is a measure of how much variation from the mean exists. For Gaussian distributions, 68% of all the data falls within one standard deviation(1σ) of the mean, 95% falls within two standard deviations (2σ), and 99.7% within three (3σ). This is often called the 68-95-99.7 rule. So if you were told that the average test score in a class was 71 with a standard deviation of 9.4, you could conclude that 95% of the students received a score between 52.2 and 89.8 if the distribution is normal (that is calculated with $71 \pm (2 * 9.4)$).

The following graph depicts the relationship between the standard deviation and the normal distribution.

```
In [16]: from gaussian_internal import display_stddev_plot
         display_stddev_plot()
         plt.show()
```

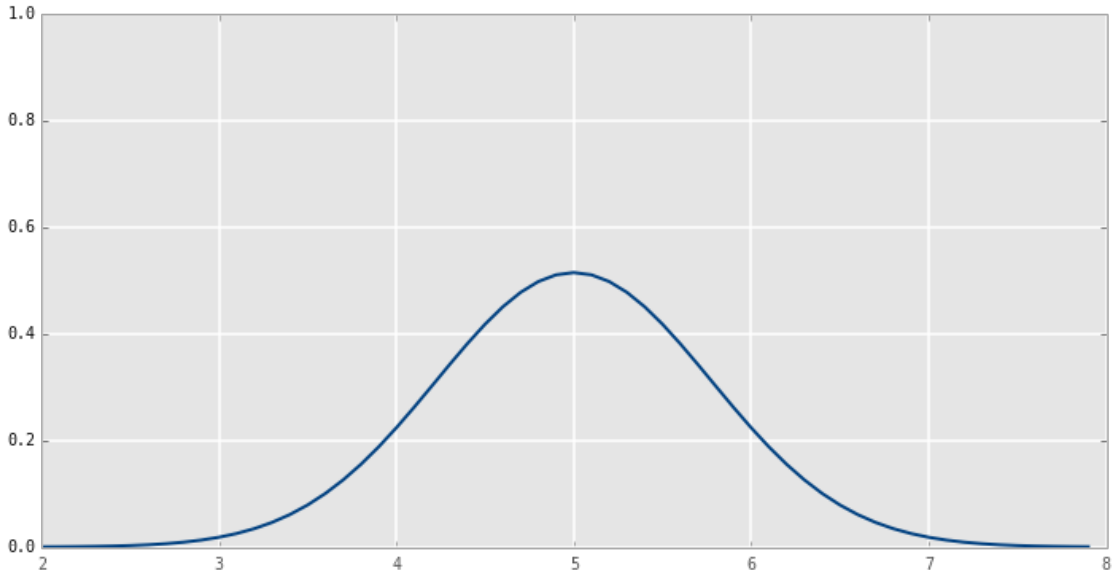
Sidebar: An equivalent formation for a Gaussian is $\mathcal{N}(\mu, 1/\tau)$ where μ is the *mean* and *tau* the *precision*. Here $1/\tau = \sigma^2$; it is the reciprocal of the variance. While we do not use this formulation in this book, it underscores that the variance is a measure of how precise our data is. A small variance yields large precision - our measurement is very precise. Conversely, a large variance yields low precision - our belief is spread out across a large area. You should become comfortable with thinking about Gaussians in these equivalent forms. Gaussians reflect our *belief* about a measurement, they express the *precision* of the measurement, and they express how much *variance* there is in the measurements. These are all different ways of stating the same fact.

5.4 Interactive Gaussians

For those that are reading this in IPython Notebook, here is an interactive version of the Gaussian plots. Use the sliders to modify μ and σ^2. Adjusting μ will move the graph to the left and right because you are adjusting the mean, and adjusting σ^2 will make the bell curve thicker and thinner.

```
In [17]: import math
         from IPython.html.widgets import interact, interactive, fixed
         import IPython.html.widgets as widgets

         def plt_g (mu,variance):
             xs = np.arange(2,8,0.1)
             ys = [gaussian (x, mu,variance) for x in xs]
             plt.plot (xs, ys)
             plt.ylim((0,1))
```

```
    plt.show()

interact (plt_g, mu=(0,10), variance=widgets.FloatSliderWidget(value=0.6,min=0.
```



Out[17]: <function __main__.plt_g>

5.5 Computational Properties of the Gaussian

Recall how our discrete Bayesian filter worked. We had a vector implemented as a numpy array representing our belief at a certain moment in time. When we performed another measurement using the `sense()` function we had to multiply probabilities together, and when we performed the motion step using the `update()` function we had to shift and add probabilities. I've promised you that the Kalman filter uses essentially the same process, and that it uses Gaussians instead of histograms, so you might reasonable expect that we will be multiplying, adding, and shifting Gaussians in the Kalman filter.

A typical textbook would directly launch into a multipage proof of the behavior of Gaussians under these operations, but I don't see the value in that right now. I think the math will be much more intuitive and clear if we just start developing a Kalman filter using Gaussians. I will provide the equations for multiplying and shifting Gaussians at the appropriate time. You will then be able to develop a physical intuition for what these operations do, rather than be forced to digest a lot of fairly abstract math.

The key point, which I will only assert for now, is that all the operations are very simple, and that they preserve the properties of the Gaussian. This is somewhat remarkable, in that the Gaussian is a nonlinear function, and typically if you multiply a nonlinear equation with itself you end up with a different equation. For example, the shape of `sin(x)sin(x)` is very

different from `sin(x)`. But the result of multiplying two Gaussians is yet another Gaussian. This is a fundamental property, and the key reason why Kalman filters are possible.

5.6 Computing Probabilities with scipy.stats

In this chapter I have used by custom written code for computing Gaussians, plotting, and so on. I chose to do that to give you a chance to look at the code and see how these functions are implemented. However, Python comes with "batteries included" as the saying goes, and it comes with a wide range of statistics functions in the module scipy.stats. I find the performance of some of the functions rather slow (the scipy.stats documentation contains a warning to this effect), but this is offset by the fact that this is standard code available to everyone, and it is well tested. So let's walk through how to use scipy.stats to compute various things.

The scipy.stats module contains a number of objects which you can use to compute attributes of various probability distributions. The full documentation for this module is here: http://http://docs.scipy.org/doc/scipy/reference/stats.html. However, we will focus on the norm variable, which implements the normal distribution. Let's look at some code that uses `scipy.stats.norm` to compute a Gaussian, and compare its value to the value returned by the `gaussian()` function.

```
In [18]: from scipy.stats import norm
         print (norm(2,3).pdf(1.5))
         print (gaussian(x=1.5, mean=2, var=3*3))

0.131146572034
0.13114657203397997
```

The call `norm(2,3)` creates what scipy calls a 'frozen' distribution - it creates and returns an object with a mean of 2 and a standard deviation of 3. You can then use this object multiple times to get the probability of various values, like so:

```
In [19]: n23 = norm(2,3)
         print ('probability of 1.5 is %.4f' % n23.pdf(1.5))
         print ('probability of 2.5 is also %.4f' % n23.pdf(2.5))
         print ('whereas probability of 2 is %.4f' % n23.pdf(2))

probability of 1.5 is 0.1311
probability of 2.5 is also 0.1311
whereas probability of 2 is 0.1330
```

If we look at the documentation for `scipy.stats.norm` here[1] we see that there are many other functions that norm provides.

For example, we can generate n samples from the distribution with the `rvs()` function.

```
In [20]: print (n23.rvs(size=15))
```

```
[ 0.38741053 -4.91803911 -2.00879426 -1.15175952  2.63354369 -0.96097707
  2.45698146  4.22587531  3.69924957 -0.27811435 -0.94132557  4.96510082
  3.43324112  4.09462176  0.6446632 ]
```

We can get the *cumulative distribution function (CDF)*, which is the probability that a randomly drawn value from the distribution is less than or equal to x.

```
In [21]: # probability that a random value is less than the mean 2
         print (n23.cdf (2))
```

```
0.5
```

We can get various properties of the distribution:

```
In [23]: print ('variance is', n23.var())
         print ('standard deviation is', n23.std())
         print ('mean is', n23.mean())
```

```
variance is 9.0
standard deviation is 3.0
mean is 2.0
```

There are many other functions available, and if you are interested I urge you to peruse the documentation. I find the documentation to be excessively terse, but with a bit of googling you can find out what a function does and some examples of how to use it. Most of this functionality is not of immediate interest to the book, so I will leave the topic in your hands to explore. The tutorial is quite approachable, and I suggest starting there. tutorial[2]

5.7 Summary and Key Points

The following points **must** be understood by you before we continue:

- Normal distributions occur throughout nature
- They express a continuous probability distribution
- They are completely described by two parameters: the mean (μ) and variance (σ^2)
- μ is the average of all possible values
- σ^2 represents how much our measurements vary from the mean

5.8 References

[1] http://docs.scipy.org/doc/scipy/reference/generated/scipy.stats.norm.html#scipy.stats.normfor
[2] http://docs.scipy.org/doc/scipy/reference/tutorial/stats.html

Chapter 6

Kalman Filters

6.1 One Dimensional Kalman Filters

Now that we understand the histogram filter and Gaussians we are prepared to implement a 1D Kalman filter. We will do this exactly as we did the histogram filter - rather than going into the theory we will just develop the code step by step. But first, let's set the book style.

6.2 Tracking A Dog

As in the histogram chapter we will be tracking a dog in a long hallway at work. However, in our latest hackathon someone created an RFID tracker that provides a reasonable accurate position for our dog. Suppose the hallway is 100m long. The sensor returns the distance of the dog from the left end of the hallway. So, 23.4 would mean the dog is 23.4 meters from the left end of the hallway.

Naturally, the sensor is not perfect. A reading of 23.4 could correspond to a real position of 23.7, or 23.0. However, it is very unlikely to correspond to a real position of say 47.6. Testing during the hackathon confirmed this result - the sensor is reasonably accurate, and while it had errors, the errors are small. Furthermore, the errors seemed to be evenly distributed on both sides of the measurement; a true position of 23m would be equally likely to be measured as 22.9 as 23.1.

Implementing and/or robustly modeling an RFID system is beyond the scope of this book, so we will write a very simple model. We will start with a simulation of the dog moving from left to right at a constant speed with some random noise added.

```
In [2]: from __future__ import print_function, division
        import matplotlib.pyplot as plt
        import numpy.random as random
        import math

        class DogSensor(object):

            def __init__(self, x0=0, velocity=1, noise=0.0):
```

```
        """ x0 - initial position
            velocity - (+=right, -=left)
            noise - scaling factor for noise, 0== no noise
        """
        self.x = x0
        self.velocity = velocity
        self.noise = math.sqrt(noise)

    def sense(self):
        self.x = self.x + self.velocity
        return self.x + random.randn() * self.noise
```

The constructor `__init()__` initializes the DogSensor class with an initial position `x0`, velocity `vel`, and an noise scaling factor. The `sense()` function has the dog move by the set velocity and returns its new position, with noise added. If you look at the code for `sense()` you will see a call to `numpy.random.randn()`. This returns a number sampled from a normal distribution with a mean of 0.0. Let's look at some example output for that.

```
In [3]: for i in range(20):
            print('{: 5.4f}'.format(random.randn()),end='\t')
            if (i+1) % 5 == 0:
                print ('')
```

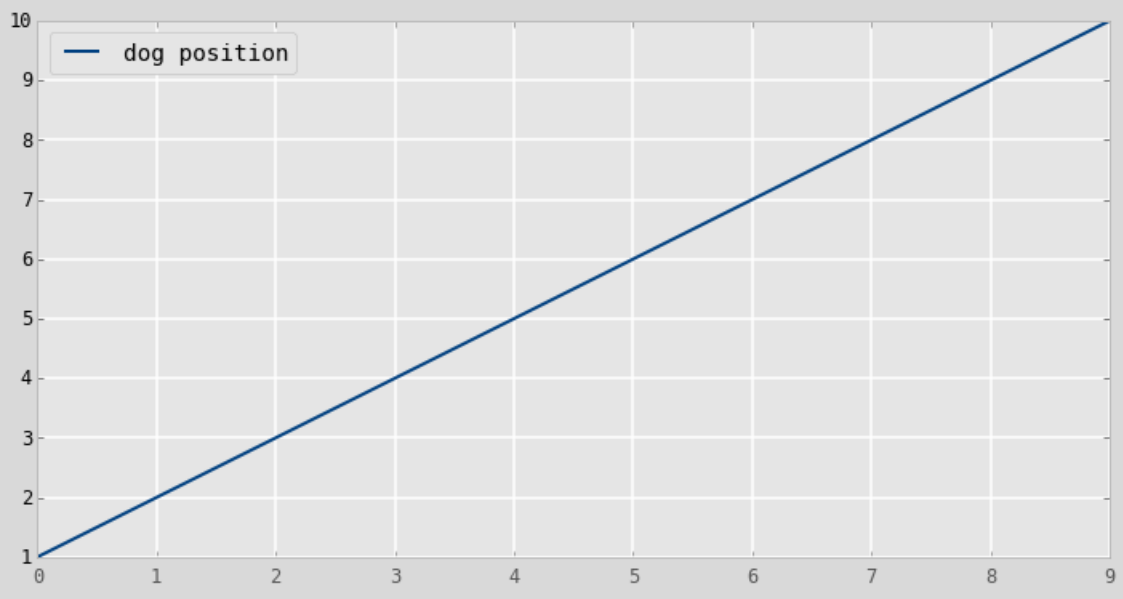
```
-1.8386         0.7546        -0.5046        -2.9576        -0.2675
 1.4816        -0.9532        -0.8862        -0.3574        -0.4382
 0.1608         1.1827         0.4886         2.0902        -0.2451
-0.4182         0.5224         0.1251         2.1121        -0.6231
```

You should see a sequence of numbers near 0, some negative and some positive. Most are probably between -1 and 1, but a few might lie somewhat outside that range. This is what we expect from a normal distribution - values are clustered around the mean, and there are fewer values the further you get from the mean.

Okay, so lets look at the output of the `DogSensor` class. We will start by setting the noise to 0 to check that the class does what we think it does

```
In [4]: import matplotlib.pyplot as plt
        import matplotlib.pylab as pylab

        dog = DogSensor (noise=0.0)
        xs = []
        for i in range(10):
            x = dog.sense()
            xs.append(x)
            print("%.4f" % x, end=' '),
        plt.plot(xs, label='dog position')
        plt.legend(loc='best')
        plt.show()
```

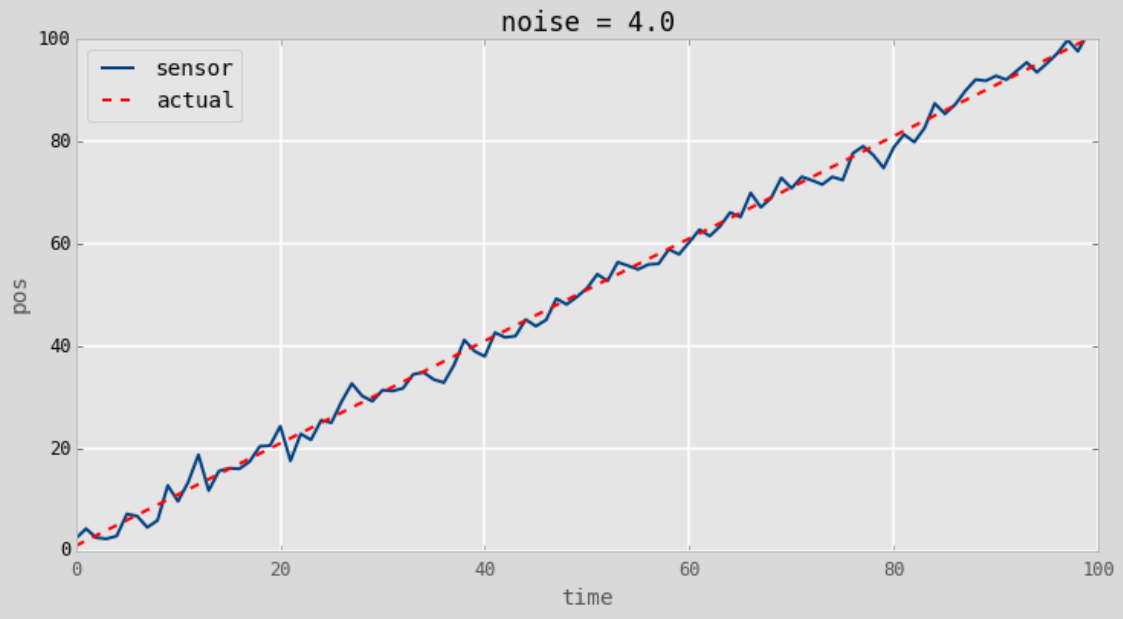
```
1.0000 2.0000 3.0000 4.0000 5.0000 6.0000 7.0000 8.0000 9.0000 10.0000
```



The constructor initialized the dog at position 0 with a velocity of 1 (move 1.0 to the right). So we would expect to see an output of 1..10, and indeed that is what we see. If you thought the correct answer should have been 0..9 recall that `sense()` returns the dog's position *after* updating his position, so the first position is 0.0 + 1, or 1.0.

Now let's inject some noise in the signal.

```
In [5]: def test_sensor(noise_scale):
            dog = DogSensor(noise=noise_scale)

            xs = []
            for i in range(100):
                x = dog.sense()
                xs.append(x)
            plt.plot(xs, label='sensor')
            plt.plot([0,99],[1,100], 'r--', label='actual')
            plt.xlabel('time')
            plt.ylabel('pos')
            plt.ylim([0,100])
            plt.title('noise = ' + str(noise_scale))
            plt.legend(loc='best')
            plt.show()

        test_sensor(4.0)
```



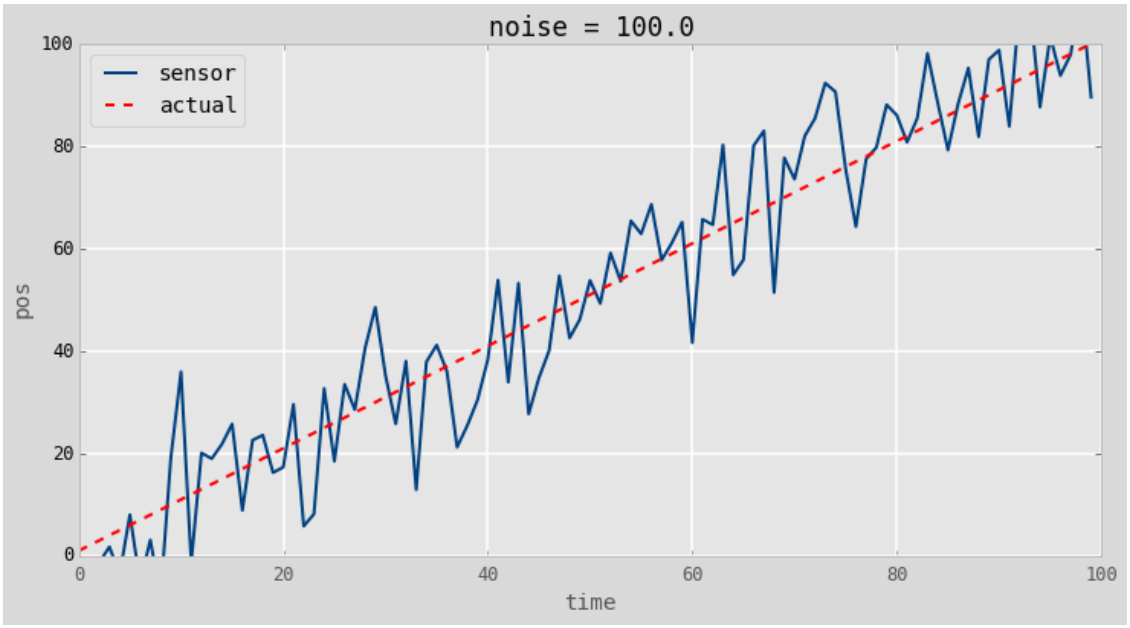
Note: numpy uses a random number generator to generate the normal distribution samples. The numbers I see as I write this are unlikely to be the ones that you see. If you run the cell above multiple times, you should get a slightly different result each time. I could use `numpy.random.seed(some_value)` to force the results to be the same each time. This would simplify my explanations in some cases, but would ruin the interactive nature of this chapter. To get a real feel for how normal distributions and Kalman filters work you will probably want to run cells several times, observing what changes, and what stays roughly the same.

So the output of the sensor should be a wavering blue line drawn over a dotted red line. The dotted red line shows the actual position of the dog, and the blue line is the noise signal produced by the simulated RFID sensor. Please note that the red dotted line was manually plotted - we do not yet have a filter that recovers that information!

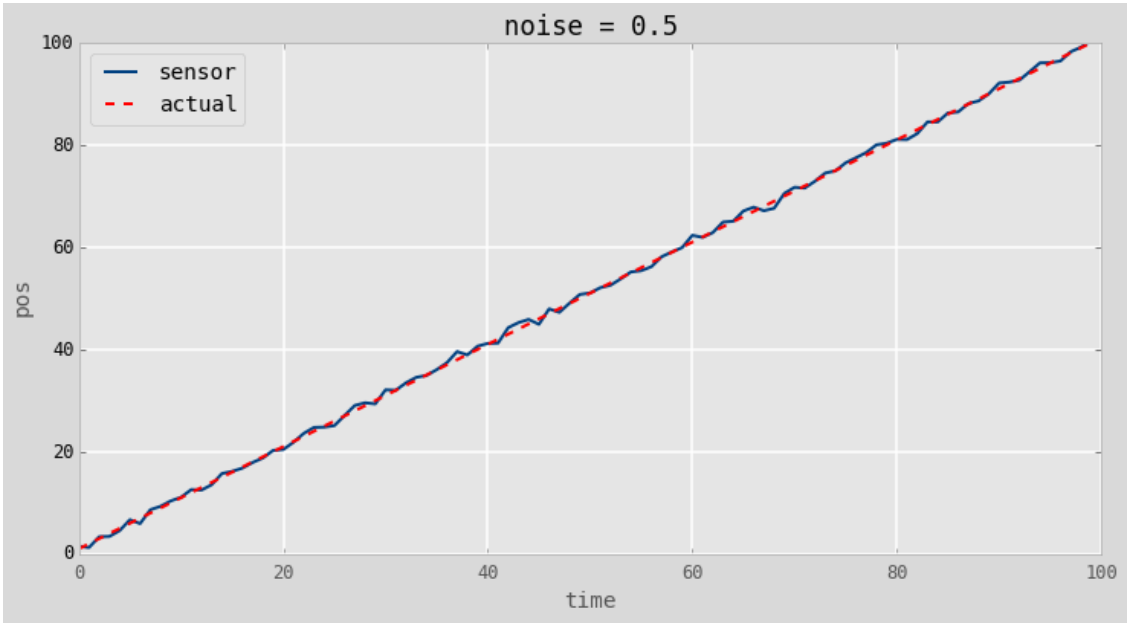
If you are running this in an interactive IPython Notebook, I strongly urge you to run the script several times in a row. You can do this by putting the cursor in the cell containing the Python code and pressing Ctrl+Enter. Each time it runs you should see a different jagged blue line wavering over the top of the dotted red line.

I also urge you to adjust the noise setting to see the result of various values. However, since you may be reading this in a read only notebook, I will show two extreme examples. The first plot shows the noise set to 100.0, and the second shows noise set to 0.5.

```
In [6]: test_sensor(100.0)
```




```
In [7]: test_sensor(0.5)
```



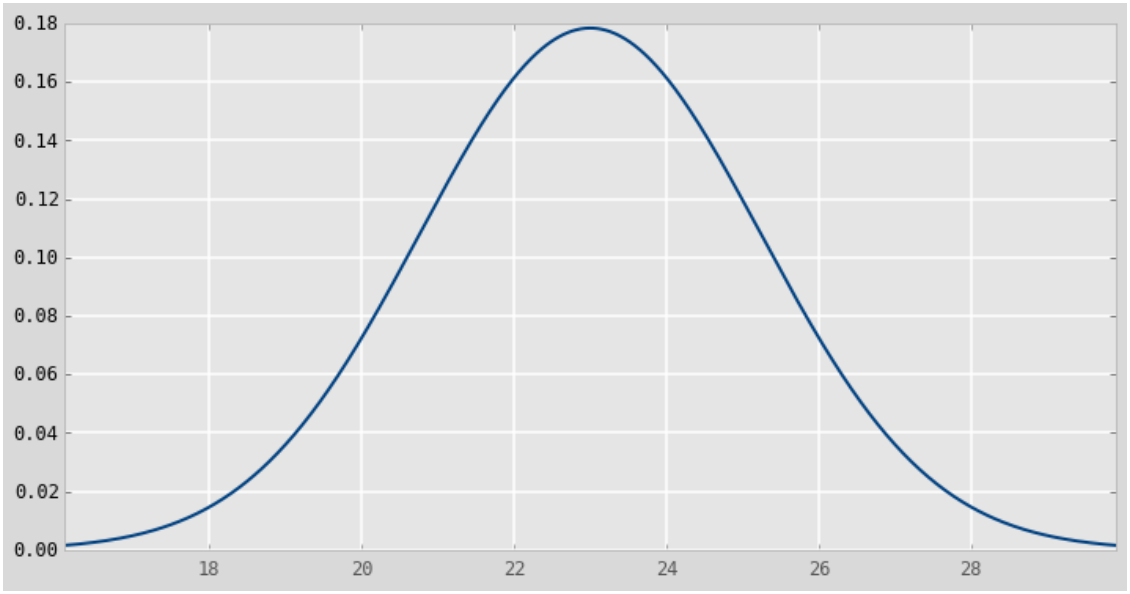
You may not have a full understanding of the exact *meaning* of a noise value of 100.0, but as it turns out if you multiply `randn()` with a number n, the result is just a normal distribution with $\sigma = \sqrt{n}$. So the example with noise = 100 is using the normal distribution $\mathcal{N}(0, 100)$. Recall the notation for a normal distribution is $\mathcal{N}(\mu, \sigma^2)$. If the square root is

confusing, recall that normal distributions use σ^2 for the variance, and σ is the standard deviation, which we do not use in this book. `DogSensor.__init__()` takes the square root of the noise setting so that the `noise * randn()` call properly computes the normal distribution.

6.3 Math with Gaussians

Let's say we believe that our dog is at 23m, and the variance is 5, or $pos_{dog} = \mathcal{N}(23, 5)$. We can represent that in a plot:

```
In [8]: import stats
        stats.plot_gaussian(23, 5)
```



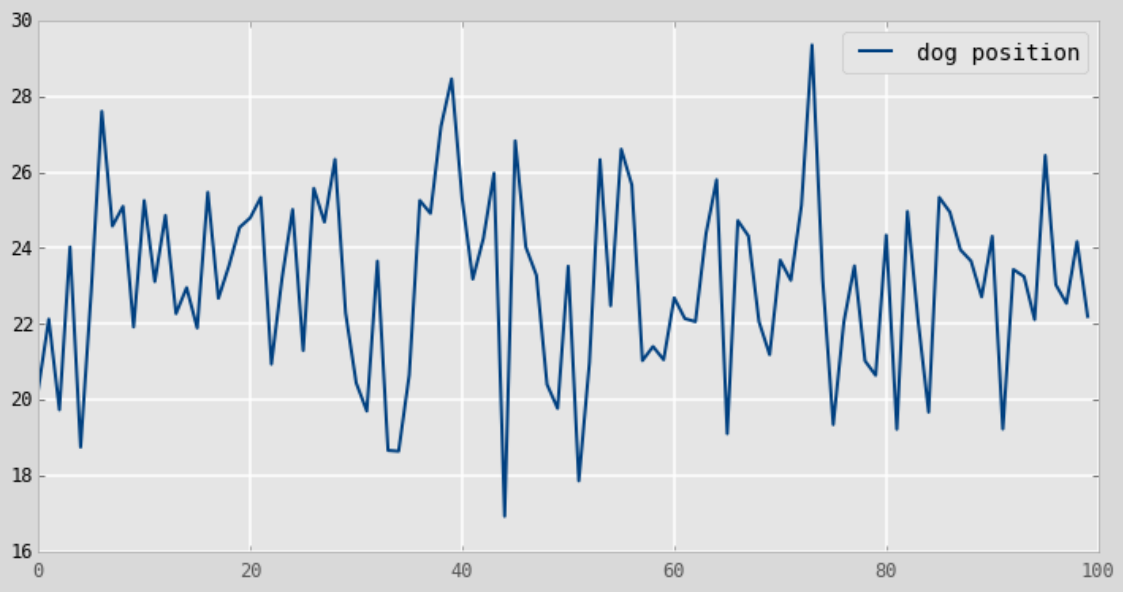
This corresponds to a fairly inexact belief. While we believe that the dog is at 23, note that roughly 21 to 25 are quite likely as well. Let's assume for the moment our dog is standing still, and we query the sensor again. This time it returns 23.2 as the position. Can we use this additional information to improve our estimate of the dog's position?

Intuition suggests 'yes'. Consider: if we read the sensor 100 times and each time it returned a value between 21 and 25, all centered around 23, we should be very confident that the dog is somewhere very near 23. Of course, a different physical interpretation is possible. Perhaps our dog was randomly wandering back and forth in a way that exactly emulated a normal distribution. But that seems extremely unlikely - I certainly have never seen a dog do that. So the only reasonable assumption is that the dog was mostly standing still at 23.0.

Let's look at 100 sensor readings in a plot:

```
In [9]: dog = DogSensor(23, 0, 5)
        xs = range(100)
```

```
    ys = []
    for i in xs:
        ys.append(dog.sense())

    plt.plot(xs,ys, label='dog position')
    plt.legend(loc='best')
    plt.show()
```



Eyeballing this confirms our intuition - no dog moves like this. However, noisy sensor data certainly looks like this. So let's proceed and try to solve this mathematically. But how?

Recall the histogram code for adding a measurement to a preexisting belief:

```
def update(pos, measure, p_hit, p_miss):
    q = array(pos, dtype=float)
    for i in range(len(hallway)):
        if hallway[i] == measure:
            q[i] = pos[i] * p_hit
        else:
            q[i] = pos[i] * p_miss
     normalize(q)
     return q
```

Note that the algorithm is essentially computing:

```
new_belief = old_belief * measurement * sensor_error
```

The measurement term might not be obvious, but recall that measurement in this case was always 1 or 0, and so it was left out for convenience.

If we are implementing this with gaussians, we might expect it to be implemented as:

```
new_gaussian = measurement * old_gaussian
```

where measurement is a Gaussian returned from the sensor. But does that make sense? Can we multiply gaussians? If we multiply a Gaussian with a Gaussian is the result another Gaussian, or something else?

It is not particularly difficult to perform the algebra to derive the equation for multiplying two gaussians, but I will just present the result:

$$N(\mu_1, \sigma_1^2) * N(\mu_2, \sigma_2^2) = N(\frac{\sigma_1^2\mu_2 + \sigma_2^2\mu_1}{\sigma_1^2 + \sigma_2^2}, \frac{1}{\frac{1}{\sigma_1^2} + \frac{1}{\sigma_2^2}})$$

In other words the result is a Gaussian with

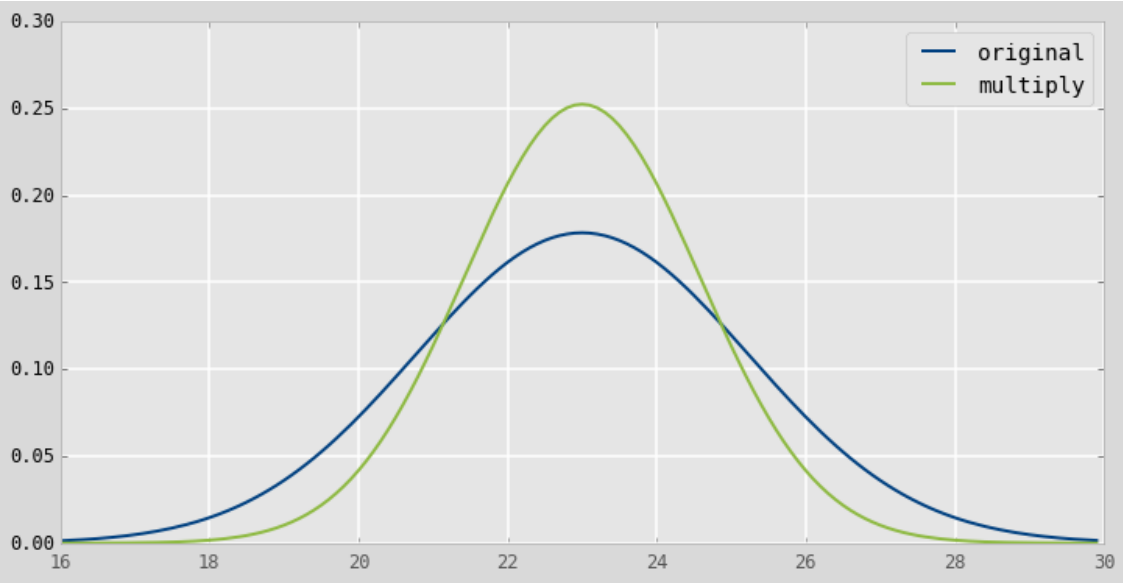
$$\mu = \frac{\sigma_1^2\mu_2 + \sigma_2^2\mu_1}{\sigma_1^2 + \sigma_2^2},$$
$$\sigma = \frac{1}{\frac{1}{\sigma_1^2} + \frac{1}{\sigma_2^2}}$$

Without doing a deep analysis we can immediately infer some things. First and most importantly the result of multiplying two Gaussians is another Gaussian. The expression for the mean is not particularly illuminating, except that it is a combination of the means and variances of the input. But the variance of the result is merely some combination of the variances of the variances of the input. We conclude from this that the variances are completely unaffected by the values of the mean!

Let's immediately look at some plots of this. First, let's look at the result of multiplying $N(23, 5)$ to itself. This corresponds to getting 23.0 as the sensor value twice in a row. But before you look at the result, what do you think the result will look like? What should the new mean be? Will the variance by wider, narrower, or the same?

```
In [10]: from __future__ import division
         import numpy as np

         def multiply(mu1, var1, mu2, var2):
             mean = (var1*mu2 + var2*mu1) / (var1+var2)
             variance = 1 / (1/var1 + 1/var2)
             return (mean, variance)

         xs = np.arange(16, 30, 0.1)

         m1,v1 = 23, 5
         m, v = multiply(m1,v1,m1,v1)
```

```
ys = [stats.gaussian(x,m1,v1) for x in xs]
plt.plot (xs, ys, label='original')

ys = [stats.gaussian(x,m,v) for x in xs]
plt.plot (xs, ys, label='multiply')

plt.legend(loc='best')
plt.show()
```



The result is either amazing or what you would expect, depending on your state of mind. I must admit I vacillate freely between the two! Note that the result of the multiplication is taller and narrow than the original Gaussian but the mean is the same. Does this match your intuition of what the result should have been?

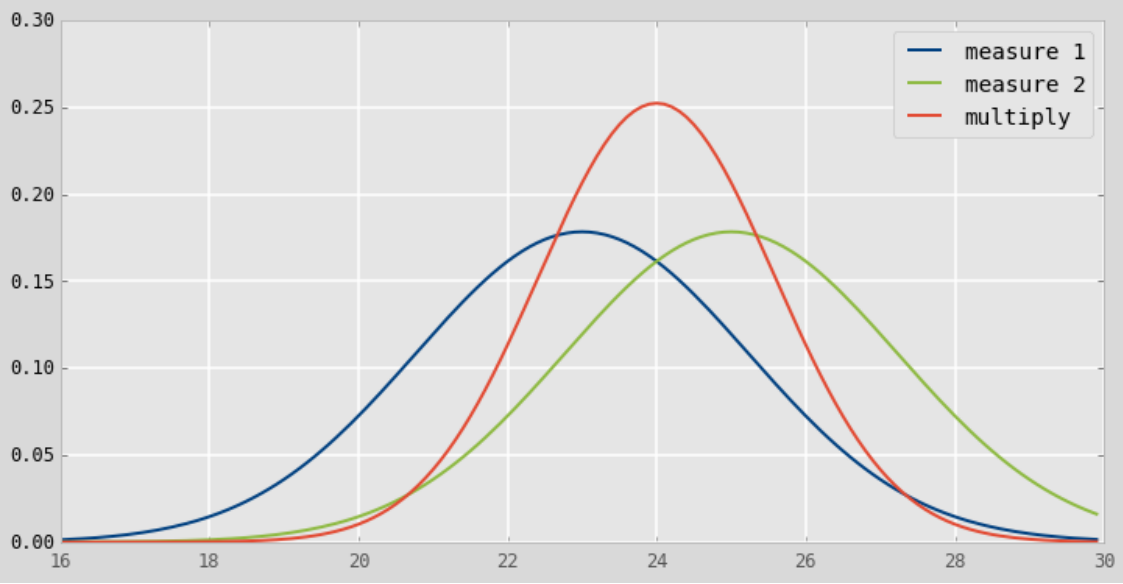
If we think of the Gaussians as two measurements, this makes sense. If I measure twice and get the same value, I should be more confident in my answer than if I just measured once. If I measure twice and get 23 meters each time, I should conclude that the length is close to 23 meters. So the mean should be 23. I am more confident with two measurements than with one, so the variance of the result should be smaller.

"Measure twice, cut once" is a useful saying and practice due to this fact! The Gaussian is just a mathematical model of this physical fact, so we should expect the math to follow our physical process.

Now let's multiply two gaussians (or equivalently, two measurements) that are partially separated. In other words, their means will be different, but their variances will be the same. What do you think the result will be? Think about it, and then look at the graph.

```
In [11]: xs = np.arange(16, 30, 0.1)
```

```
m1, v1 = 23, 5
m2, v2 = 25, 5
m, s = multiply(m1,v1,m2,v2)

ys = [stats.gaussian(x,m1,v1) for x in xs]
plt.plot (xs, ys, label='measure 1')

ys = [stats.gaussian(x,m2,v2) for x in xs]
plt.plot (xs, ys, label='measure 2')

ys = [stats.gaussian(x,m,v) for x in xs]
plt.plot(xs, ys,label='multiply')
plt.legend()
plt.show()
```



Another beautiful result! If I handed you a measuring tape and asked you to measure the distance from table to a wall, and you got 23m, and then a friend make the same measurement and got 25m, your best guess must be 24m.

That is fairly counter-intuitive, so let's consider it further. Perhaps a more reasonable assumption would be that either you or your coworker just made a mistake, and the true distance is either 23 or 25, but certainly not 24. Surely that is possible. However, suppose the two measurements you reported as 24.01 and 23.99. In that case you would agree that in this case the best guess for the correct value is 24? Which interpretation we choose depends on the properties of the sensors we are using. Humans make galling mistakes, physical sensors do not.

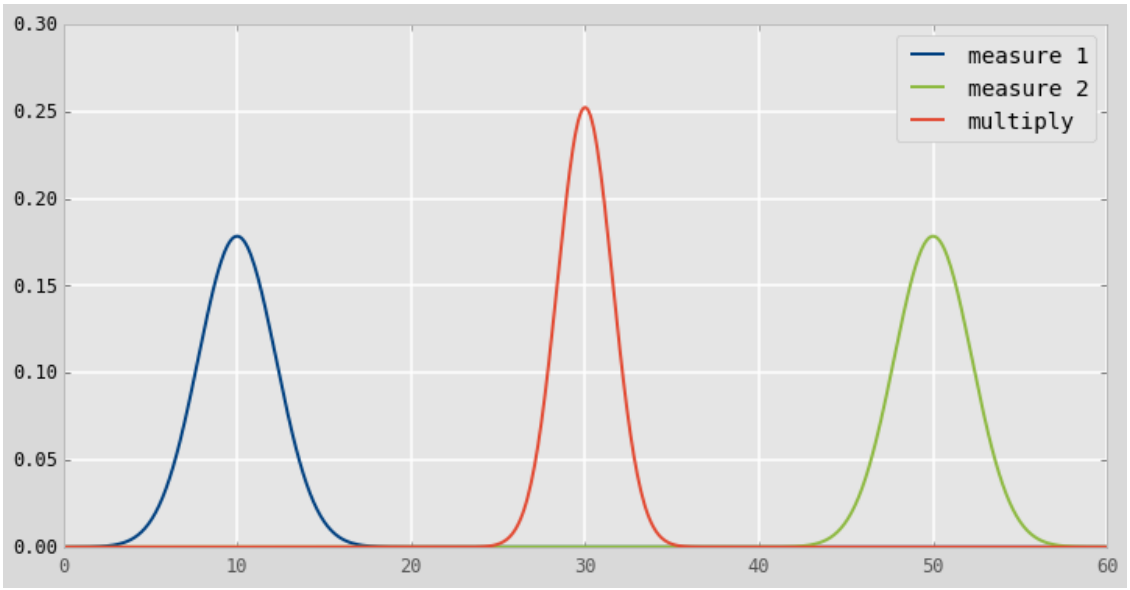
This topic is fairly deep, and I will explore it once we have completed our Kalman filter. For now I will merely say that the Kalman filter requires the interpretation that

measurements are accurate, with Gaussian noise, and that a large error caused by misreading a measuring tape is not Gaussian noise.

For now I ask that you trust me. The math is correct, so we have no choice but to accept it and use it. We will see how the Kalman filter deals with movements vs error very soon. In the meantime, accept that 24 is the correct answer to this problem.

One final test of your intuition. What if the two measurements are widely separated?

```
In [12]: xs = np.arange(0, 60, 0.1)

         m1, v1 = 10, 5
         m2, v2 = 50, 5
         m, v = multiply(m1,v1,m2,v2)

         ys = [stats.gaussian(x,m1,v1) for x in xs]
         plt.plot (xs, ys, label='measure 1')

         ys = [stats.gaussian(x,m2,v2) for x in xs]
         plt.plot (xs, ys, label='measure 2')

         ys = [stats.gaussian(x,m,v) for x in xs]
         plt.plot(xs, ys, label='multiply')
         plt.legend()
         plt.show()
```



This result bothered me quite a bit when I first learned it. If my first measurement was 10, and the next one was 50, why would I choose 30 as a result? And why would I be *more* confident? Doesn't it make sense that either one of the measurements is wrong, or that I am

measuring a moving object? Shouldn't the result be nearer 50? And, shouldn't the variance be larger, not smaller?

Well, no. Recall the g-h filter chapter. In that chapter we agreed that if I weighed myself on two scales, and the first read 160lbs while the second read 170lbs, and both were equally accurate, the best estimate was 165lbs. Furthermore I should be a bit more confident about 165lbs vs 160lbs or 170lbs because I know have two readings, both near this estimate, increasing my confidence that neither is wildly wrong.

Let's look at the math again to convince ourselves that the physical interpretation of the Gaussian equations makes sense.

$$\mu = \frac{\sigma_1^2\mu_2 + \sigma_2^2\mu_1}{\sigma_1^2 + \sigma_2^2}$$

If both scales have the same accuracy, then $\sigma_1^2 = \sigma_2^2$, and the resulting equation is

$$\mu = \frac{\mu_1 + \mu_2}{2}$$

which is just the average of the two weighings. If we look at the extreme cases, assume the first scale is very much more accurate than than the second one. At the limit, we can set $\sigma_1^2 = 0$, yielding

$$\mu = \frac{0 * \mu_2 + \sigma_2^2\mu_1}{\sigma_2^2},$$

or just

$$\mu = \mu_1$$

Finally, if we set $\sigma_1^2 = 9\sigma_2^2$, then the resulting equation is

$$\mu = \frac{9\sigma_2^2\mu_2 + \sigma_2^2\mu_1}{9\sigma_2^2 + \sigma_2^2}$$

or just

$$\mu = \frac{1}{10}\mu_1 + \frac{9}{10}\mu_2$$

This again fits our physical intuition of favoring the second, accurate scale over the first, inaccurate scale.

6.4 Implementing the Update Step

Recall the histogram filter uses a numpy array to encode our belief about the position of our dog at any time. That array stored our belief of our dog's position in the hallway using 10 discrete positions. This was very crude, because with a 100m hallway that corresponded to positions 10m apart. It would have been trivial to expand the number of positions to say 1,000, and that is what we would do if using it for a real problem. But the problem remains that the distribution is discrete and multimodal - it can express strong belief that the dog is in two positions at the same time.

Therefore, we will use a single Gaussian to reflect our current belief of the dog's position. In other words, we will use $dog_{pos} = \mathcal{N}(\mu, \sigma^2)$. Gaussians extend to infinity on both sides of the mean, so the single Gaussian will cover the entire hallway. They are unimodal, and seem to reflect the behavior of real-world sensors - most errors are small and clustered around the mean. Here is the entire implementation of the update function for a Kalman filter:

```
In [13]: def update(mean, variance, measurement, measurement_variance):
             return multiply(mean, variance, measurement, measurement_variance)
```

Kalman filters are supposed to be hard! But this is very short and straightforward. All we are doing is multiplying the Gaussian that reflects our belief of where the dog was with the new measurement. Perhaps this would be clearer if we used more specific names:

```
In [14]: def update_dog(dog_pos, dog_variance, measurement, measurement_variance):
             return multiply(dog_pos, dog_sigma, measurement, measurement_variance)
```

That is less abstract, which perhaps helps with comprehension, but it is poor coding practice. We are writing a Kalman filter that works for any problem, not just tracking dogs in a hallway, so we don't use variable names with 'dog' in them. Still, the `update_dog()` function should make what we are doing very clear.

Let's look at an example. We will suppose that our current belief for the dog's position is $N(2, 5)$. Don't worry about where that number came from. It may appear that we have a chicken and egg problem, in that how do we know the position before we sense it, but we will resolve that shortly. We will create a `DogSensor` object initialized to be at position 0.0, and with no velocity, and modest noise. This corresponds to the dog standing still at the far left side of the hallway. Note that we mistakenly believe the dog is at position 2.0, not 0.0.

```
In [15]: dog = DogSensor(velocity=0, noise=1)

         pos,s = 2, 5
         for i in range(20):
             pos,s = update(pos, s, dog.sense(), 5)
             print('time:', i, '\tposition =', "%.3f" % pos, '\tvariance =', "%.3f" % s)
```

```
time: 0         position = 0.827         variance = 2.500
time: 1         position = 0.427         variance = 1.667
time: 2         position = 0.192         variance = 1.250
time: 3         position = 0.548         variance = 1.000
time: 4         position = 0.416         variance = 0.833
time: 5         position = 0.409         variance = 0.714
time: 6         position = 0.297         variance = 0.625
time: 7         position = 0.490         variance = 0.556
time: 8         position = 0.407         variance = 0.500
time: 9         position = 0.291         variance = 0.455
time: 10         position = 0.120         variance = 0.417
time: 11         position = -0.043         variance = 0.385
```

```
time: 12         position = -0.082         variance = 0.357
time: 13         position = -0.130         variance = 0.333
time: 14         position = -0.208         variance = 0.312
time: 15         position = -0.144         variance = 0.294
time: 16         position = -0.075         variance = 0.278
time: 17         position = -0.073         variance = 0.263
time: 18         position = -0.030         variance = 0.250
time: 19         position = -0.045         variance = 0.238
```

Because of the random numbers I do not know the exact values that you see, but the position should have converged very quickly to almost 0 despite the initial error of believing that the position was 2.0. Furthermore, the variance should have quickly converged from the initial value of 5.0 to 0.238.

By now the fact that we converged to a position of 0.0 should not be terribly surprising. All we are doing is computing `new_pos = old_pos * measurement` and the measurement is a normal distribution around 0, so we should get very close to 0 after 20 iterations. But the truly amazing part of this code is how the variance became 0.238 despite every measurement having a variance of 5.0.

If we think about the physical interpretation of this is should be clear that this is what should happen. If you sent 20 people into the hall with a tape measure to physically measure the position of the dog you would be very confident in the result after 20 measurements - more confident than after 1 or 2 measurements. So it makes sense that as we make more measurements the variance gets smaller.

Mathematically it makes sense as well. Recall the computation for the variance after the multiplication: $\sigma^2 = 1/(\frac{1}{\sigma_1^2} + \frac{1}{\sigma_2^2})$. We take the reciprocals of the sigma from the measurement and prior belief, add them, and take the reciprocal of the result. Think about that for a moment, and you will see that this will always result in smaller numbers as we proceed.

6.5 Implementing Predictions

That is a beautiful result, but it is not yet a filter. We assumed that the dog was sitting still, an extremely dubious assumption. Certainly it is a useless one - who would need to write a filter to track non-moving objects? The histogram used a loop of sense and update functions, and we must do the same to accommodate movement.

How how do we perform the predict function with gaussians? Recall the histogram method:

```
def predict(pos, move, p_correct, p_under, p_over):
    n = len(pos)
    result = array(pos, dtype=float)
    for i in range(n):
            result[i] =  \
            pos[(i-move) % n]   * p_correct + \
            pos[(i-move-1) % n] * p_over + \
```

```
            pos[(i-move+1) % n] * p_under
    return result
```

In a nutshell, we shift the probability vector by the amount we believe the animal moved, and adjust the probability. How do we do that with gaussians?

It turns out that we just add gaussians. Think of the case without gaussians. I think my dog is at 7.3m, and he moves 2.6m to right, where is he now? Obviously, $7.3 + 2.6 = 9.9$. He is at 9.9m. Abstractly, the algorithm is `new_pos = old_pos + dist_moved`. It does not matter if we use floating point numbers or gaussians for these values, the algorithm must be the same.

How is addition for gaussians performed? It turns out to be very simple:

$$N(\mu_1, {\sigma_1}^2) + N(\mu_2, {\sigma_2}^2) = N(\mu_1 + \mu_2, {\sigma_1}^2 + {\sigma_2}^2)$$

All we do is add the means and the variance separately! Does that make sense? Think of the physical representation of this abstract equation. μ_1 is the old position, and μ_2 is the distance moved. Surely it makes sense that our new position is $\mu_1 + \mu_2$. What about the variance? It is perhaps harder to form an intuition about this. However, recall that with the `update()` function for the histogram filter we always lost information - our confidence after the update was lower than our confidence before the update. Perhaps this makes sense - we don't really know where the dog is moving, so perhaps the confidence should get smaller (variance gets larger). I assure you that the equation for gaussian addition is correct, and derived by basic algebra. Therefore it is reasonable to expect that if we are using gaussians to model physical events, the results must correctly describe those events.

I recognize the amount of hand waving in that argument. Now is a good time to either work through the algebra to convince yourself of the mathematical correctness of the algorithm, or to work through some examples and see that it behaves reasonably. This book will do the latter.

So, here is our implementation of the predict function:

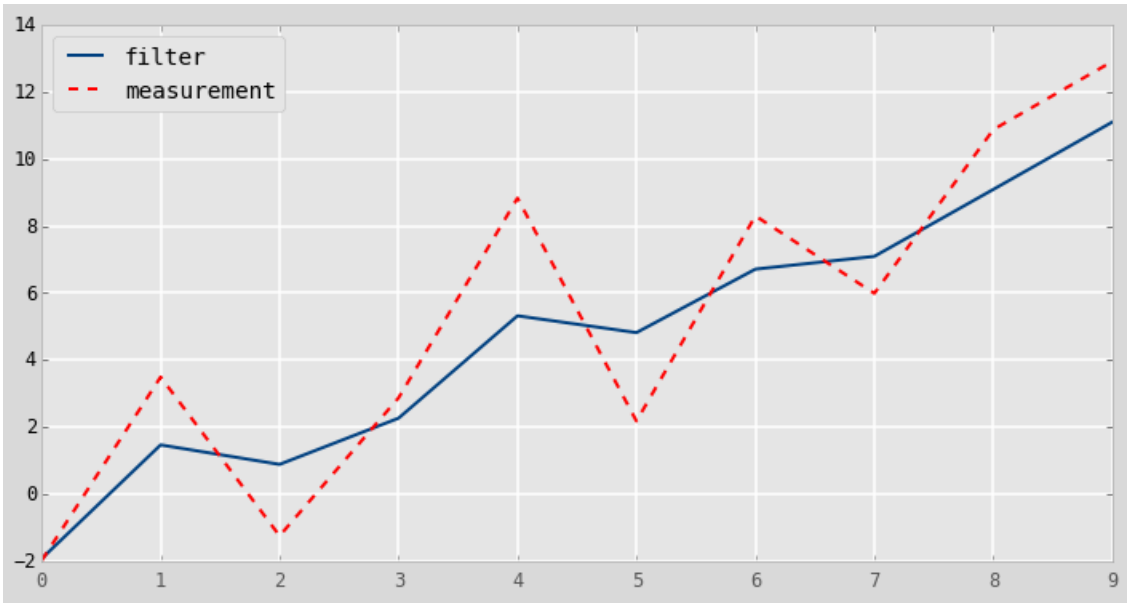
```
In [16]: def predict(pos, variance, movement, movement_variance):
             return (pos + movement, variance + movement_variance)
```

What is left? Just calling these functions. The histogram did nothing more than loop over the `sense()` and `update()` functions, so let's do the same.

```
In [17]: # assume dog is always moving 1m to the right
         movement = 1
         movement_error = 2
         sensor_error = 10
         pos = (0, 500)   # gaussian N(0,50)

         dog = DogSensor(pos[0], velocity=movement, noise=sensor_error)
```

```
zs = []
ps = []

for i in range(10):
    pos = predict(pos[0], pos[1], movement, movement_error)
    print('PREDICT: {: 10.4f} {: 10.4f}'.format(pos[0], pos[1]),end='\t')

    Z = dog.sense()
    zs.append(Z)

    pos = update(pos[0], pos[1], Z, sensor_error)
    ps.append(pos[0])

    print('UPDATE: {: 10.4f} {: 10.4f}'.format(pos[0], pos[1]))


plt.plot(ps, label='filter')
plt.plot(zs, c='r', linestyle='dashed', label='measurement')
plt.legend(loc='best')
plt.show()
```

```
PREDICT:     1.0000   502.0000        UPDATE:    -1.9271     9.8047
PREDICT:    -0.9271    11.8047        UPDATE:     1.4652     5.4138
PREDICT:     2.4652     7.4138        UPDATE:     0.8840     4.2574
PREDICT:     1.8840     6.2574        UPDATE:     2.2629     3.8490
PREDICT:     3.2629     5.8490        UPDATE:     5.3172     3.6904
PREDICT:     6.3172     5.6904        UPDATE:     4.8154     3.6267
PREDICT:     5.8154     5.6267        UPDATE:     6.7095     3.6007
PREDICT:     7.7095     5.6007        UPDATE:     7.0910     3.5900
PREDICT:     8.0910     5.5900        UPDATE:     9.0888     3.5856
PREDICT:    10.0888     5.5856        UPDATE:    11.0984     3.5838
```



There is a fair bit of arbitrary constants code above, but don't worry about it. What does require explanation are the first few lines:

```
movement = 1
movement_error = 2
```

For the moment we are assuming that we have some other sensor that detects how the dog is moving. For example, there could be an inertial sensor clipped onto the dog's collar, and it reports how far the dog moved each time it is triggered. The details don't matter. The upshot is that we have a sensor, it has noise, and so we represent it with a Gaussian. Later we will learn what to do if we do not have a sensor for the `predict()` step.

For now let's walk through the code and output bit by bit.

```
movement = 1
movement_error = 2
sensor_error = 10
pos = (0, 500)   # gaussian N(0,500)
```

The first lines just set up the initial conditions for our filter. We are assuming that the dog moves steadily to the right 1m at a time. We have a relatively low error of 2 for the movement sensor, and a higher error of 10 for the RFID position sensor. Finally, we set our belief of the dog's initial position as $N(0, 500)$. Why those numbers. Well, 0 is as good as any number if we don't know where the dog is. But we set the variance to 500 to denote that we have no confidence in this value at all. 100m is almost as likely as 0 with this value for the variance.

Next we initialize the RFID simulator with

```
dog = DogSensor(pos[0], velocity=movement, noise=sensor_error)
```

It may seem very 'convenient' to set the simulator to the same position as our guess, and it is. Do not fret. In the next example we will see the effect of a wildly inaccurate guess for the dog's initial position.

The next code allocates an array to store the output of the measurements and filtered positions.

```
zs = []
ps = []
```

This is the first time that I am introducing standard nomenclature used by the Kalman filtering literature. It is traditional to call our measurement Z, and so I follow that convention here. As an aside, I find the nomenclature used by the literature very obscure. However, if you wish to read the literature you will have to become used to it, so I will not use a much more readable variable name such as m or *measure*.

Now we just enter our `update() ... predict()` loop.

```
for i in range(10):
    pos = predict(pos[0], pos[1], movement, sensor_error)
    print 'PREDICT:', "%.4f" %pos[0], ", %.4f" %pos[1]
```

Wait, why `predict()` before `update()`? It turns out the order does not matter once, but the first call to `,DogSensor.sense()` assumes that the dog has already moved, so we start with the update step. In practice you will order these calls based on the details of your sensor, and you will very typically do the `sense()` first.

So we call the update function with the gaussian representing our current belief about our position, the another gaussian representing our belief as to where the dog is moving, and then print the output. Your output will differ, but when writing this I get this as output:

```
PREDICT: 1.000 502.000
```

What is this saying? After the prediction, we believe that we are at 1.0, and the variance is now 502.0. Recall we started at 500.0. The variance got worse, which is always what happens during the prediction step.

```
Z = dog.sense()
zs.append(Z)
```

Here we sense the dog's position, and store it in our array so we can plot the results later.

Finally we call the update function of our filter, save the result in our *ps* array, and print the updated position belief:

```
pos = update(pos[0], pos[1], Z, movement_error)
ps.append(pos[0])
print 'UPDATE:', "%.4f" %pos[0], ", %.4f" %pos[1]
```

Your result will be different, but I get

```
UPDATE: 1.6279 , 9.8047
```

as the result. What is happening? Well, at this point the dog is really at 1.0, however the predicted position is 1.6279. What is happening is the RFID sensor has a fair amount of noise, and so we compute the position as 1.6279. That is pretty far off from 1, but this is just are first time through the loop. Intuition tells us that the results will get better as we make more measurements, so let's hope that this is true for our filter as well. Now look at the variance: 9.8047. It has dropped tremendously from 502.0. Why? Well, the RFID has a reasonably small variance of 2.0, so we trust it far more than our previous belief. At this point there is no way to know for sure that the RFID is outputting reliable data, so the variance is not 2.0, but is has gotten much better.

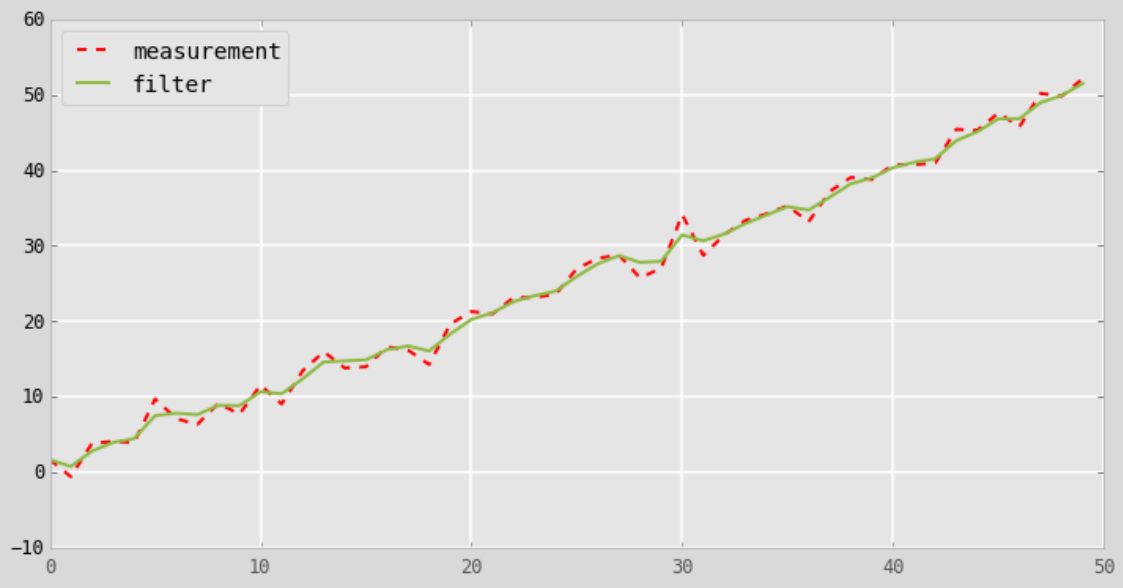
Now the software just loops, calling `predict()` and `update()` in turn. Because of the random sampling I do not know exactly what numbers you are seeing, but the final position is probably between 9 and 11, and the final variance is probably around 3.5. After several runs I did see the final position nearer 7, which would have been the result of several measurements with relatively large errors.

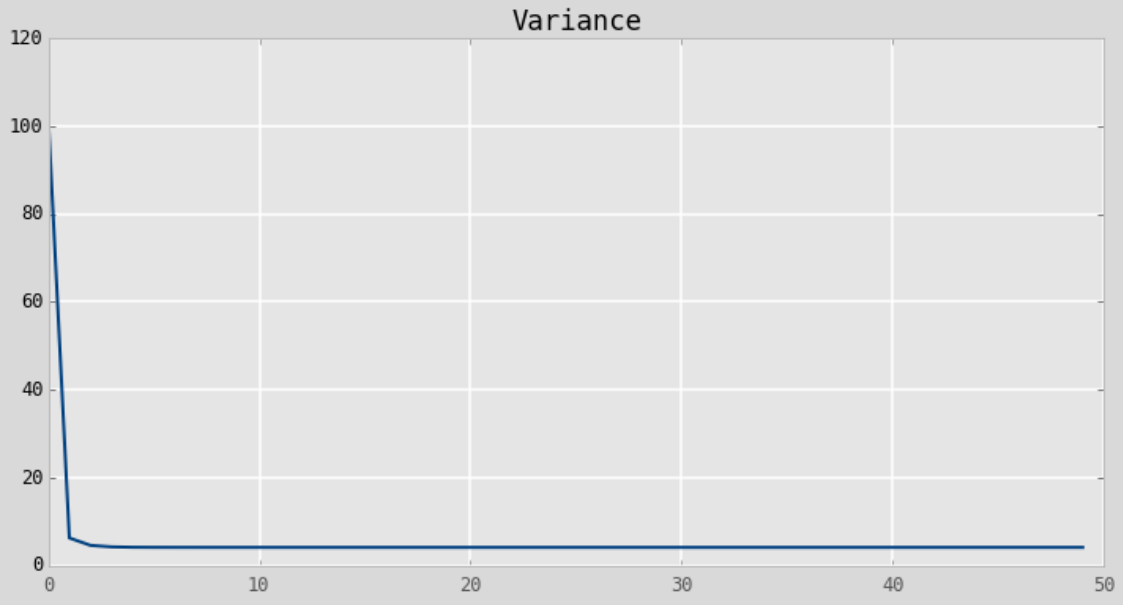
Now look at the plot. The noisy measurements are plotted in with a dotted red line, and the filter results are in the solid blue line. Both are quite noisy, but notice how much noisier the measurements (red line) are. This is your first Kalman filter shown to work!

In this example I only plotted 10 data points so the output from the print statements would not overwhelm us. Now let's look at the filter's performance with more data. This time we will plot both the output of the filter and the variance.

```
In [18]: %precision 2
         # assume dog is always moving 1m to the right
         movement = 1
         movement_error = 2
         sensor_error = 4.5
         pos = (0, 100)   # gaussian N(0,50)

         dog = DogSensor(pos[0], velocity=movement, noise=sensor_error)

         zs = []
         ps = []
         vs = []

         for i in range(50):
             pos = predict(pos[0], pos[1], movement, movement_error)
             Z = dog.sense()
             zs.append(Z)
             vs.append(pos[1])

             pos = update(pos[0], pos[1], Z, sensor_error)
             ps.append(pos[0])
```

```
#plt.subplot(121)
p1, = plt.plot(zs,c='r', linestyle='dashed')
p2, = plt.plot(ps,)
plt.legend([p1,p2], ['measurement', 'filter'], 2)
plt.show()

plt.plot(vs)
plt.title('Variance')
plt.show()
print ([float("%0.4f" % v) for v in vs])
```





```
[102.0, 6.3099, 4.6267, 4.2812, 4.1939, 4.1708, 4.1646, 4.1629, 4.1624, 4.1623, 4.1623,
```

Here we can see that the variance converges very quickly to roughly 4.1623 in 10 steps. We interpret this as meaning that we become very confident in our position estimate very quickly. The first few measurements are unsure due to our uncertainty in our guess at the initial position, but the filter is able to quickly determine an accurate estimate.

> Before I go on, I want to emphasize that this code fully implements a 1D Kalman filter. If you have tried to read the literature, you are perhaps surprised, because this looks nothing like the complex, endless pages of math in those books. To be fair, the math gets a bit more complicated in multiple dimensions, but not by much. So long as we worry about *using* the equations rather than *deriving* them we can create Kalman filters without a lot of effort. Moreover, I hope you'll agree that you have a decent intuitive grasp of what is happening. We represent our beliefs with Gaussians, and our beliefs get better over time because more measurement means more data to work with. "Measure twice, cut once!"

6.6 Relationship to the g-h Filter

In the first chapter I stated that the Kalman filter is a form of g-h filter. However, we have been reasoning about the probability of Gaussians, and not used any of the reasoning or equations of the first chapter. A trivial amount of algebra will reveal the relationship, so let's do that now. It's not particularly illuminating algebra, so feel free to skip to the bottom to see the final equation that relates g to the variances.

The equation for our estimate is:

$$\mu_{x'} = \frac{\sigma_1^2\mu_2 + \sigma_2^2\mu_1}{\sigma_1^2 + \sigma_2^2}$$

which I will make more friendly for our eyes as:

$$\mu_{x'} = \frac{ya + xb}{a + b}$$

We can easily put this into the g-h form with the following algebra

$$\begin{aligned}
\mu_{x'} &= (x - x) + \frac{ya + xb}{a + b} \\
\mu_{x'} &= x - \frac{a + b}{a + b}x + \frac{ya + xb}{a + b} \\
\mu_{x'} &= x + \frac{-x(a + b) + xb + ya}{a + b} \\
\mu_{x'} &= x + \frac{-xa + ya}{a + b} \\
\mu_{x'} &= x + \frac{a}{a + b}(y - x)
\end{aligned}$$

We are almost done, but recall that the variance of estimate is given by

$$\sigma^2_{x'} = \frac{1}{\frac{1}{\sigma^2_1} + \frac{1}{\sigma^2_2}} = \frac{1}{\frac{1}{a} + \frac{1}{b}}$$

We can incorporate that term into our equation above by observing that

$$\begin{aligned}
\frac{a}{a+b} &= \frac{a/a}{(a+b)/a} = \frac{1}{(a+b)/a} \\
&= \frac{1}{1 + \frac{b}{a}} = \frac{1}{\frac{b}{b} + \frac{b}{a}} \\
&= \frac{1}{b}\frac{1}{\frac{1}{b} + \frac{1}{a}} \\
&= \frac{\sigma^2_{x'}}{b}
\end{aligned}$$

We can tie all of this together with

$$\begin{aligned}
\mu_{x'} &= x + \frac{a}{a+b}(y - x) \\
&= x + \frac{\sigma^2_{x'}}{b}(y - x) \\
&= x + g_n(y - x)
\end{aligned}$$

■

where

$$g_n = \frac{\sigma^2_{x'}}{\sigma^2_y}$$

The end result is multipying the residual of the two measurements by a constant and adding to our previous value, which is the g equation for the g-h filter. g is the variance of the new estimate divided by the variance of the measurement. Of course in this case g is not truly a constant, as it varies with each time step as the variance changes, but it is truly the same formula. We can also derive the formula for h in the same way but I don't find this a particularly interesting derivation. The end result is

$$h_n = \frac{COV(x, \dot{x})}{\sigma^2_y}$$

The takeaway point is that g and h are specified fully by the variance and covariances of the measurement and preditions at time n. In other words, we are just picking a point between the measurement and prediction by a scale factor determined by the quality of each of those two inputs. That is all the Kalman filter is.

Exercise: Modify the values of `movement_error` and `sensor_error` and note the effect on the filter and on the variance. Which has a larger effect on the value that variance converges to. For example, which results in a smaller variance:

```
movement_error = 40
sensor_error = 2
```

or:

```
movement_error = 2
sensor_error = 40
```

6.7 Introduction to Designing a Filter

So far we have developed our filter based on the dog sensors introduced in the Discrete Bayesian filter chapter. We are used to this problem by now, and may feel ill-equipped to implement a Kalman filter for a different problem. To be honest, there is still quite a bit of information missing from this presentation. The next chapter will fill in the gaps. Still, lets get a feel for it by designing and implementing a Kalman filter for a thermometer. The sensor for the thermometer outputs a voltage that corresponds to the temperature that is being measured. We have read the manufacturer's specifications for the sensor, and it tells us that the sensor exhibits white noise with a standard deviation of 2.13.

We do not have a real sensor to read, so we will simulate the sensor with the following function. We have hard-coded the voltage to 16.3 - obviously the voltage will differ based on the temperature, but that is not important to our filter design.

```
In [19]: temp_variance = 2.13**2
         def volt():
             return random.randn()*temp_variance + 16.3
```

We generate white noise with a given variance using the equation `random.randn() * variance`. The specification gives us the standard deviation of the noise, not the variance, but recall that variance is just the square of the standard deviation. Hence we raise 2.13 to the second power.

> **Sidebar**: spec sheets are just what they sound like - specifications. Any individual sensor will exhibit different performance based on normal manufacturing variations. Numbers given are often maximums - the spec is a guarantee that the performance will be at least that good. So, our sensor might have standard deviation of 1.8. If you buy an expensive piece of equipment it often comes with a sheet of paper displaying the test results of your specific item; this is usually very trustworthy. On the other hand, if this is a cheap sensor it is likely it received little to no testing prior to being sold. Manufacturers typically test a small subset of their output to verify that everything falls within the desired performance range. If you have a critical application you will need to read the specification sheet carefully to figure out exactly what they mean by their ranges. Do they guarantee their number is a maximum, or is it, say, the 3σ error rate? Is every item tested? Is the variance normal, or some other distribution. Finally, manufacturing is not perfect. Your part might be defective and not match the performance on the sheet.

For example, I just randomly looked up a data sheet for an airflow sensor. There is a field *Repeatability*, with the value $\pm 0.50\%$. Is this a Gaussian? Is there a bias? For example, perhaps the repeatability is nearly 0.0% at low temperatures, and always nearly +0.50 at high temperatures. Data sheets for electrical components often contain a section of "Typical Performance Characteristics". These are used to capture information that cannot be easily conveyed in a table. For example, I am looking at a chart showing output voltage vs current for a LM555 timer. There are three curves showing the performance at different temperatures. The response is ideally linear, but all three lines are curved. This clarifies that errors in voltage outputs are probably not Gaussian - in this chip's case higher temperatures leads to lower voltage output, and the voltage output is quite nonlinear if the input current is very high.

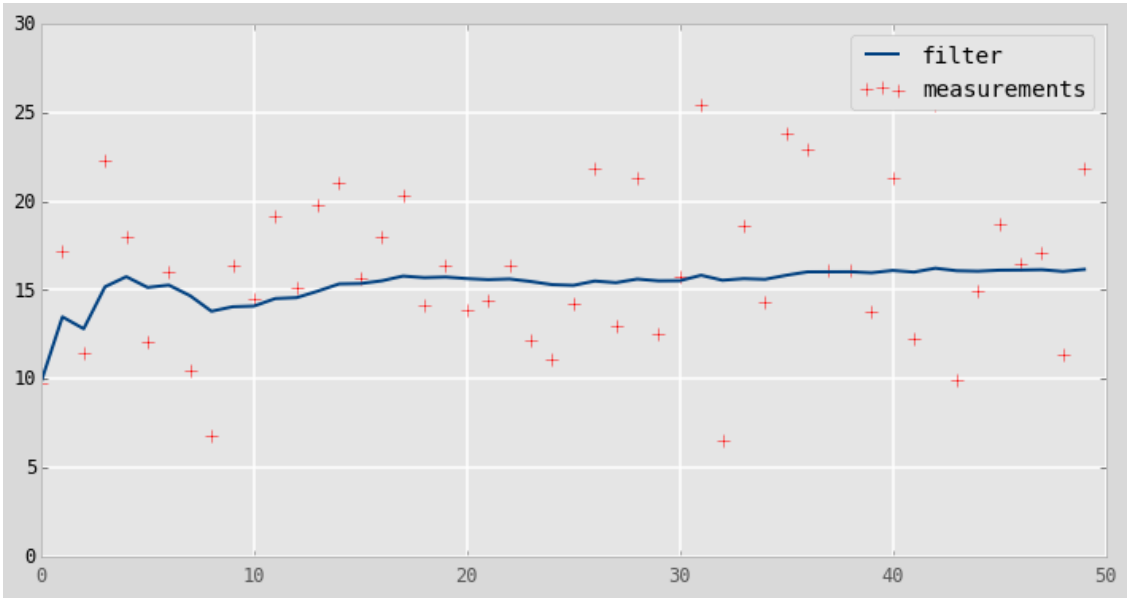
As you might guess, modeling the performance of your sensors is one of the harder parts of creating good Kalman filter.

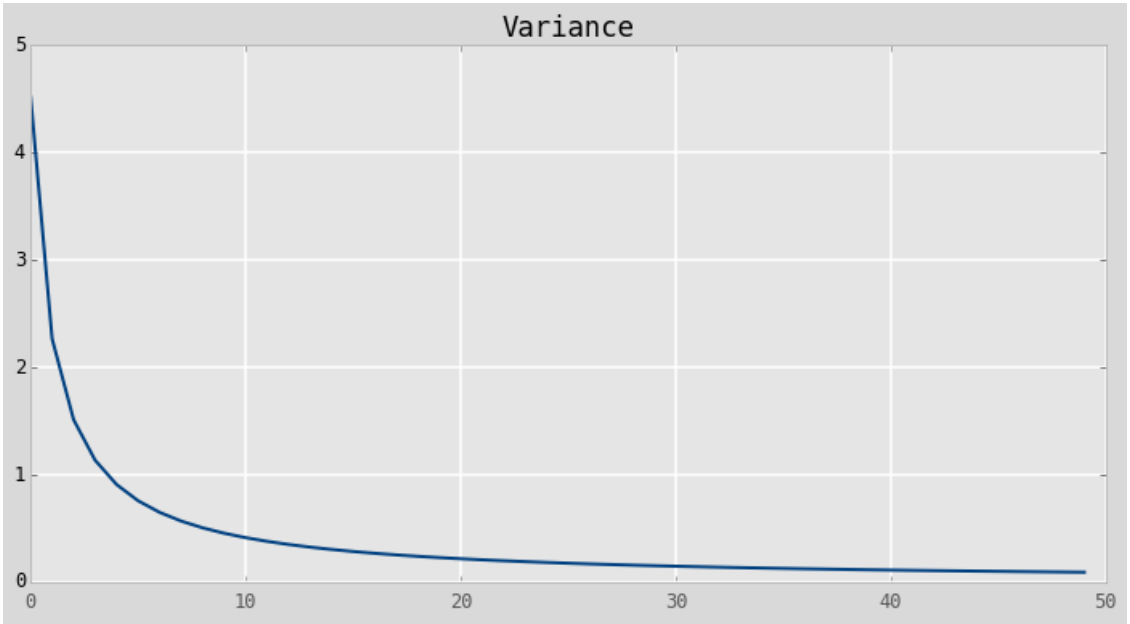
Now we need to write the Kalman filter processing loop. As with our previous problem, we need to perform a cycle of sensing and updating. The sensing step probably seems clear - call `volt()` to get the measurement, pass the result into `update()` function, but what about the update step? We do not have a sensor to detect 'movement' in the voltage, and for any small duration we expect the voltage to remain constant. How shall we handle this?

As always, we will trust in the math. We have no movement, and no error associated with them, so we will just set both to zero. Let's see what happens.

```
In [20]: sensor_error = temp_variance
         movement_error = 0
         movement = 0
         voltage = (25,1000) #who knows what the first value is?

         zs = []
         ps = []
         vs = []
         N=50

         for i in range(N):
             Z = volt()
             zs.append(Z)

             voltage = update(voltage[0], voltage[1], Z, sensor_error)
             ps.append(voltage[0])
             vs.append(voltage[1])

             voltage = predict(voltage[0], voltage[1], movement, movement_error)

         plt.scatter(range(N), zs, marker='+', s=64, color='r', label='measurements')
```

```
p1, = plt.plot(ps, label='filter')
plt.legend(loc='best')
plt.xlim((0,N));plt.ylim((0,30))
plt.show()
plt.plot(vs)
plt.title('Variance')
plt.show()
print('Variance converges to',vs[-1])
print('Last voltage is',voltage[0])
```





```
Variance converges to 0.09072976736236911
Last voltage is 16.160958715064073
```

The first plot shows the individual sensor measurements marked with '+'s vs the filter output. Despite a lot of noise in the sensor we quickly discover the approximate voltage of the sensor. In the run I just completed at the time of authorship, the last voltage output from the filter is 16.213, which is quite close to the 16.4 used by the `volt()` function. On other runs I have gotten up to around 16.9 as an output and also as low as 15.5 or so.

The second plot shows how the variance converges over time. Compare this plot to the variance plot for the dog sensor. While this does converge to a very small value, it is much slower than the dog problem. The next section **Explaining the Results - Multi-Sensor Fusion** explains why this happens.

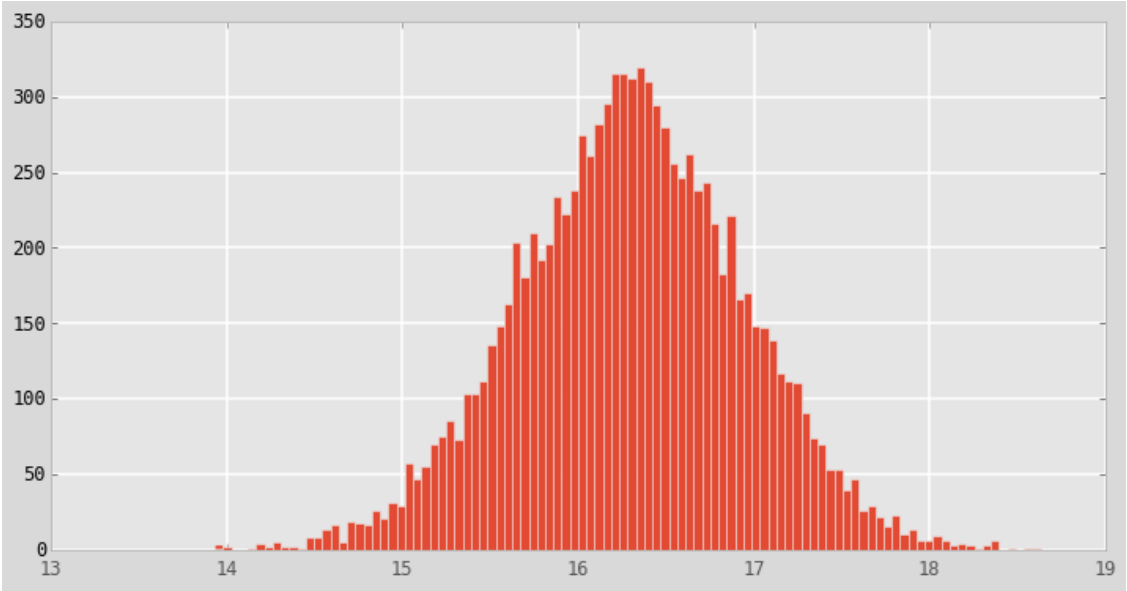
Exercise(optional): Write a function that runs the Kalman filter many times and record what value the voltage converges to each time. Plot this as a histogram. After 10,000 runs do the results look normally distributed? Does this match your intuition of what should happen?

use plt.hist(data,bins=100) to plot the histogram.

```
In [21]: #Your code here
```

Solution

```
In [22]: sensor_error = temp_variance

         def VKF():
             voltage=(14,1000)
             for i in range(N):
                 Z = volt()
                 voltage = update(voltage[0], voltage[1], Z, sensor_error)
             return voltage[0]

         vs = []
         for i in range (10000):
             vs.append (VKF())
         plt.hist(vs, bins=100, color='#e24a33')
         plt.show()
```



Discussion

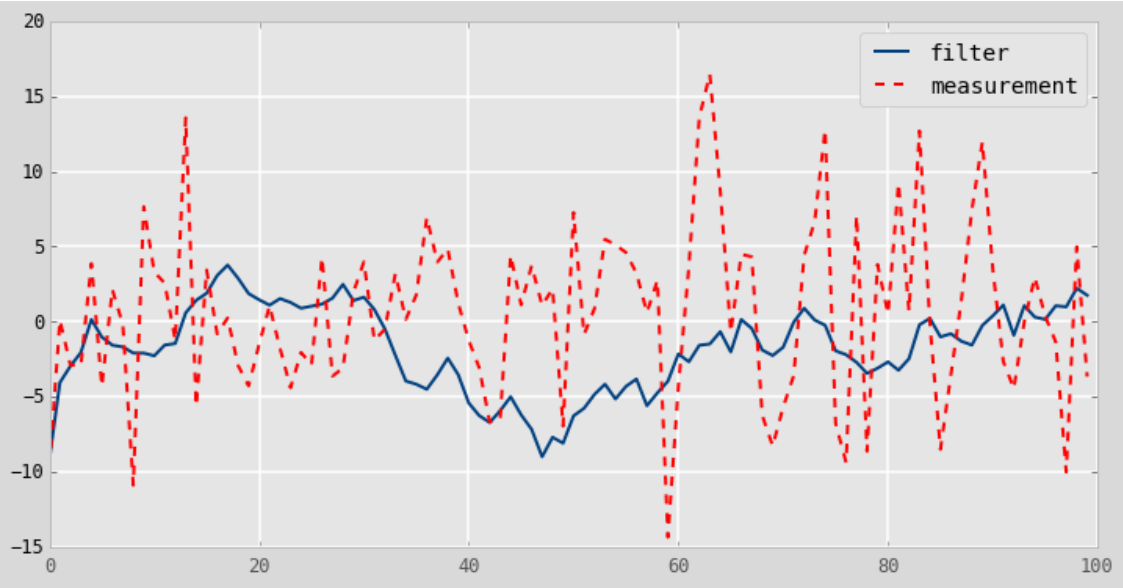
The results do in fact look like a normal distribution. Each voltage is Gaussian, and the **Central Limit Theorem** guarantees that a large number of Gaussians is normally distributed. We will discuss this more in a subsequent math chapter.

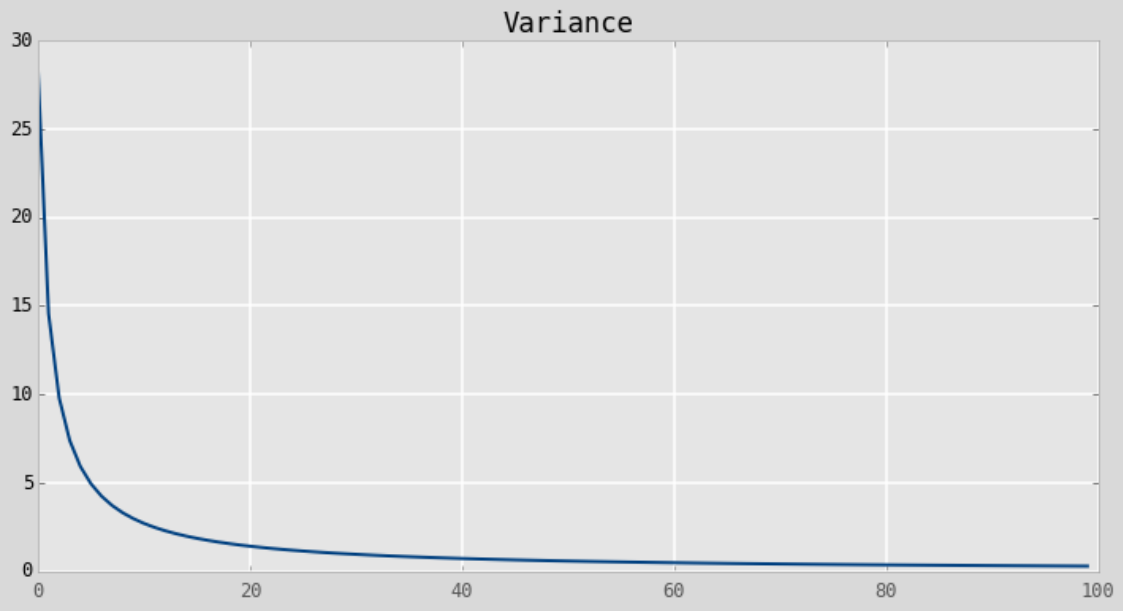
6.8 Explaining the Results - Multi-Sensor Fusion

So how does the Kalman filter do so well? I have glossed over one aspect of the filter as it becomes confusing to address too many points at the same time. We will return to the dog tracking problem. We used two sensors to track the dog - the RFID sensor that detects position, and the inertial tracker that tracked movement. However, we have focused all of our attention on the position sensor. Let's change focus and see how the filter performs if the inertial tracker is also noisy. This will provide us with an vital insight into the performance of Kalman filters.

```
In [23]: sensor_error = 30
         movement_sensor = 30
         pos = (0,500)

         dog = DogSensor(0, velocity=movement, noise=sensor_error)

         zs = []
         ps = []
         vs = []

         for i in range(100):
```

```
        Z = dog.sense()
        zs.append(Z)

        pos = update(pos[0], pos[1], Z, sensor_error)
        ps.append(pos[0])
        vs.append(pos[1])

        pos = predict(pos[0], pos[1], movement+ random.randn(), movement_error)

plt.plot(ps, label='filter')
plt.plot(zs, linestyle='dashed', c='r', label='measurement')
plt.legend()
plt.show()
plt.plot(vs)
plt.title('Variance')
plt.show()
```





This result is worse than the example where only the measurement sensor was noisy. Instead of being mostly straight, this time the filter's output is distinctly jagged. But, it still mostly tracks the dog. What is happening here?

This illustrates the effects of *multi-sensor fusion*. Suppose we get a position reading of -28.78 followed by 31.43. From that information alone it is impossible to tell if the dog is standing still during very noisy measurements, or perhaps sprinting from -29 to 31 and being accurately measured. But we have a second source of information, his velocity. Even when the velocity is also noisy, it constrains what our beliefs might be. For example, suppose that with the 31.43 position reading we get a velocity reading of 59. That matches the difference between the two positions quite well, so this will lead us to believe the RFID sensor and the velocity sensor. Now suppose we got a velocity reading of 1.7. This doesn't match our RFID reading very well - it suggests that the dog is standing still or moving slowly.

When sensors measure different aspects of the system and they all agree we have strong evidence that the sensors are accurate. And when they do not agree it is a strong indication that one or more of them are inaccurate.

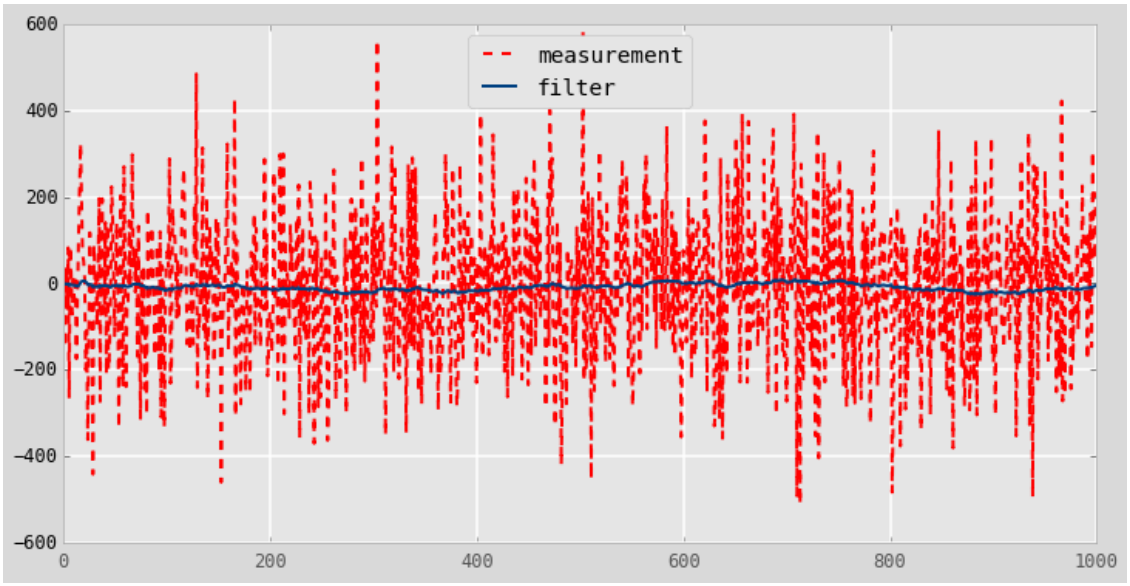
We will formalize this mathematically in the next chapter; for now trust this intuitive explanation. We use this sort of reasoning every day in our lives. If one person tells us something that seems far fetched we are inclined to doubt them. But if several people independently relay the same information we attach higher credence to the data. If one person disagrees with several other people, we tend to distrust the outlier. If we know the people that might alter our belief. If a friend is inclined to practical jokes and tall tales we may put very little trust in what they say. If one lawyer and three lay people opine on some fact of law, and the lawyer disagrees with the three you'll probably lend more credence to what the lawyer says because of her expertise. In the next chapter we will learn how to mathematical model this sort of reasoning.

6.9 More examples

6.9.1 Example: Extreme Amounts of Noise

So I didn't put a lot of noise in the signal, and I also 'correctly guessed' that the dog was at position 0. How does the filter perform in real world conditions? Let's explore and find out. I will start by injecting a lot of noise in the RFID sensor. I will inject an extreme amount of noise - noise that apparently swamps the actual measurement. What does your intuition tell about how the filter will perform if the noise is allowed to be anywhere from -300 or 300. In other words, an actual position of 1.0 might be reported as 287.9, or -189.6, or any other number in that range. Think about it before you scroll down.

```
In [24]: sensor_error = 30000
         movement_error = 2
         pos = (0,500)

         dog = DogSensor(pos[0], velocity=movement, noise=sensor_error)

         zs = []
         ps = []

         for i in range(1000):
             pos = predict(pos[0], pos[1], movement, movement_error)

             Z = dog.sense()
             zs.append(Z)

             pos = update(pos[0], pos[1], Z, sensor_error)
             ps.append(pos[0])


         p1, = plt.plot(zs,c='r', linestyle='dashed', label='measurement')
         p2, = plt.plot(ps, c='#004080', label='filter')
         plt.legend(loc='best')
         plt.show()
```



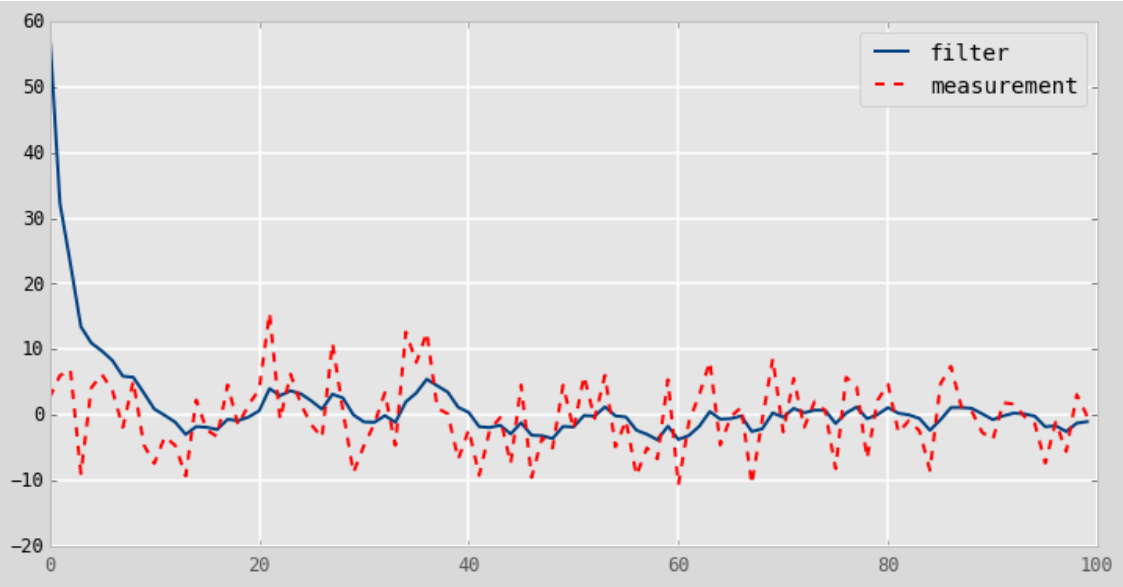
In this example the noise is extreme yet the filter still outputs a nearly straight line! This is an astonishing result! What do you think might be the cause of this performance? If you are not sure, don't worry, we will discuss it latter.

6.9.2 Example: Bad Initial Estimate

Now let's lets look at the results when we make a bad initial estimate of position. To avoid obscuring the results I'll reduce the sensor variance to 30, but set the initial position to 1000m. Can the filter recover from a 1000m initial error?

```
In [25]: sensor_error = 30
         movement_error = 2
         pos = (1000,500)

         dog = DogSensor(0, velocity=movement, noise=sensor_error)

         zs = []
         ps = []

         for i in range(100):
             pos = predict(pos[0], pos[1], movement, movement_error)

             Z = dog.sense()
             zs.append(Z)

             pos = update(pos[0], pos[1], Z, sensor_error)
             ps.append(pos[0])
```

```
plt.plot(ps, label='filter')
plt.plot(zs,c='r', linestyle='dashed', label='measurement')
plt.legend(loc='best')
plt.show()
```



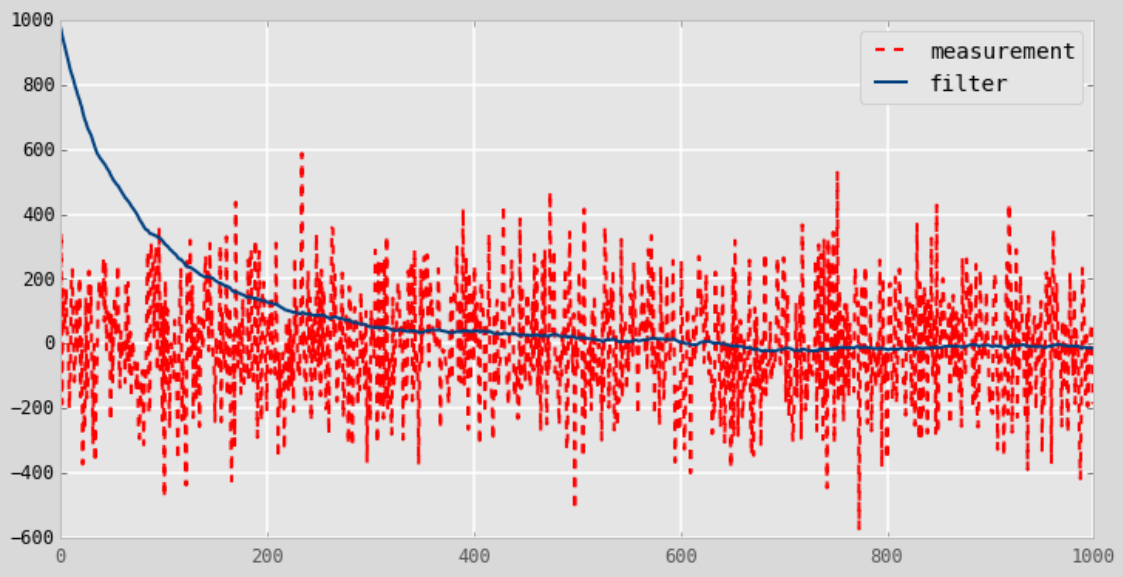
Again the answer is yes! Because we are relatively sure about our belief in the sensor ($\sigma = 30$) even after the first step we have changed our belief in the first position from 1000 to somewhere around 60.0 or so. After another 5-10 measurements we have converged to the correct value! So this is how we get around the chicken and egg problem of initial guesses. In practice we would probably just assign the first measurement from the sensor as the initial value, but you can see it doesn't matter much if we wildly guess at the initial conditions - the Kalman filter still converges very quickly.

6.9.3 Example: Large Noise and Bad Initial Estimate

What about the worst of both worlds, large noise and a bad initial estimate?

```
In [26]: sensor_error = 30000
         movement_error = 2
         pos = (1000,500)


         dog = DogSensor(0, velocity=movement, noise=sensor_error)
         zs = []
         ps = []
```

```
for i in range(1000):
    pos = predict(pos[0], pos[1], movement, movement_error)

    Z = dog.sense()
    zs.append(Z)

    pos = update(pos[0], pos[1], Z, sensor_error)
    ps.append(pos[0])

plt.plot(zs,c='r', linestyle='dashed', label='measurement')
plt.plot(ps, c='#004080', label='filter')
plt.legend(loc='best')
plt.show()
```

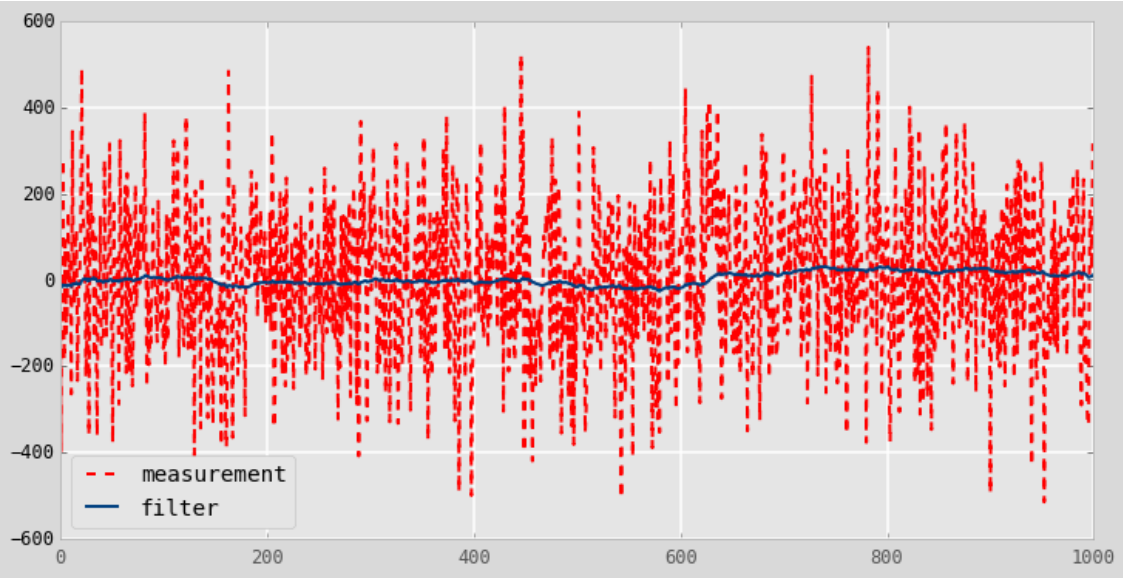


This time the filter does struggle. Notice that the previous example only computed 100 updates, whereas this example uses 1000. By my eye it takes the filter 400 or so iterations to become reasonable accurate, but maybe over 600 before the results are good. Kalman filters are good, but we cannot expect miracles. If we have extremely noisy data and extremely bad initial conditions, this is as good as it gets.

Finally, let's make the suggest change of making our initial position guess just be the first sensor measurement.

```
In [27]: sensor_error = 30000
         movement_error = 2
         pos = None

         dog = DogSensor(0, velocity=movement, noise=sensor_error)
```

```
zs = []
ps = []

for i in range(1000):
    Z = dog.sense()
    zs.append(Z)
    if pos == None:
        pos = (Z, 500)

    pos = update(pos[0], pos[1], Z, sensor_error)
    ps.append(pos[0])

    pos = predict(pos[0], pos[1], movement, movement_error)

plt.plot(zs,c='r', linestyle='dashed', label='measurement')
plt.plot(ps, c='#004080', label='filter')
plt.legend(loc='best')
plt.show()
```



This simple change significantly improves the results. On some runs it takes 200 iterations or so to settle to a good solution, but other runs it converges very rapidly. This all depends on whether the initial measurement Z had a small amount or large amount of noise.

200 iterations may seem like a lot, but the amount of noise we are injecting is truly huge. In the real world we use sensors like thermometers, laser rangefinders, GPS satellites, computer vision, and so on. None have the enormous error as shown here. A reasonable value for the variance for a cheap thermometer might be 10, for example, and our code is using 30,000 for the variance.

6.9.4 Exercise: Interactive Plots

Implement the Kalman filter using IPython Notebook's animation features to allow you to modify the various constants in real time using sliders. Refer to the section **Interactive Gaussians** in the Gaussian chapter to see how to do this. You will use the `interact()` function to call a calculation and plotting function. Each parameter passed into `interact()` automatically gets a slider created for it. I have built the boilerplate for this; just fill in the required code.

```
In [28]: from IPython.html.widgets import interact, interactive, fixed
         import IPython.html.widgets as widgets
         def plot_kalman_filter(start_pos, sensor_noise, movement, movement_noise, noise
             # your code goes here
             pass

         interact(plot_kalman_filter,
                  start_pos=(-10,10),
                  sensor_noise=widgets.IntSliderWidget(value=5,min=0,max=100),
                  movement=widgets.FloatSliderWidget(value=1,min=-2.,max=2.),
                  movement_noise=widgets.FloatSliderWidget(value=5,min=0,max=100.),
                  noise_scale=widgets.FloatSliderWidget(value=1,min=0,max=2.))
```

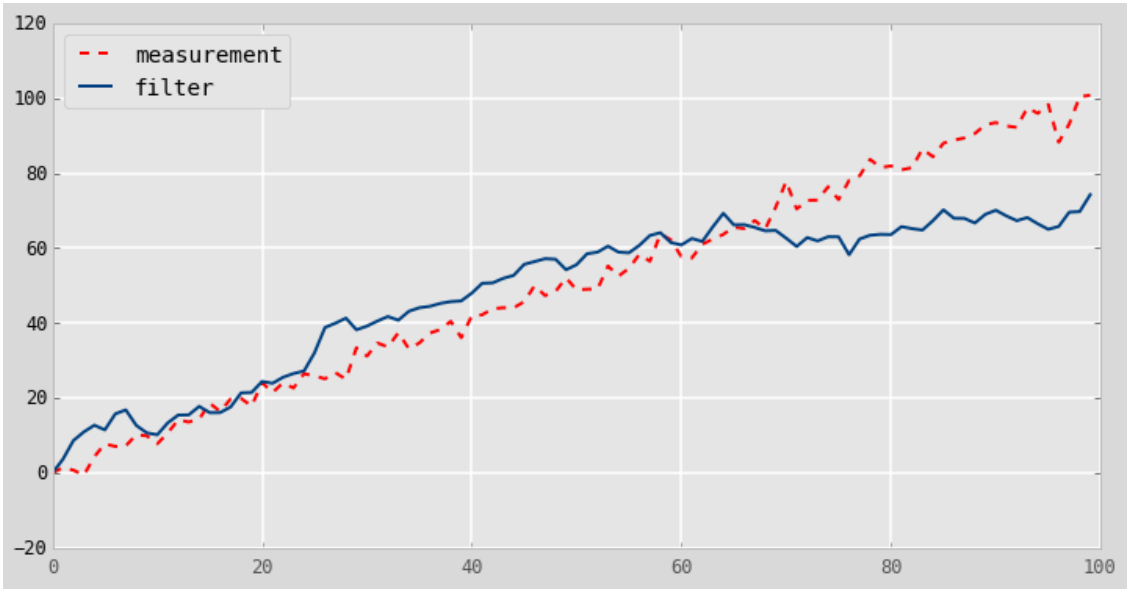
```
Out[28]: <function __main__.plot_kalman_filter>
```

Solution

One possible solution follows.

```
In [29]: zs = np.zeros(100)
         ps = np.zeros(100)
         def plot_kalman_filter(start_pos, sensor_noise, movement, movement_noise,noise_
             dog = DogSensor(start_pos, velocity=movement, noise=sensor_noise)
             random.seed(303)
             pos = (0,100)

             for i in range(100):
                 Z = dog.sense() + random.randn()*noise_scale
                 zs[i] = Z

                 pos = update(pos[0], pos[1], Z, sensor_error)
                 ps[i] = pos[0]

                 pos = predict(pos[0], pos[1], movement + random.randn()*movement_noise,

             plt.plot(zs,c='r', linestyle='dashed', label='measurement')
             plt.plot(ps, c='#004080', label='filter')
             plt.legend(loc='best')
```

```
        plt.show()

    interact(plot_kalman_filter,
             start_pos=(-10,10),
             sensor_noise=widgets.IntSliderWidget(value=5,min=0,max=100),
             movement=widgets.FloatSliderWidget(value=1,min=-2.,max=2.),
             movement_noise=widgets.FloatSliderWidget(value=2,min=0,max=100.),
             noise_scale=widgets.FloatSliderWidget(value=1,min=0,max=20.))
```



Out[29]: <function __main__.plot_kalman_filter>

6.9.5 Exercise - Nonlinear Systems

Our equations are linear:

$$new\_pos = old\_pos + dist\_moved$$
$$new\_position = old\_position * measurement$$

Do you suppose that this filter works well or poorly with nonlinear systems?

Implement a Kalman filter that uses the following equation to generate the measurement value for i in range(100):

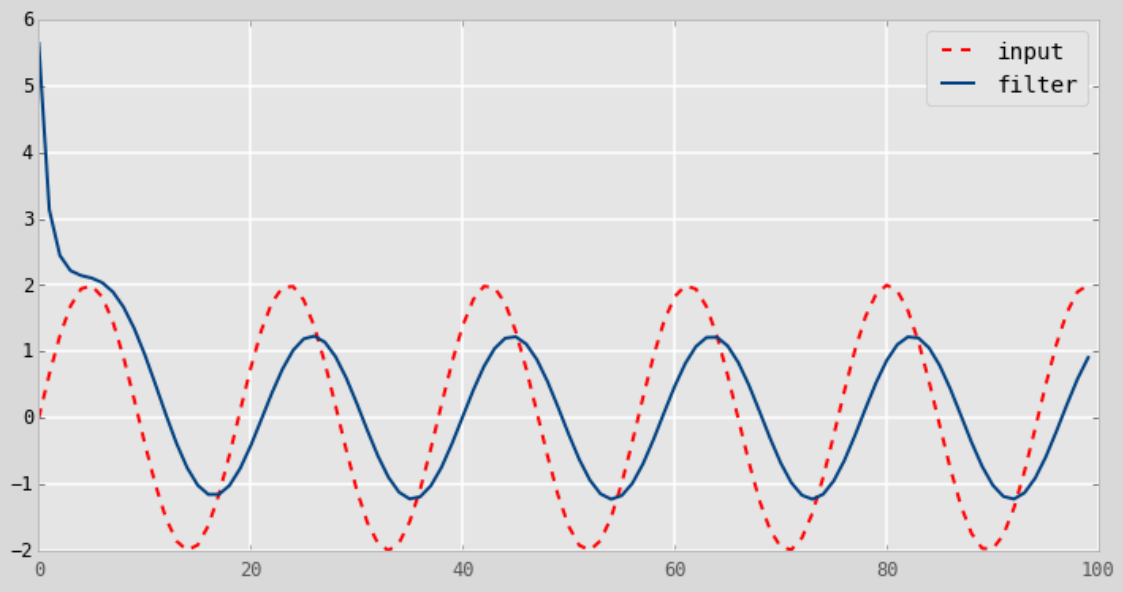
```
Z = math.sin(i/3.) * 2
```

Adjust the variance and initial positions to see the effect. What is, for example, the result of a very bad initial guess?

```
In [30]: #enter your code here.
```

Solution:

```
In [31]: sensor_error = 30
         movement_error = 2
         pos = (100,500)

         zs = []
         ps = []


         for i in range(100):
             pos = predict(pos[0], pos[1], movement, movement_error)

             Z = math.sin(i/3.)*2
             zs.append(Z)

             pos = update(pos[0], pos[1], Z, sensor_error)
             ps.append(pos[0])

         plt.plot(zs,c='r', linestyle='dashed', label='input')
         plt.plot(ps, c='#004080', label='filter')
         plt.legend(loc='best')
         plt.show()
```



Discussion

Here we set a bad initial guess of 100. We can see that the filter never 'acquires' the signal. Note now the peak of the filter output always lags the peak of the signal by a small amount, and how the filtered signal does not come very close to capturing the high and low peaks of the input signal.

If we recall the g-h filter chapter we can understand what is happening here. The structure of the g-h filter requires that the filter output chooses a value part way between the prediction and measurement. A varying signal like this one is always accelerating, whereas our process model assumes constant velocity, so the filter is mathematically guaranteed to always lag the input signal.

Maybe we just didn't adjust things 'quite right'. After all, the output looks like a sin wave, it is just offset some. Let's test this assumption.

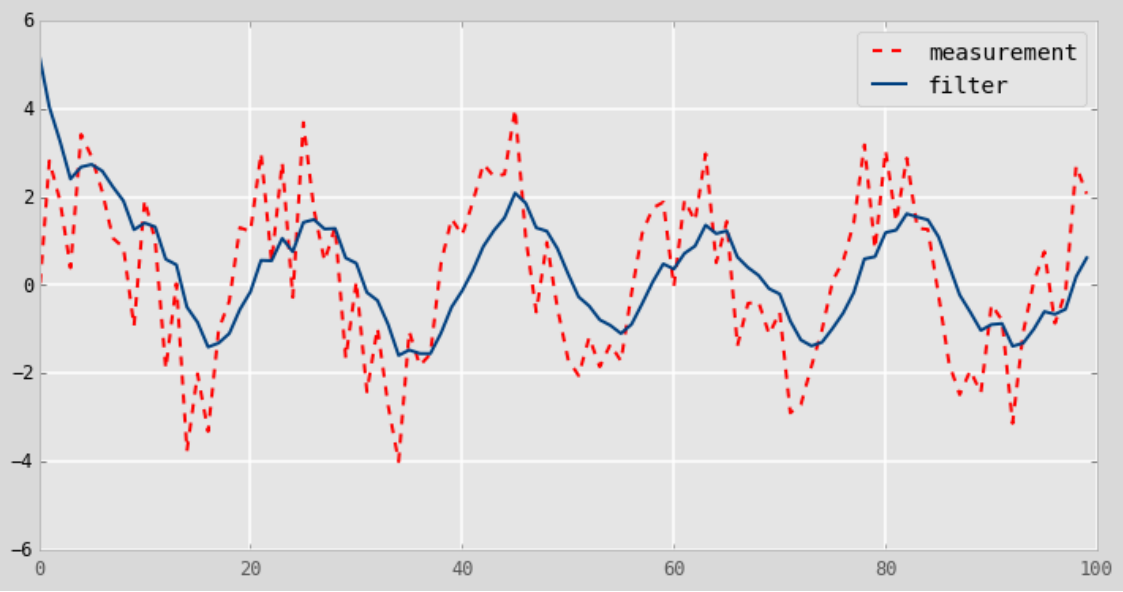
6.9.6 Exercise - Noisy Nonlinear Systems

Implement the same system, but add noise to the measurement.

In [32]:
```
#enter your code here
```

Solution

In [33]:
```
sensor_error = 30
movement_error = 2
pos = (100,500)

zs = []
ps = []

for i in range(100):
    pos = predict(pos[0], pos[1], movement, movement_error)

    Z = math.sin(i/3.)*2 + random.randn()*1.2
    zs.append(Z)

    pos = update(pos[0], pos[1], Z, sensor_error)
    ps.append(pos[0])

p1, = plt.plot(zs,c='r', linestyle='dashed', label='measurement')
p2, = plt.plot(ps, c='#004080', label='filter')
plt.legend(loc='best')
plt.show()
```



Discussion

This is terrible! The output is not at all like a sin wave, except in the grossest way. With linear systems we could add extreme amounts of noise to our signal and still extract a very accurate result, but here even modest noise creates a very bad result.

Very shortly after practitioners began implementing Kalman filters they recognized the poor performance of them for nonlinear systems and began devising ways of dealing with it. Much of this book is devoted to this problem and its various solutions.

6.10 Summary

This information in this chapter takes some time to assimilate. To truly understand this you will probably have to work through this chapter several times. I encourage you to change the various constants and observe the results. Convince yourself that Gaussians are a good representation of a unimodal belief of something like the position of a dog in a hallway. Then convince yourself that multiplying Gaussians truly does compute a new belief from your prior belief and the new measurement. Finally, convince yourself that if you are measuring movement, that adding the Gaussians correctly updates your belief. That is all the Kalman filter does. Even now I alternate between complacency and amazement at the results.

If you understand this, you will be able to understand multidimensional Kalman filters and the various extensions that have been make on them. If you do not fully understand this, I strongly suggest rereading this chapter. Try implementing the filter from scratch, just by looking at the equations and reading the text. Change the constants. Maybe try to implement a different tracking problem, like tracking stock prices. Experimentation will build your intuition and understanding of how these marvelous filters work.

In [33]:

author notes: clean up the code - same stuff duplicated over and over - write a 'clean implementation' at the end.

Chapter 7

Multivariate Kalman Filters

7.1 Introduction

The techniques in the last chapter are very powerful, but they only work in one dimension. The gaussians represent a mean and variance that are scalars - real numbers. They provide no way to represent multidimensional data, such as the position of a dog in a field. You may retort that you could use two Kalman filters for that case, one tracks the x coordinate and the other tracks the y coordinate. That does work in some cases, but put that thought aside, because soon you will see some enormous benefits to implementing the multidimensional case.

In this chapter I am purposefully glossing over many aspects of the mathematics behind Kalman filters. If you are familiar with the topic you will read statements that you disagree with because they contain simplifications that do not necessarily hold in more general cases. If you are not familiar with the topic, expect some paragraphs to be somewhat 'magical' - it will not be clear how I derived a certain result. I prefer that you develop an intuition for how these filters work through several worked examples. If I started by presenting a rigorous mathematical formulation you would be left scratching your head about what all these terms mean and how you might apply them to your problem. In later chapters I will provide a more rigorous mathematical foundation, and at that time I will have to either correct approximations that I made in this chapter or provide additional information that I did not cover here.

7.2 Multivariate Normal Distributions

What might a *multivariate normal distribution* look like? In this context, multivariate just means multiple variables. Our goal is to be able to represent a normal distribution across multiple dimensions. Consider the 2 dimensional case. Let's say we believe that $x = 2$ and $y = 17$. Therefore we can see that for N dimensions, we need N means, like so:

$$\mu = \begin{bmatrix} \mu_1 \\ \mu_2 \\ \vdots \\ \mu_n \end{bmatrix}$$

Therefore for this example we would have

$$\mu = \begin{bmatrix} 2 \\ 17 \end{bmatrix}$$

The next step is representing our variances. At first blush we might think we would also need N variances for N dimensions. We might want to say the variance for x is 10 and the variance for y is 4, like so.

$$\sigma^2 = \begin{bmatrix} 10 \\ 4 \end{bmatrix}$$

While this is possible, it does not consider the more general case. For example, suppose we were tracking house prices vs total m^2 of the floor plan. These numbers are *correlated*. It is not an exact correlation, but in general houses in the same neighborhood are more expensive if they have a larger floor plan. We want a way to express not only what we think the variance is in the price and the m^2, but also the degree to which they are correlated. It turns out that we use the following matrix to denote *covariances* with multivariate normal distributions. You might guess, correctly, that *covariance* is short for *correlated variances*.

$$\Sigma = \begin{bmatrix} \sigma_1^2 & \sigma_{12} & \cdots & \sigma_{1n} \\ \sigma_{21} & \sigma_2^2 & \cdots & \sigma_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ \sigma_{n1} & \sigma_{n2} & \cdots & \sigma_n^2 \end{bmatrix}$$

If you haven't seen this before it is probably a bit confusing at the moment. Rather than explain the math right now, we will take our usual tactic of building our intuition first with various physical models. At this point, note that the diagonal contains the variance for each state variable, and that all off-diagonal elements (covariances) are represent how much the ith (row) and jth (column) state variable are linearly correlated to each other. In other words, it is a measure for how much they change together. No correlation will have a covariance of 0. So, for example, if the variance for x is 10, the variance for y is 4, and there is no linear correlation between x and y, then we would say

$$\Sigma = \begin{bmatrix} 10 & 0 \\ 0 & 4 \end{bmatrix}$$

If there was a small amount of correlation between x and y we might have

$$\Sigma = \begin{bmatrix} 10 & 1.2 \\ 1.2 & 4 \end{bmatrix}$$

where 1.2 is the covariance between x and y. Note that this is always symmetric - the covariance between x and y is always equal to the covariance between y and x. That is, $\sigma_{xy} = \sigma_{yx}$ for any x and y.

Now, without explanation, here is the full equation for the multivariate normal distribution in n dimensions.

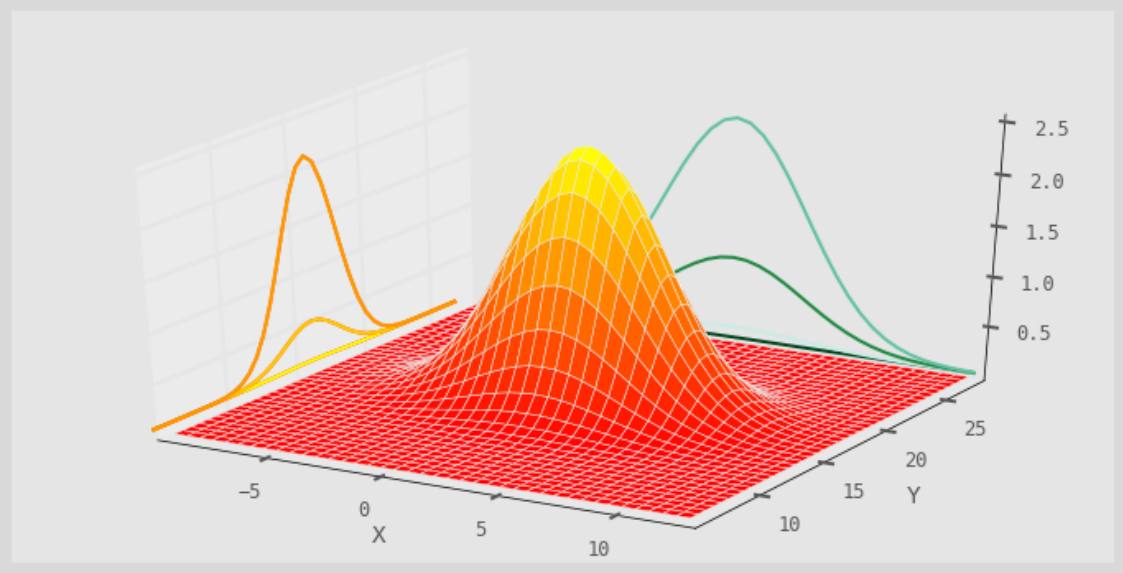
$$\mathcal{N}(\mu, \Sigma) = (2\pi)^{-\frac{n}{2}}|\Sigma|^{-\frac{1}{2}}\, e^{-\frac{1}{2}(\mathbf{x}-\mu)'\Sigma^{-1}(\mathbf{x}-\mu)}$$

I urge you to not try to remember this function. We will program it in a Python function and then call it when we need to compute a specific value. However, if you look at it briefly you will note that it looks quite similar to the *univariate normal distribution* except it uses matrices instead of scalar values, and the root of π is scaled by n. Here is the *univariate* equation for reference:

$$f(x, \mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{1}{2}(x-\mu)^2/\sigma^2}$$

If you are reasonably well-versed in linear algebra this equation should look quite manageable; if not, don't worry! Let's just plot it and see what it looks like.

```
In [2]: import mkf_internal
        import numpy as np
        mkf_internal.plot_3d_covariance((2,17), np.array([[10.,0],[0,4.]]))
```



Here we have plotted a two dimensional multivariate Gaussian with a mean of $\mu = \left[\begin{smallmatrix}2\\17\end{smallmatrix}\right]$ and a covariance of $\Sigma = \left[\begin{smallmatrix}8 & 0\\0 & 10\end{smallmatrix}\right]$. The three dimensional shape shows the probability of for any value of (x,y) in the z-axis. I have projected just the variance for x and y onto the walls of the chart - you can see that they take on the normal Gaussian bell curve shape. You can also see that, as we might hope, that the curve for x is wider than the curve for y, which

is explained by $\sigma_x^2 = 10$ and $\sigma_y^2 = 4$. Also, the highest point of the curve is centered over (2,17), the means for x and y. I hope this demystifies the equation for you. Any multivariate Gaussian will create this sort of shape. If we think of this as a the Gaussian for our dog's position in a two dimensional field, the z-value at each point of (x,y) indicates the probability of the dog being at that position. So, he has the highest probability of being at (2,17), a modest probability of being at (5,14), and a very low probability of being at (10,10).

We will discuss the mathematical description of covariances in the Kalman Filter math chapter. For this chapter we just need to understand the following.

1. The diagonal of the matrix contains the variance for each variable.
2. Each off-diagonal element contains σ_{ij} - the covariance between i and j. This tells us how much linear correlation there is between the two variables. 0 means no correlation, and as the number gets higher the correlation gets greater.
3. $\sigma_{ij} = \sigma_{ji}$
4. The covariance between x and itself is just the variance of x: $\sigma_{xx} = \sigma_x^2$.
5. This chart only shows a 2 dimensional Gaussian, but the equation works for any number of dimensions >= 1. It's kind of hard to show a chart for the higher dimensions.

I have programmed the multivariate Gaussian equation and saved it in the file `stats.py` with the function name `multivariate_gaussian`. I am not showing the code here because I have taken advantage of the linear algebra solving apparatus of numpy to efficiently compute a solution - the code does not correspond to the equation in a one to one manner. If you wish to view the code, I urge you to either load it in an editor, or load it into this worksheet by putting `%load -s multivariate_gaussian stats.py` in the next cell and executing it with ctrl-enter.

However, please note that the Kalman filter equations incorporate this computation automatically; you will not be using this function very often in this book, so I would not spend a lot of time mastering this function unless it interests you.

> As of version 0.14 scipy.stats has implemented the multivariate normal equation with the function `multivariate_normal()`. It implements a 'frozen' form where you set the mean and covariance once, and then calculate the probability for any number of values for x over any arbitrary number of calls. This is much more efficient then recomputing everything in each call. So, if you have version 0.14 or later you may want to substitute my function for the built in version. Use `scipy.version.version` to get the version number. I deliberately named my function `multivariate_gaussian()` to ensure it is never confused with the built in version. I will say that for a single call, where the frozen variables do not matter, mine consistently runs faster as measured by the `timeit` function.
>
> The tutorial[1] for the `scipy.stats` module explains 'freezing' distributions and other very useful features. As of this date, it includes an example of using the multivariate_normal function, which does work a bit differently from my function.

```
In [3]: from stats import gaussian, multivariate_gaussian
```

Let's use it to compute a few values just to make sure we know how to call and use the function, and then move on to more interesting things.

First, let's find the probability for our dog being at (2.5, 7.3) if we believe he is at (2,7) with a variance of 8 for x and a variance of 10 for y.

Start by setting x to (2.5,7.3):

```
In [4]: x = [2.5, 7.3]
```

Next, we set the mean of our belief:

```
In [5]: mu = [2.0, 7.0]
```

Finally, we have to define our covariance matrix. In the problem statement we did not mention any correlation between x and y, and we will assume there is none. This makes sense; a dog can choose to independently wander in either the x direction or y direction without affecting the other. If there is no correlation between the values you just fill in the diagonal of the covariance matrix with the variances. I will use the seemingly arbitrary name **P** for the covariance matrix. The Kalman filters use the name **P** for this matrix, so I will introduce the terminology now to avoid explaining why I change the name later.

```
In [6]: P = [[8.,  0.],
             [0., 10.]]
```

Now just call the function

```
In [7]: print(multivariate_gaussian(x,mu,P))
```

```
0.017439537440741816
```

> Note that the function can accept lists, np.array, or np.matrix as arguments, or even scalars. Type `multivariate_gaussian?` in a cell and press ctrl-enter to get the help for this function.

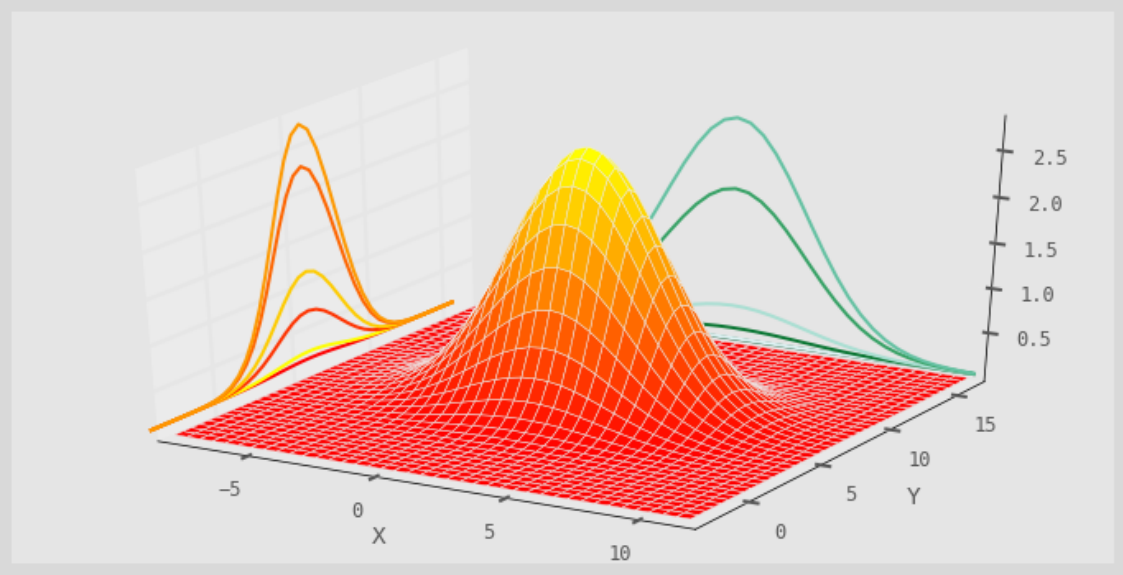
Let's check the probability for the dog being at exactly (2,7)

```
In [8]: from __future__ import print_function
        import numpy as np

        x = np.array([2,7]) # using array to show we can use lists and arrays
        prob = multivariate_gaussian(x,mu,P) * 100.

        print("Probability dog is at (2,7) is {:.3}%".format(prob))
```

```
Probability dog is at (2,7) is 1.78%
```

These numbers are not easy to interpret. Let's plot this in 3D, with the z (up) coordinate being the probability.

```
In [9]: import mkf_internal
        mkf_internal.plot_3d_covariance((2,7), np.array([[8.,0],[0,4.]]))
```

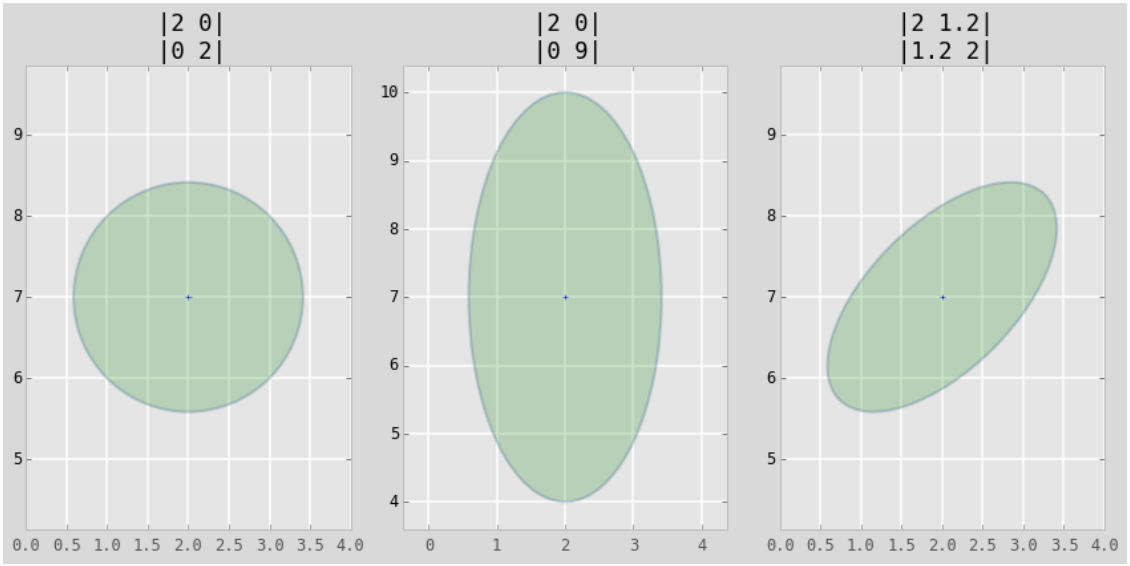


The result is clearly a 3D bell shaped curve. We can see that the gaussian is centered around (2,7), and that the probability quickly drops away in all directions. On the sides of the plot I have drawn the Gaussians for x in greens and for y in orange.

As beautiful as this is, it is perhaps a bit hard to get useful information. For example, it is not easy to tell if x and y both have the same variance or not. So for most of the rest of this book we will display multidimensional Gaussian using contour plots. I will use some helper functions in `stats.py` to plot them. If you are interested in linear algebra go ahead and look at the code used to produce these contours, otherwise feel free to ignore it.

```
In [10]: import stats

         P = np.array([[2,0],[0,2]])
         plt.subplot(131)
         stats.plot_covariance_ellipse((2,7), cov=P, facecolor='g', alpha=0.2,
                                       title='|2 0|\n|0 2|')

         plt.subplot(132)
         P = np.array([[2,0],[0,9]])
         stats.plot_covariance_ellipse((2,7), P,  facecolor='g', alpha=0.2,
                                       title='|2 0|\n|0 9|')
```

```
plt.subplot(133)
P = np.array([[2,1.2],[1.2,2]])
stats.plot_covariance_ellipse((2,7), P,  facecolor='g', alpha=0.2,
                              title='|2 1.2|\n|1.2 2|')

plt.tight_layout()
plt.show()
```



From a mathematical perspective these display the values that the multivariate gaussian takes for a specific sigma (in this case $\sigma^2 = 1$. Think of it as taking a horizontal slice through the 3D surface plot we did above. However, thinking about the physical interpretation of these plots clarifies their meaning.

The first plot uses the mean and covariance matrices of

$$\mu = \begin{bmatrix} 2 \\ 7 \end{bmatrix}$$

$$\Sigma = \begin{bmatrix} 2 & 0 \\ 0 & 2 \end{bmatrix}$$

Let this be our current belief about the position of our dog in a field. In other words, we believe that he is positioned at (2,7) with a variance of $\sigma^2 = 2$ for both x and y. The contour plot shows where we believe the dog is located with the '+' in the center of the ellipse. The ellipse shows the boundary for the $1\sigma^2$ probability - points where the dog is quite likely to be based on our current knowledge. Of course, the dog might be very far from this point, as Gaussians allow the mean to be any value. For example, the dog could be at (3234.76,189989.62), but that has vanishing low probability of being true. Generally speaking displaying the $1\sigma^2$ to $2\sigma^2$ contour captures the most likely values for the distribution. An equivalent way of thinking about this is the circle/ellipse shows us the amount of error in

our belief. A tiny circle would indicate that we have a very small error, and a very large circle indicates a lot of error in our belief. We will use this throughout the rest of the book to display and evaluate the accuracy of our filters at any point in time.

The second plot uses the mean and covariance matrices of

$$\mu = \begin{bmatrix}2\\7\end{bmatrix}$$
$$\Sigma = \begin{bmatrix}2 & 0\\0 & 9\end{bmatrix}$$

This time we use a different variance for x (2) vs y (9). The result is an ellipse. When we look at it we can immediately tell that we have a lot more uncertainty in the y value vs the x value. Our belief that the value is (2,7) is the same in both cases, but errors are different. This sort of thing happens naturally as we track objects in the world - one sensor has a better view of the object, or is closer, than another sensor, and so we end up with different error rates in the different axis.

The third plot uses the mean and covariance matrices of:

$$\mu = \begin{bmatrix}2\\7\end{bmatrix}$$
$$\Sigma = \begin{bmatrix}2 & 1.2\\1.2 & 2\end{bmatrix}$$

This is the first contour that has values in the off-diagonal elements of *cov*, and this is the first contour plot with a slanted ellipse. This is not a coincidence. The two facts are telling use the same thing. A slanted ellipse tells us that the x and y values are somehow **correlated**. We denote that in the covariance matrix with values off the diagonal. What does this mean in physical terms? Think of trying to park your car in a parking spot. You can not pull up beside the spot and then move sideways into the space because most cars cannot go purely sideways. x and y are not independent. This is a consequence of the steering system in a car. When your tires are turned the car rotates around its rear axle while moving forward. Or think of a horse attached to a pivoting exercise bar in a corral. The horse can only walk in circles, he cannot vary x and y independently, which means he cannot walk straight forward to to the side. If x changes, y must also change in a defined way.

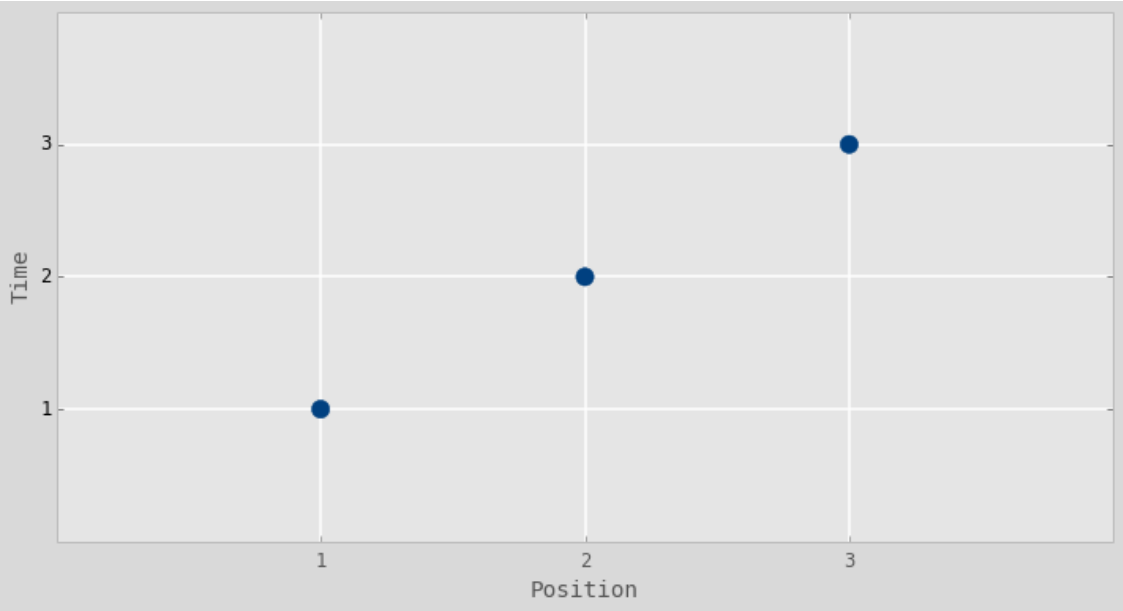
So when we see this ellipse we know that x and y are correlated, and that the correlation is "strong". The size of the ellipse shows how much error we have in each axis, and the slant shows how strongly correlated the values are.

A word about **correlation** and **independence**. If variables are **independent** they can vary separately. If you walk in an open field, you can move in the x direction (east-west), the y direction(north-south), or any combination thereof. Independent variables are always also **uncorrelated**. Except in special cases, the reverse does not hold true. Variables can be uncorrelated, but dependent. For example, consider the pair(x, y) where $y = x^2$. Correlation is a linear measurement, so x and y are uncorrelated. However, they are obviously dependent on each other.

7.3 Unobserved Variables

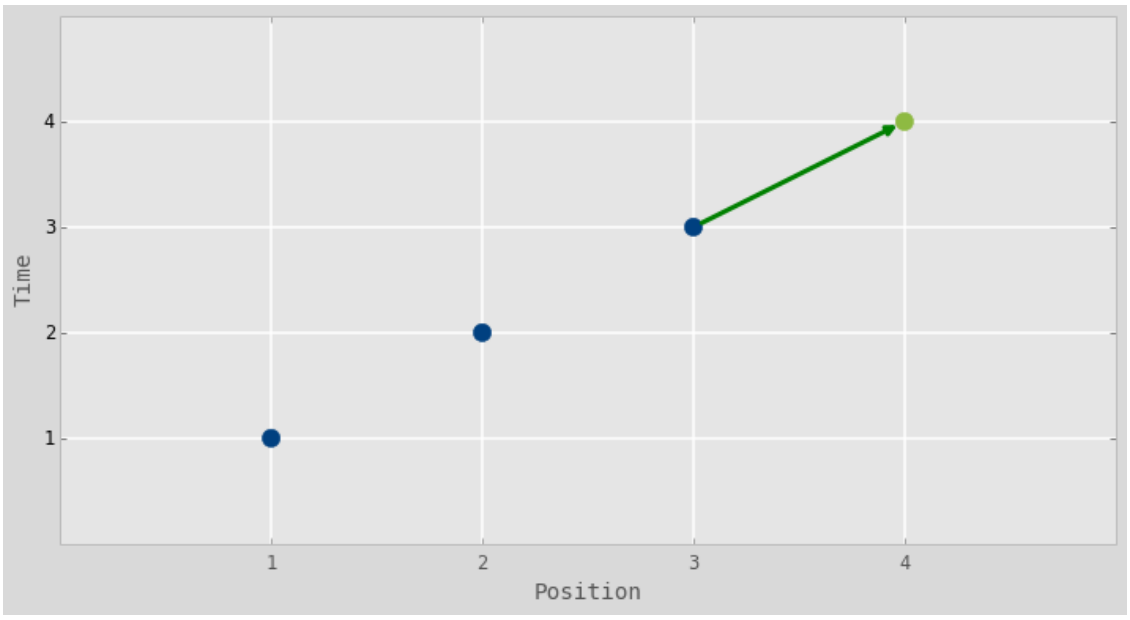
Let's say we are tracking an aircraft and we get the following data for the x coordinate at time t=1,2, and 3 seconds. What does your intuition tell you the value of x will be at time t=4 seconds?

```
In [11]: import mkf_internal
         mkf_internal.show_position_chart()
```



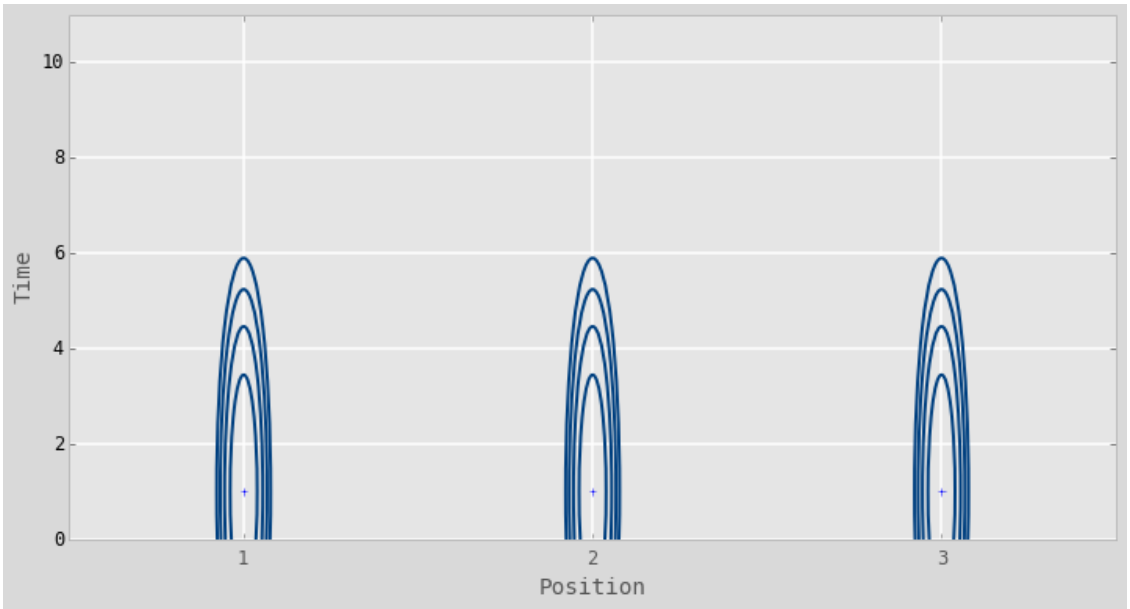
It appears that the aircraft is flying in a straight line because we can draw a line between the three points, and we know that aircraft cannot turn on a dime. The most reasonable guess is that x=4 at t=4. I will depict that with a green arrow.

```
In [12]: mkf_internal.show_position_prediction_chart()
```



If this is data from a Kalman filter, then each point has both a mean and variance. Let's try to show that by showing the approximate error for each point. Don't worry about why I am using a covariance matrix to depict the variance at this point, it will become clear in a few paragraphs. The intent at this point is to show that while we have x=1,2,3 that there is a lot of error associated with each measurement.

```
In [13]: mkf_internal.show_x_error_chart()
```

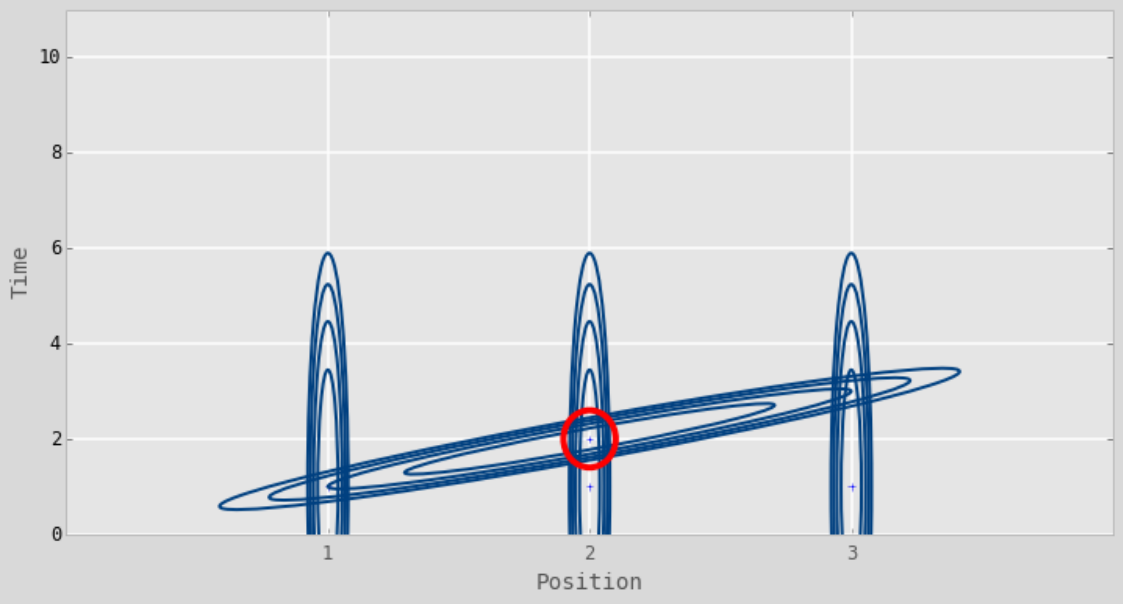


We can see that there is a lot of error associated with each value of x. We could write a 1D Kalman filter as we did in the last chapter, but suppose this is the output of that filter, and not just raw sensor measurements. Are we out of luck?

Let us think about how we predicted that x=4 at t=4. In one sense we just drew a straight line between the points and saw where it lay at t=4. My constant refrain: what is the physical interpretation of that? What is the difference in x over time? In other words, what is $\frac{\partial x}{\partial t}$? The derivative, or difference in distance over time is *velocity*.

This is the **key point** in Kalman filters, so read carefully! Our sensor is only detecting the position of the aircraft (how doesn't matter). It does not have any kind of sensor that provides velocity to us. But based on the position estimates we can compute velocity. In Kalman filters we would call the velocity an *unobserved variable*. Unobserved means what it sounds like - there is no sensor that is measuring velocity directly. Since the velocity is based on the position, and the position has error, the velocity will have error as well. What happens if we draw the velocity errors over the positions errors?

```
In [14]: mkf_internal.show_x_with_unobserved()
```



Think about what this plot means. We have a lot of error in our position estimates. We therefore have a lot of error in our velocity estimates. But look at the intersections between the velocity and the positions. Take the intersection at t=2. The intersection between the velocity and the position is where our aircraft is most likely to be, which I have roughly depicted with a red ellipse ('roughly' because I set the size via eyeball, not via math). The size of the error is much smaller than the error of the positions, despite the fact that velocity was derived from position.

What makes this possible? Imagine for a moment that we superimposed the velocity from a *different* airplane over the position graph. Clearly the two are not related, and there is

no way that combining the two could possibly yield any additional information. In contrast, the velocity of the this airplane tells us something very important - the direction and speed of travel. So long as the aircraft does not alter its velocity the velocity allows us to predict where the next position is. After a relatively small amount of error in velocity the probability that it is a good match with the position is very small. Think about it - if you suddenly change direction your position is also going to change a lot. If the position measurement is not in the direction of the assumed velocity change it is very unlikely to be true. The two are correlated, so if the velocity changes so must the position, and in a predictable way.

7.4 Kalman Filter Algorithm

So in general terms we can show how a multidimensional Kalman filter works. In the example above, we compute velocity from the previous position measurements using something called the *measurement function*. Then we predict the next position by using the current estimate and something called the *state transition function*. In our example above,

$$new\_position = old\_position + velocity * time$$

Next, we take the measurement from the sensor, and compare it to the prediction we just made. In a world with perfect sensors and perfect airplanes the prediction will always match the measured value. In the real world they will always be at least slightly different. We call the difference between the two the *residual*. Finally, we use something called the *Kalman gain* to update our estimate to be somewhere between the measured position and the predicted position. I will not describe how the gain is set, but suppose we had perfect confidence in our measurement - no error is possible. Then, clearly, we would set the gain so that 100% of the position came from the measurement, and 0% from the prediction. At the other extreme, if he have no confidence at all in the sensor (maybe it reported a hardware fault), we would set the gain so that 100% of the position came from the prediction, and 0% from the measurement. In normal cases, we will take a ratio of the two: maybe 53% of the measurement, and 47% of the prediction. The gain is updated on every cycle based on the variance of the variables (in a way yet to be explained). It should be clear that if the variance of the measurement is low, and the variance of the prediction is high we will favor the measurement, and vice versa.

The chart shows a prior estimate of $\hat{x} = 2$ and a velocity $\dot{x} = 1$.

> We use the caret notation $\hat{x}$ to denote an *estimate* - the output of the filter. We use the familar dot notation $\dot{x}$ to denote the derivative of x.

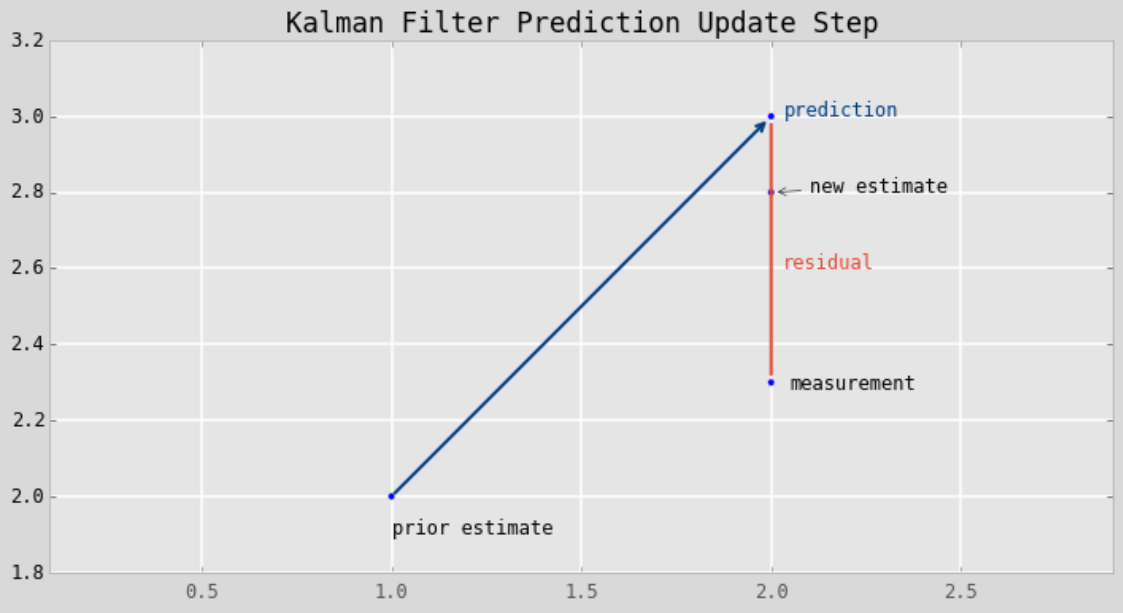
Therefore we predict $x^- = 2 + 1 = 3$.

> We use the notation x^- to denote a *prediction*.

However, the new measurement is $x^* = 2.3$, giving a residual $r = 0.7$. Finally, the Kalman filter gain K gives us a new estimate of $\hat{x} = 2.8$.

We use the symbolology x^* to denote a measurement. I will address symbology in more detail later. It is an unfortunate reality that nearly every text on Kalman filtering uses different symbology and variables - there is almost no agreement across texts. Be sure to read the introductory material very carefully to avoid being led astray.

```
In [15]: from mkf_internal import *
         show_residual_chart()
```



7.5 The Equations

The brilliance of the Kalman filter is taking the insights of the chapter up to this point and finding an optimal mathematical solution. The Kalman filter finds what is called a *least squared fit* to the set of measurements to produce an optimal output. We will not trouble ourselves with the derivation of these equations. It runs to several pages, and offers a lot less insight than the words above, in my opinion. Furthermore, to create a Kalman filter for your application you will not be manipulating these equations, but only specifying a number of parameters that are used by them. It would be going too far to say that you will never need to understand these equations; but to start we can pass them by and I will present the code that implements them. So, first, let's see the equations. > Kalman Filter Predict Step:

$$\hat{\mathbf{x}}^-_{k+1} = \mathbf{F}_k\hat{\mathbf{x}}_k + \mathbf{B}_k\mathbf{u}_k \qquad (1)$$

$$\mathbf{P}^-_{k+1} = \mathbf{F}_k\mathbf{P}_k\mathbf{F}_k^T + \mathbf{Q}_k \qquad (2)$$

Kalman Filter Update Step:

$$\mathbf{y}_k = \mathbf{z}_k - \mathbf{H}_k\hat{x}_k^- \quad (3)$$
$$\mathbf{S}_k = \mathbf{H}_k\mathbf{P}_k^-\mathbf{H}_k^T + \mathbf{R}_k \quad (4)$$
$$\mathbf{K}_k = \mathbf{P}_k^-\mathbf{H}_k^T\mathbf{S}_k^{-1} \quad (5)$$
$$\hat{\mathbf{x}}_k = \hat{\mathbf{x}}_k^- + \mathbf{K}_k\mathbf{y} \quad (6)$$
$$\mathbf{P}_k = (\mathbf{I} - \mathbf{K}_k\mathbf{H}_k)\mathbf{P}_k^- \quad (7)$$

Dash off, wipe the blood out of your eyes, and we'll disuss what this means.

These are nothing more than linear algebra equations that implement the algorithm we used in the last chapter, but using multidimensional Gaussians instead of univariate Gaussians, and optimized for a least squares fit.

The subscripts indicate which time step the data comes from; k is now, $k+1$ is the next step. A^T is the transpose of the matrix A, and A^{-1} is the inverse. Finally, the hat denotes an estimate, so $\hat{x}_k$ is the estimate of x at time k.

Different texts use different notation and variable names for the Kalman filter. Later we will expose you to these different forms to prepare you for reading the original literature. In the equations above I have adopted the variable names used by the Wikipedia article[2] on Kalman filters. Each bold letter denotes a matrix or vector. The subscripts indicate which time step the data comes from; k is now, $k+1$ is the next step. The caret ($\hat{}$) indicates that the value is an estimate. Finally, I particularly like how Brown [3] uses a raised $^-$ to denote a prediction, and so I have adopted that approach. For a matrix $\mathbf{A}$, $\mathbf{A}^T$ signifies its transpose, and $\mathbf{A}^{-1}$ its inverse. So, taken together, $\hat{\mathbf{x}}_{k+1}^-$ represents the prediction for the estimate of $\mathbf{x}$ at time step $k+1$, where $\mathbf{x}$ is some vector in the form $\mathbf{x} = \begin{bmatrix} x_1 & x_2 & .. & x_n \end{bmatrix}^T$. The notation does not specify that $\mathbf{x}$ is a column vector - we will learn the shapes and sizes of all of the variables later in the chapter.

author's note: do we really want to explain notation here?

7.5.1 Kalman Equations Expressed as an Algorithm

However, I still find the notation to be a bit dense, and unnecessarily complicated for writing code. The subscripts indicate the time step, but when we right code it is very clear what is being calculated at each time step. For most of this book I'm going to use the following simplified equations, which express an algorithm.

Predict Step

$$\mathbf{x}^- := \mathbf{F}\mathbf{x} + \mathbf{B}\mathbf{u} \quad (1)$$
$$\mathbf{P} := \mathbf{F}\mathbf{P}\mathbf{F}^T + \mathbf{Q} \quad (2)$$

Update Step

$$\mathbf{y} := \mathbf{z} - \mathbf{H}\mathbf{x}^- \quad (3)$$
$$\mathbf{S} := \mathbf{H}\mathbf{P}\mathbf{H}^T + \mathbf{R} \quad (4)$$
$$\mathbf{K} := \mathbf{P}\mathbf{H}^T\mathbf{S}^{-1} \quad (5)$$
$$\mathbf{x} := \mathbf{x}^- + \mathbf{K}\mathbf{y} \quad (6)$$
$$\mathbf{P} := (\mathbf{I} - \mathbf{K}\mathbf{H})\mathbf{P} \quad (7)$$

This is an algorithm, so := denotes assignment, not equality. For example, equation (6) has P on both sides of the :=. This equation updates the value of P by the computation on the right hand side; it does not imply that the two sides of the equation are equal (they are not).

What do all of the variables mean? What is **P**, for example? Don't worry right now. Instead, I am just going to design a Kalman filter, and introduce the names as we go. Then we will just pass them into Python function that implement the equations above, and we will have our solution. Later sections will then delve into more detail about each step and equation. I think learning by example and practice is far easier than trying to memorize a dozen abstract facts at once.

7.6 Implementation in Python

Before we go any further let's gain some familiarity with the equations by programming them in Python. I have written a production quality implementation of the Kalman filter equations in my `filterpy` library, and we will be using that later in the chapter and the remainder of the book. We could just look at that code, but it contains a significant amount of code to ensure that the computations are numerically stable, that you do not pass in bad data, and so on. Let's just try to program this.

The filter equations are *linear algebra* equations, so we will use the Python library that implements linear algebra - `numpy`. In the filter equations a **bold** variable denotes a matrix. Numpy provides two types to implement matrices: `numpy.array` and `numpy.matrix`. You might suspect that the latter is the one we want to use. As it turns out `numpy.matrix` does support linear algebra well, except for one problem - most of the rest of `numpy` uses `numpy.array`, not `numpy.matrix`. You can pass a `numpy.matrix` into a function, and get a `numpy.array` back as a result. Hence, the standard advice is that `numpy.matrix` is deprecated, and you should always use `numpy.array` even when `numpy.matrix` is more convienient. I ignored this advice in a early version of this code and ended up regretting that choice, and so now I use 'numpy.array' only.

`numpy.array` implements a any-dimensional array. You can construct it with any list like object. The following constructs a 1-D array from a list:

```
In [16]: import numpy as np
         x = np.array([1,2,3])
         print(x)
         print(type(x))

[1 2 3]
<class 'numpy.ndarray'>
```

You can create a 2D array with nested lists:

```
In [17]: x = np.array([[1,2,3],
                       [4,5,6]])
         print(x)

[[1 2 3]
 [4 5 6]]
```

You can create arrays of 3 or more dimensions, but we have no need for that here, and so I will not elaborate.

By default the arrays use the data type of the values in the list; if there are multiple types than it will choose the type that most accurately represents all the values. So, for example, if your list contains a mix of `int` and `float` the data type of the array would be of type `float`. You can override this with the `dtype` parameter.

```
In [18]: x = np.array([1,2,3],dtype=float)
         print(x)

[ 1.  2.  3.]
```

You can perform matrix addition with the `+` operator, but matrix multiplication requires the `dot` method or function. The `*` operator performs element-wise multiplication, which is **not** what you want for linear algebra.

```
In [19]: x = np.array([[1,2],[3,4]], dtype=float)
         print('addition:\n', x+x)
         print('element-wise multiplication\n', x*x)
         print('multiplication\n', np.dot(x,x))
         print('dot is also a member\n', x.dot(x))

addition:
 [[ 2.  4.]
 [ 6.  8.]]
element-wise multiplication
 [[  1.   4.]
 [  9.  16.]]
multiplication
 [[  7.  10.]
```

```
 [ 15.  22.]]
dot is also a member
 [[  7.  10.]
 [ 15.  22.]]
```

You can get the transpose with `.T`, and the inverse with `numpy.linalg.inv`.

```
In [20]: print('transpose\n', x.T)
         print('inverse\n', np.linalg.inv(x))

transpose
 [[ 1.  3.]
 [ 2.  4.]]
inverse
 [[-2.   1. ]
 [ 1.5 -0.5]]
```

Finally, there are helper functions like `zeros` to create a matrix of all zeros, `ones` to get all ones, and `eye` to get the identity matrix.

```
In [21]: print('zeros\n', np.zeros((3,2)))
         print('\neye\n', np.eye(3))

zeros
 [[ 0.  0.]
 [ 0.  0.]
 [ 0.  0.]]

eye
 [[ 1.  0.  0.]
 [ 0.  1.  0.]
 [ 0.  0.  1.]]
```

There is a lot of useful functionality in `numpy`, but let's move on to implementing the Kalman filter. Let's start with the prediction equations.

$$\mathbf{x}^- := \mathbf{Fx} + \mathbf{Bu} \qquad (1)$$

$$\mathbf{P} := \mathbf{FPF}^T + \mathbf{Q} \qquad (2)$$

Those are linear algebra equations using matrix multiplication and addition. Assuming each variable is already defined somewhere, we could write:

```
x = dot(F,x) + dot(B,u)
P = F.dot(P).dot(F.T) + Q
```

That is all there is to it! Okay, we need to put these in a function or a class somehow, but that is the 'hard' code, which is actually pretty easy.

Now let's do the update step. Again, they consist of matrix multiplication and addition.

$$\mathbf{y} := \mathbf{z} - \mathbf{H}\mathbf{x}^- \tag{3}$$
$$\mathbf{S} := \mathbf{H}\mathbf{P}\mathbf{H}^T + \mathbf{R} \tag{4}$$
$$\mathbf{K} := \mathbf{P}\mathbf{H}^T\mathbf{S}^{-1} \tag{5}$$
$$\mathbf{x} := \mathbf{x}^- + \mathbf{K}\mathbf{y} \tag{6}$$
$$\mathbf{P} := (\mathbf{I} - \mathbf{K}\mathbf{H})\mathbf{P} \tag{7}$$

In Python we would write:

```
y = z - dot(H, x)
S = H.dot(P).dot(H.T) + R
K = P.dot(H.T).dot(np.linalg.inv(S))
x = x + dot(K,y)
P = (I - dot(K, H)).dot(P)
```

And that is it, we have implemented a Kalman filter!

Well, you probably do not want to cut and paste that code into every project that uses a Kalman filter. So let's put this into a class. I don't intend to teach you how to program here, so I will instead point you to my `KalmanFilter` class from my filterpy module, available on github [4]. However, I have written a simplified version of that class below for your inspection.

```
In [22]: import numpy as np
         import scipy.linalg as linalg
         import matplotlib.pyplot as plt
         import numpy.random as random
         from numpy import dot

         class KalmanFilter:

             def __init__(self, dim_x, dim_z, dim_u=0):
                 """ Create a Kalman filter. You are responsible for setting the
                 various state variables to reasonable values; the defaults below will
                 not give you a functional filter.

                 Parameters
                 ----------
                 dim_x : int
                     Number of state variables for the Kalman filter. For example, if
                     you are tracking the position and velocity of an object in two
                     dimensions, dim_x would be 4.

                     This is used to set the default size of P, Q, and u
```

```
        dim_z : int
            Number of of measurement inputs. For example, if the sensor
            provides you with position in (x,y), dim_z would be 2.

        dim_u : int (optional)
            size of the control input, if it is being used.
            Default value of 0 indicates it is not used.
        """

        self.x = np.zeros((dim_x,1)) # state
        self.P = np.eye(dim_x)       # uncertainty covariance
        self.Q = np.eye(dim_x)       # process uncertainty
        self.u = np.zeros((dim_x,1)) # motion vector
        self.B = 0                   # control transition matrix
        self.F = 0                   # state transition matrix
        self.H = 0                   # Measurement function
        self.R = np.eye(dim_z)       # state uncertainty

        # identity matrix. Do not alter this.
        self._I = np.eye(dim_x)

        if use_short_form:
            self.update = self.update_short_form


    def update(self, Z, R=None):
        """
        Add a new measurement (Z) to the kalman filter. If Z is None, nothing
        is changed.

        Parameters
        ----------
        Z : np.array
            measurement for this update.

        R : np.array, scalar, or None
            Optionally provide R to override the measurement noise for this
            one call, otherwise  self.R will be used.
        """

        if Z is None:
            return

        if R is None:
```

```
            R = self.R
        elif np.isscalar(R):
            R = np.eye(self.dim_z) * R

        # error (residual) between measurement and prediction
        y = Z - dot(H, x)

        # project system uncertainty into measurement space
        S = dot(H,P).dot(H.T) + R

        # map system uncertainty into kalman gain
        K = dot(P, H.T).dot(linalg.inv(S))

        # predict new x with residual scaled by the kalman gain
        self.x = self.x + dot(K, y)

        I_KH = self._I - dot (K, H)
        self.P = dot(I_KH).dot(P).dot(I_KH.T) + dot(K, R).dot(K.T)

    def predict(self, u=0):
        """ Predict next position.
        Parameters
        ----------
        u : np.array
            Optional control vector. If non-zero, it is multiplied by B
            to create the control input into the system.
        """

        self.x = np.dot(self.F, self.x) + np.dot(self.B, u)
        self.P = self.F.dot(self.P).dot(self.F.T) + self.Q
```

We will see how to use this class in the rest of the chapter, so I will not belabor its use here. There are several additions to the version in filterpy that make it more usable. For example, instead of using variables for the R, P, and so on, the `filterpy` version uses properties. This allows you to write something like:

```
dog_filter.R = 3
```

and the class will recognize that R is actually supposed to be a matrix and convert the 3 into an appropriate matrix (we don't yet know what an 'appropriate' matrix for $R = 3$ would be, but we will learn that soon).

You can import the class using the following Python:

```
In [23]: from filterpy.kalman import KalmanFilter
```

7.7 Tracking a Dog

Let's go back to our tried and true problem of tracking our dog. This time we will include the fundamental insight of this chapter - that of using *unobserved variables* to improve our estimates. In simple terms, our algorithm is:

```
1. predict the next value for x with "x + vel*time"
2. get measurement for x
3. compute residual as: "x - x_prediction"
4. compute kalman gain based on noise levels
5. compute new position as "residual * kalman gain"
```

That is the entire Kalman filter algorithm. It is both what we described above in words, and it is what the rather obscure Kalman Filter equations do. The Kalman filter equations just express this algorithm by using linear algebra.

As I mentioned above, there is actually very little programming involved in creating a Kalman filter. We will just be defining several matrices and parameters that get passed into the Kalman filter algorithm code. Rather than try to explain each of the steps ahead of time, which can be a bit abstract and hard to follow, let's just do it for our by now well known dog tracking problem. Naturally this one example will not cover every use case of the Kalman filter, but we will learn by starting with a simple problem and then slowly start addressing more complicated situations.

Step 1: Choose the State Variables and Set Initial Conditions In the previous chapter we tracked a dog in one dimension by using a Gaussian. The mean (μ) represented the most likely position, and the variance (σ^2) represented the probability distribution of the position. In that problem the position is the *state* of the system, and we call μ the *state variable*.

In this chapter we will be tracking both the position and velocity of the dog, so we have two state variables. State variables can either be *observed variables* - directly measured by a sensor, or *unobserved variables* - inferred from the observed variables. For our dog tracking problem, our observed state variable is position, and th unobserved variable is velocity.

In the previous chapter would denote the dog's position being 3.2 as:

$$\mu = 3.2$$

In this chapter we will use the multivariate Gaussian as described at the beginning of this chapter. For example, if we wanted to specify a position of 10.0 and a velocity of 4.5, we would write:

$$\mu = \begin{bmatrix} 10.0 \\ 4.5 \end{bmatrix}$$

The Kalman filter is implemented using linear algebra. We use an $n \times 1$ matrix to store n state variables. For the dog tracking problem, we use x to denote position, and the first derivative of x, $\dot{x}$, for velocity. The Kalman filter equations use $\mathbf{x}$ for the state, so we define $\mathbf{x}$ as:

$$\mathbf{x} = \begin{bmatrix} x \\ \dot{x} \end{bmatrix}$$

We use $\mathbf{x}$ instead of μ, but recognize this is just the mean of the multivariate Gaussian.

The other half of the Gaussian is the covariance Σ. The Kalman filter equations use the alternative symbol $\mathbf{P}$, but it means the same thing. In the one dimensional Kalman filter we specified an initial value for σ^2, and then the filter took care of updating it's value as measurements were added to the filter. The same thing happens in the multidimensional Kalman filter.

In the last chapter we initialized the dog's position at 0.0, and set the $\sigma^2 = 500$ to indicate that we were very unsure about this initial value. We need to do the same thing for the multidimensional Kalman filter. We will set the initial position to 0.0, the initial velocity to 0.0, and then set σ^2 to a 500 for both the position and velocity to reflect our uncertainty.

Recall that the diagonals of the covariance matrix contains the variance of each variable. So to initialize the Kalman filter to the values in the previous paragraph we would write:

$$\mathbf{x} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$
$$\mathbf{P} = \begin{bmatrix} 500 & 0 \\ 0 & 500 \end{bmatrix}$$

I am often frustrated when books use the same value for multiple variables in an example as it can be unclear which value corresponds to which variable. To ensure that there is no confusion let's look at the example of setting the initial position to 1, the initial velocity to 2.3, the σ^2 of the position to 500, and the σ^2 of the velocity to 400. In that case we would write:

$$\mathbf{x} = \begin{bmatrix} 1 \\ 2.3 \end{bmatrix}$$
$$\mathbf{P} = \begin{bmatrix} 500 & 0 \\ 0 & 400 \end{bmatrix}$$

We have chosen our state variables and set our initial conditions, so this step is complete.

Step 2: Design State Transition Function The next step in designing a Kalman filter is telling it how to predict the next state from the current state by providing it with equations that describe the physical model of the system. For example, for our dog tracking problem we are tracking a moving object, so we just need to provide it with the Newtonian equations for motion. If we were tracking a thrown ball we would have to provide equations for how a ball moves in a gravitational field, and perhaps include the effects of things like air drag. If we were writing a Kalman filter for a rocket we would have to tell it how the rocket responds to its thrusters and main engine. A Kalman filter for a bowling ball would incorporate the effects of friction and ball rotation. You get the idea.

In the language of Kalman filters the physical model is call the *process model*. That is probably a better term than *physical model* because the Kalman filter can be used to track

non-physical things like stock prices. We describe the process model with a set of equations we call the *State Transition Function.*

We know from elementary physics how to compute a future position given our current position and velocity. Let x be our current position, and Δt be the amount of time in the future, and x^- be our predicted position. The velocity is then the derivative of x, which we notate as $\dot{x}$. We can then write

$$x^- = \dot{x}\Delta t + x$$

Equation (1) of the Kalman filter $\mathbf{x}^- = \mathbf{Fx} + \mathbf{Bu}$ implements the *state transition function* that we are discussing. This requires us to formulate the motion equation above with matrices, so let's learn how to do that now. For the moment we will ignore the $\mathbf{Bu}$ term, as for our problem it turns out that it is equal to zero. Thus, we must express our equations in the form $\mathbf{x}^- = \mathbf{Fx}$.

A quick review on how to represent linear equations with matrices. Take the following two equations:

$$2x + 3y = 83x - y = 1$$

We can put this in matrix form by writing:

$$\begin{bmatrix}2 & 3\\ 3 & -1\end{bmatrix}\begin{bmatrix}x\\ y\end{bmatrix} = \begin{bmatrix}8\\ 1\end{bmatrix}$$

If you perform the matrix multiplication in this equation the result will be the two equations above.

So, given that $\mathbf{x} = \begin{bmatrix}x & \dot{x}\end{bmatrix}^T$ we can write:

$$\begin{aligned}\mathbf{x}^- &= \mathbf{Fx}\\ \begin{bmatrix}x\\ \dot{x}\end{bmatrix}^- &= \mathbf{F}\begin{bmatrix}x\\ \dot{x}\end{bmatrix}\end{aligned}$$

Since $\mathbf{x}$ is a 2×1 matrix $\mathbf{F}$ must be a 2×2 matrix to yield another 2×1 matrix as a result. The first row of the F is easy to derive:

$$\begin{bmatrix}x\\ \dot{x}\end{bmatrix}^- = \begin{bmatrix}1 & \Delta t\\ ? & ?\end{bmatrix} \times \begin{bmatrix}x\\ \dot{x}\end{bmatrix}$$

When we multiply the first row of $\mathbf{F}$ that out we get:

$$\begin{aligned}x^- &= 1x + \Delta t\dot{x}, \text{ or}\\ x^- &= \dot{x}\Delta t + x\end{aligned}$$

which is our equation for computing the new position based on velocity, time, and the previous position.

Now we have to account for the second row. I've let it somewhat unstated up to now, but we are assuming constant velocity for this problem. Naturally this assumption is not true; if our dog moves it must accelerate and decelerate. If you cast your mind back to the *g-h Filter* chapter we explored the effect of assuming constant velocity. So long as the acceleration is small compared to Δt the filter will still perform well.

Therefore we will assume that

$$\dot{x}^- = \dot{x}$$

which gives us the second row of $\mathbf{F}$ as follows, once we set $\Delta t = 1$:

$$\begin{bmatrix} x \\ \dot{x} \end{bmatrix}^- = \begin{bmatrix} 1 & 1 \\ 0 & 1 \end{bmatrix} \times \begin{bmatrix} x \\ \dot{x} \end{bmatrix}$$

Which, when multiplied out, yields our desired equations:

$$\begin{aligned} x^- &= x + \dot{x} \\ \dot{x}^- &= \dot{x} \end{aligned}$$

In the vocabulary of Kalman filters we call this *transforming the state matrix*. We take our state matrix, which for us is $\left(\begin{smallmatrix} x \\ \dot{x} \end{smallmatrix}\right)$, and multiply it by a matrix we will call $\mathbf{F}$ to compute the new state. In this case, $\mathbf{F} = \left(\begin{smallmatrix} 1 & 1 \\ 0 & 1 \end{smallmatrix}\right)$.

You will do this for every Kalman filter you ever design. Your state matrix will change depending on how many state random variables you have, and then you will create $\mathbf{F}$ so that it updates your state based on whatever the physics of your problem dictates. $\mathbf{F}$ is always a matrix of constants. Each row in $\mathbf{F}$ is If this is not fully clear, don't worry, we will do this many times in this book.

Step 3: Design the Motion Function The Kalman filter does not just filter data, it allows us to incorporate control inputs for systems like robots and airplanes. Consider the state transition function we wrote for the dog:

$$x_t = \dot{x}(\Delta t) + x_{t-1}$$

Suppose that instead of passively tracking our dog we were actively controlling a robot. At each time step we would send control signals to the robot based on our current position vs desired position. Kalman filter equations incorporate that knowledge into the filter equations, creating a predicted position based both on current velocity *and* control inputs to the drive motors.

We will cover this use case later, but for now passive tracking applications we set those terms to 0. In step 2 there was the unexplained term $\mathbf{Bu}$ in equation (1):

$$\hat{\mathbf{x}} = \mathbf{Fx} + \mathbf{Bu}$$

.

Here $\mathbf{u}$ is the control input, and $\mathbf{B}$ is its transfer function. For example, $\mathbf{u}$ might be a voltage controlling how fast the wheel's motor turns, and multiplying by $\mathbf{B}$ yields $\left(\begin{smallmatrix} x \\ \dot{x} \end{smallmatrix}\right)$. Since we do not need these terms we will set them both to zero and not concern ourselves with them for now.

Step 4: Design the Measurement Function The Kalman filter computes the update step in what we call *measurement space*. We mostly ignored this issue in the previous chapter because of the complication it adds. In the last chapter we tracked our dog's position using a sensor that reported his position. Computing the *residual* was easy - subtract the filter's predicted position from the measurement:

$$residual = measurement - position$$

However, consider what would happen if we were trying to track temperature using a thermometer that varies a voltage output depending on the temperature. The equation for the residual computation would be nonsense; you can't subtract a temperature from a voltage.

$$residual = z_{volts} - temp_C \quad (BAD!)$$

The Kalman filter generalizes this problem by having you supply a *measurement function*. It is somewhat counterintuitive at first. As I already stated the Kalman filter performs its calculations in *measurement space*. It needs to do that because it only really makes sense to talk about the residual of the measurement in terms of the measurement. So it does something like this:

```
residual = measurement - convert_to_measurement(predicted state)
```

In other words, for the thermometer tracking problem, it would take the filter's current prediction of temperature, convert that to whatever voltage would represent that temperature, and then subtract it from the current thermometer voltage output. This gives it a residual in the correct units (volts).

It does this with a *measurement function* matrix that you provide it. At first it might seem counterintuitive: to use the thermometer we need to know how to convert the output voltage into a temperature, but we tell the Kalman filter how to convert a temperature into a voltage!. But if you think about it, what you are really telling the filter is how your sensor works. Your sensor converts temperature into voltage, and you are just telling the Kalman filter how it does it. The Kalman filter equations can take that information and figure out how to perform the inverse operation without you explicitly telling it the computation.

The Kalman filter equation that performs this step is:

$$\mathbf{y} := \mathbf{z} - \mathbf{H}\mathbf{x}^- \quad (3)$$

where $\mathbf{y}$ is the residual, $\mathbf{x}^-$ is the predicted value for $\mathbf{x}$, $\mathbf{z}$ is the measurement, and $\mathbf{H}$ is the measurement function. It is just a matrix that we multiply the state into to convert it into a measurement.

For our dog tracking problem we have a sensor that measures position, but no sensor that measures velocity. So for a given state $\mathbf{x} = \begin{bmatrix} x & \dot{x} \end{bmatrix}^T$ we will want to multiply the position x by 1 to get the corresponding measurement of the position, and multiply the velocity $\dot{x}$ by 0 to get the corresponding measurement of velocity (of which there is none).

We only have 1 measurement in this example, so the dimension of the residual matrix needs to be 1×1. $\mathbf{x}$ is 2×1, so $\mathbf{H}$ needs to be 1×2 to get the right result. If we put this in linear algebra terms we get:

$$\begin{aligned}\mathbf{y} = \mathbf{z} - & \begin{bmatrix}1 & 0\end{bmatrix} \begin{bmatrix}x \\ \dot{x}\end{bmatrix}, or \\ \mathbf{y} = \mathbf{z} - & \quad \mathbf{H} \begin{bmatrix}x \\ \dot{x}\end{bmatrix}\end{aligned}$$

And so, for our Kalman filter we set

$$\mathbf{H} = \begin{bmatrix}1 & 0\end{bmatrix}$$

Believe it or not, we have designed the majority of our Kalman filter!! All that is left is to model the noise in our sensors.

Step 5: Design the Measurement Noise Matrix The *measurement noise* is a matrix that models the noise in our sensors as a covariance matrix. This can be admittedly a very difficult thing to do in practice. A complicated system may have many sensors, the correlation between them might not be clear, and usually their noise is not a pure Gaussian. For example, a sensor might be biased to read high if the temperature is high, and so the noise is not distributed equally on both sides of the mean. Later we will address this topic in detail. For now I just want you to get used to the idea of the measurement noise matrix so we will keep it deliberately simple.

In the last chapter we used a variance of 5 for our position sensor. Let's use the same value here. The Kalman filter equations uses the symbol R for this matrix.

$$R = 5$$

In general the matrix will have dimension $m \times m$, where m is the number of sensors. It is $m \times m$ because it is a covariance matrix, as there may be correlations between the sensors. We have only 1 sensor here so we write:

$$R = \begin{bmatrix}5\end{bmatrix}$$

Step 6: Design the Process Noise Matrix What is *process noise*? Consider the motion of a thrown ball. In a vacuum and with constant gravitational force it moves in a parabola. However, if you throw the ball on the surface of the earth you will also need to model factors like rotation and air drag. However, even when you have done all of that there is usually things you cannot account for. For example, consider wind. On a windy day the ball's trajectory will differ from the computed trajectory, perhaps by a significant amount. Without wind sensors, we may have no way to model the wind. The Kalman filter models this as *process noise*, and calls it $\mathbf{Q}$.

Astute readers will realize that we can inspect the ball's path and extract wind as an unobserved state variable, but the point to grasp here is there will always be some unmodeled noise in our process, and the Kalman filter gives us a way to model it.

Designing the process noise matrix can be quite demanding, and we will put it off until the Kalman math chapter. In this chapter we will focus on building an intuitive understanding on how modifying this matrix alters the behavior of the filter.

As you might expect, the Kalman filter uses the process noise matrix during the prediction step because the prediction step is the step that uses the process model to predict the next state. It is used in equation (2) from the Kalman filter equations:

$$\mathbf{P} = \mathbf{FPF}^T + \mathbf{Q}$$

If you look back at step one you will recall that $\mathbf{P}$ is the covariance matrix. It will be of size $n \times n$ where n is the number of state variables. $\mathbf{FPF}^T$ is just some linear algebra 'magic' that switches $\mathbf{P}$ into state space. We will cover this in detail in the Kalman math chapter; for now I will just say that when the Kalman filter performs the math for Step 4 above it needed to convert $\mathbf{P}$ into measurement space to compute the residual and Kalman gain, so here it it converted back into state space to perform the state prediction.

In pseudocode we might express this equation as:

```
P = to_state_space(P_in_measurement_space) + process_noise
```

This is the multidimensional linear algebra analogue of the predict step in the one dimensional case, where we added the variance of the filter to the variance of the movement:

```
sigma = sigma + movement_sigma
```

$\mathbf{P}$ is dimensioned $n \times n$, so $\mathbf{Q}$ must have the same dimensions. We are just adding matrices, so hopefully it is clear that each element in $\mathbf{Q}$ specifies how much uncertainty is added to the system due to the process noise. We have not given the math for this yet, but if you suspect the math is difficult you would be correct.

Fortunately you can get a long way with approximations. The filtered result will not be optimal, but in my opinion the promise of optimal results from Kalman filters is mostly wishful thinking. Consider, for example, tracking a car. In that problem the process noise would include things like potholes, wind gusts, changing drag due to turning, rolling down windows, and many more factors. We cannot realistically model that analytically, and so in practice we work out a simplified model, compute $\mathbf{Q}$ based on that simplified model, and then add *a bit* to $\mathbf{Q}$ in hopes of taking the uncalculable factors into account. Then we use a lot of simulations and trial runs to see if the filter behaves well; if it doesn't we adjust $\mathbf{Q}$ until the filter performs well. In this chapter we will focus on forming an intuitive understanding on how adjusting $\mathbf{Q}$ affects the output of the filter. In the Kalman Filter Math chapter we will discuss the analytic computation of $\mathbf{Q}$, and also provide code that will compute it automatically for you.

For our first example, we will set the diagonal of $\mathbf{Q}$ to a small value, and the off-diagonal terms to zero. This is typically not a particularly good choice for a real filter, but it is enough for us to begin forming an understanding of the performance of the filter for various values of $\mathbf{Q}$.

Some books and papers use **R** for measurement noise and **Q** for the process noise. Others do the opposite, using **Q** for measurement noise and **R** for the process noise! Read carefully, and make sure you don't get confused. I use the following mnemonic. Radars are used to measure positions, and they have measurement error. So, for me, **R** is the **R**adar's measurement noise. I've read a lot of Kalman filter literature in the context of radar tracking, so it makes sense to me. I don't have a good one for **Q**, other than to note that it alphabetically follows the p in **P**rocess.

7.8 Implementing the Kalman Filter

As we already explained, the Kalman filter equations are already implemented for you in the `filterpy` library, so let's start by importing it and creating a filter.

```
In [24]: import numpy as np
         from filterpy.kalman import KalmanFilter

         dog_filter = KalmanFilter (dim_x=2, dim_z=1)
```

That's it. We import the filter, and create a filter that uses 2 state variables. We specify the number of state variables with the 'dim=2' expression (dim means dimensions).

The Kalman filter class contains a number of variables that you need to set. x is the state, F is the state transition function, and so on. Rather than talk about it, let's just do it!

```
In [25]: dog_filter.x = np.array([[0], [0]])      # initial state (location and velocity
         dog_filter.F = np.array([[1,1], [0,1]]) # state transition matrix
         dog_filter.H = np.array([[1,0]])        # Measurement function
         dog_filter.R *= 5                       # measurement noise
         dog_filter.Q *= 0                       # process noise
         dog_filter.P *= 500.                    # covariance matrix
```

Let's look at this line by line.

1: We just assign the initial value for our state. Here we just initialize both the position and velocity to zero.

2: We set $\mathbf{F} = \begin{pmatrix} 1 & 1 \\ 0 & 1 \end{pmatrix}$, as in design step 2 above.

3: We set $\mathbf{H} = \begin{pmatrix} 1 & 0 \end{pmatrix}$, as in design step 3 above.

4: We set $\mathbf{R} = 5$ and $\mathbf{Q} = 0$ as in steps 5 and 6.

5: Recall in the last chapter we set our initial belief to $\mathcal{N}(\mu, \sigma^2) = \mathcal{N}(0, 500)$ to signify our lack of knowledge about the initial conditions. We implemented this in Python with a list that contained both μ and σ^2 in the variable *pos*:

```
pos = (0,500)
```

Multidimensional Kalman filters stores the state variables in $\mathbf{x}$ and their *covariance* in $\mathbf{P}$. These are `f.x` and `f.P` in the code above. Notionally, this is similar as the one dimension case, but instead of having a mean and variance we have a mean and covariance. For the multidimensional case, we have

$$\mathcal{N}(\mu, \sigma^2) = \mathcal{N}(\mathbf{x}, \mathbf{P})$$

$\mathbf{P}$ is initialized to the identity matrix of size $n \times n$, so multiplying by 500 assigns a variance of 500 to x and $\dot{x}$. So `f.P` contains

$$\begin{bmatrix} 500 & 0 \\ 0 & 500 \end{bmatrix}$$

This will become much clearer once we look at the covariance matrix in detail in later sessions. For now recognize that each diagonal element e_{ii} is the variance for the ith state variable, and that the *500* is just a statement that we are very uncertain about our initial value by some *amount*.

> Summary: For our dog tracking problem, in the 1-D case μ was the position, and σ^2 was the variance. In the 2-D case $\mathbf{x}$ is our position and velocity, and $\mathbf{P}$ is the *covariance* of the position and velocity. It is the same thing, just in higher dimensions!

All that is left is to run the code! The `DogSensor` class from the previous chapter has been placed in `DogSensor.py`.

```
In [26]: import numpy as np
         from DogSensor import DogSensor
         from filterpy.kalman import KalmanFilter

         def dog_tracking_filter(R,Q=0,cov=1.):
             dog_filter = KalmanFilter (dim_x=2, dim_z=1)
             dog_filter.x = np.array([[0],
                                      [0]])   # initial state (location and velocity)
             dog_filter.F = np.array([[1,1],
                                      [0,1]])  # state transition matrix
             dog_filter.H = np.array([[1,0]])  # Measurement function
             dog_filter.R *= R                 # measurement uncertainty
             dog_filter.P *= cov               # covariance matrix
             if np.isscalar(Q):
                 dog_filter.Q = np.array([[0,0],
                                          [0,Q]])
             else:
                 dog_filter.Q = Q
             return dog_filter
```

```
def filter_dog(noise=0, count=0, R=0, Q=0, P=500., data=None, initial_x=None):
    """ Kalman filter 'count' readings from the DogSensor.
    'noise' is the noise scaling factor for the DogSensor.
    'data' provides the measurements. If set, noise will
    be ignored and data will not be generated for you.

    returns a tuple of (positions, measurements, covariance)
    """
    if data is None:
        dog = DogSensor(velocity=1, noise=noise)
        zs = [dog.sense() for t in range(count)]
    else:
        zs = data

    dog_filter = dog_tracking_filter(R=R, Q=Q, cov=P)
    if initial_x is not None:
        dog_filter.x = initial_x

    pos = [None] * count
    cov = [None] * count

    for t in range(count):
        z = zs[t]
        pos[t] = dog_filter.x[0,0]
        cov[t] = dog_filter.P

        # perform the kalman filter steps
        dog_filter.update (z)
        dog_filter.predict()

    return (pos, zs, cov)
```

This is the complete code for the filter, and most of it is just boilerplate. The first function `dog_tracking_filter()` is a helper function that creates a `KalmanFilter` object with specified $\mathbf{R}$, $\mathbf{Q}$ and $\mathbf{P}$ matrices. We've shown this code already, so I will not discuss it more here.

The function `filter_dog()` implements the filter itself. Lets work through it line by line. The first line creates the simulation of the DogSensor, as we have seen in the previous chapter.

```
dog = DogSensor(velocity=1, noise=noise)
```

The next line uses our helper function to create a Kalman filter.

```
dog_filter = dog_tracking_filter(R=R, Q=Q, cov=500.)
```

We will want to plot the filtered position, the measurements, and the covariance, so we will need to store them in lists. The next three lines initialize empty lists of length *count* in a pythonic way.

```
pos = [None] * count
zs  = [None] * count
cov = [None] * count
```

Finally we get to the filter. All we need to do is perform the update and predict steps of the Kalman filter for each measurement. The `KalmanFilter` class provides the two functions `update()` and `predict()` for this purpose. `update()` performs the measurement update step of the Kalman filter, and so it takes a variable containing the sensor measurement.

Absent the bookkeeping work of storing the filter's data, the for loop reads:

```
for t in range (count):
    z = dog.sense()
    dog_filter.update (z)
    dog_filter.predict()
```

It really cannot get much simpler than that. As we tackle more complicated problems this code will remain largely the same; all of the work goes into setting up the `KalmanFilter` variables; executing the filter is trivial.

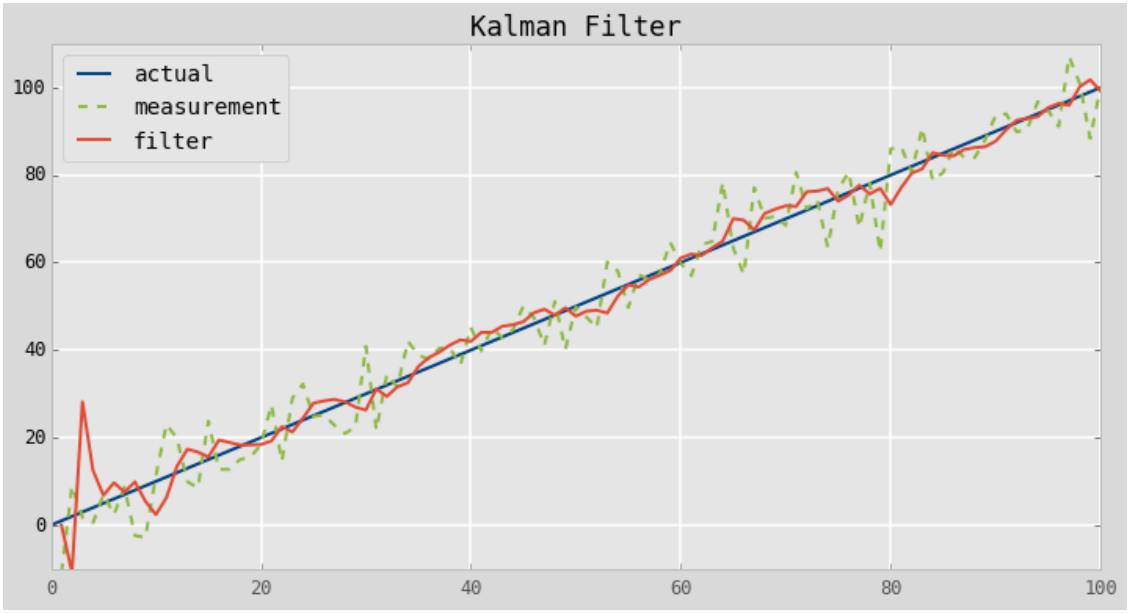
Now let's look at the result. Here is some code that calls `filter_track()` and then plots the result. It is fairly uninteresting code, so I will not walk through it.

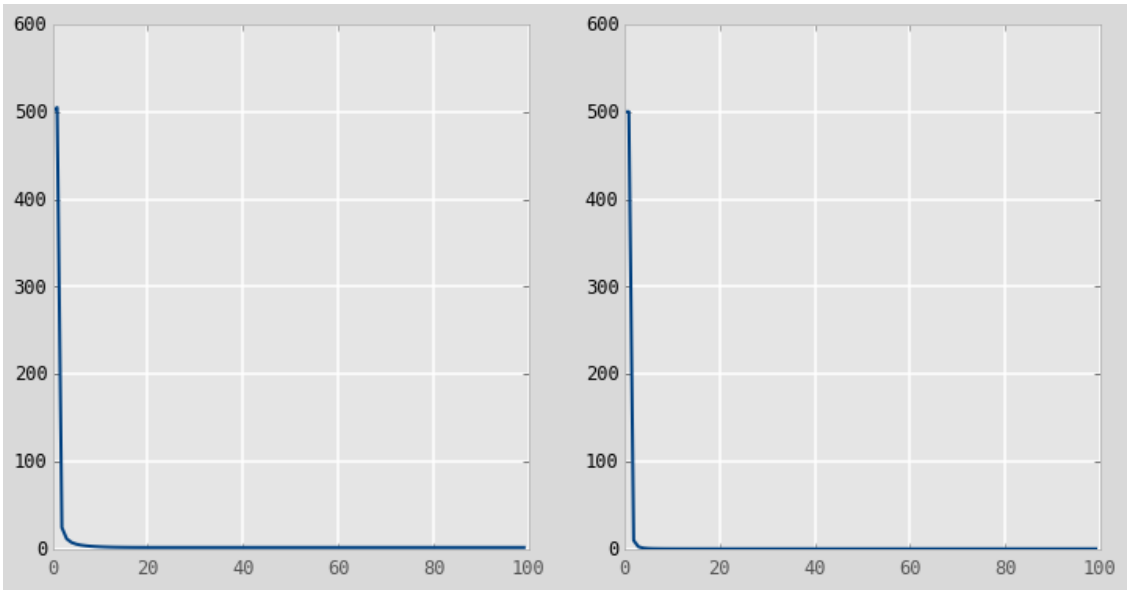
```
In [27]: def plot_track(noise=None, count=0, R=0, Q=0, P=500., initial_x=None,
                        data=None, plot_P=True, title='Kalman Filter'):

             ps, zs, cov = filter_dog(noise=noise, data=data, count=count,
                                      R=R, Q=Q, P=P, initial_x=initial_x)

             p0, = plt.plot([0,count],[0,count])
             p1, = plt.plot(range(1,count+1),zs, linestyle='dashed')
             p2, = plt.plot(range(1,count+1),ps)
             plt.legend([p0,p1,p2], ['actual','measurement', 'filter'], 2)
             plt.ylim((0-10,count+10))
             plt.title(title)
             plt.show()

             if plot_P:
                 plt.subplot(121)
                 plot_covariance(cov, (0,0))
                 plt.subplot(122)
                 plot_covariance(cov, (1,1))
                 plt.show()
```

```
def plot_covariance(P, index=(0,0)):
    ps = []
    for p in P:
        ps.append(p[index[0],index[1]])
    plt.plot(ps)
```

Finally, call it. We will start by filtering 100 measurements with a noise factor of 30, $\mathbf{R} = 5$ and $\mathbf{Q} = 0$.

```
In [28]: plot_track (noise=30, R=5, Q=0.01, count=100)
```





There is still a lot to learn, but we have implemented our first, full Kalman filter using the same theory and equations as published by Nobert Kalman! Code very much like this runs inside of your GPS and phone, inside every airliner, inside of robots, and so on.

The first plot plots the output of the Kalman filter against the measurements and the actual position of our dog (drawn in green). After the initial settling in period the filter should track the dog's position very closely.

The next two plots show the variance of x and of $\dot{x}$. If you look at the code, you will see that I have plotted the diagonals of $\mathbf{P}$ over time. Recall that the diagonal of a covariance matrix contains the variance of each state variable. So $\mathbf{P}[0,0]$ is the variance of x, and $\mathbf{P}[1,1]$ is the variance of $\dot{x}$. You can see that despite initializing $\mathbf{P} = \left(\begin{smallmatrix} 500 & 0 \\ 0 & 500 \end{smallmatrix}\right)$ we quickly converge to small variances for both the position and velocity. We will spend a lot of time on the covariance matrix later, so for now I will leave it at that.

In the previous chapter we filtered very noisy signals with much simpler code than the code above. However, realize that right now we are working with a very simple example - an object moving through 1-D space and one sensor. That is about the limit of what we can compute with the code in the last chapter. In contrast, we can implement very complicated, multidimensional filter with this code merely by altering are assignments to the filter's variables. Perhaps we want to track 100 dimensions in financial models. Or we have an aircraft with a GPS, INS, TACAN, radar altimeter, baro altimeter, and airspeed indicator, and we want to integrate all those sensors into a model that predicts position, velocity, and accelerations in 3D (which requires 9 state variables). We can do that with the code in this chapter.

7.9 Compare to Univariate Kalman Filter

The equations in this chapter look very different from the equations in the last chapter, yet I claimed the last chapter implemented a full 1-D (univariate) Kalman filter.

Recall that the univariate equations for the update step are:

$$\begin{aligned}\mu &= \frac{\sigma_1^2\mu_2 + \sigma_2^2\mu_1}{\sigma_1^2 + \sigma_2^2}, \\ \sigma^2 &= \frac{1}{\frac{1}{\sigma_1^2} + \frac{1}{\sigma_2^2}}\end{aligned}$$

and that the 1-D equations for the predict step are:

$$\begin{aligned}\mu &= \mu_1 + \mu_2, \\ \sigma^2 &= \sigma_1^2 + \sigma_2^2\end{aligned}$$

Let's implement a simple 1-D kalman filter using the Kalman filter from this chapter, and compare its output to the kalman filter from the previous chapter by plotting it. We will use a simple model of tracking an object that starts at x=0 and moves by 1 at each

step. We will assume the arbitrary value 5 for the measurement noise and .02 for the process noise.

First, let's implement the filter from the last chapter:

```
In [29]: from __future__ import division
         import numpy as np
         from numpy.random import randn
         from filterpy.kalman import KalmanFilter

         # 1-D Kalman filter equations
         def predict(pos, variance, movement, movement_variance):
             return (pos + movement, variance + movement_variance)


         def update (mu1, var1, mu2, var2):
             mean = (var1*mu2 + var2*mu1) / (var1+var2)
             variance = 1 / (1/var1 + 1/var2)
             return (mean, variance)
```

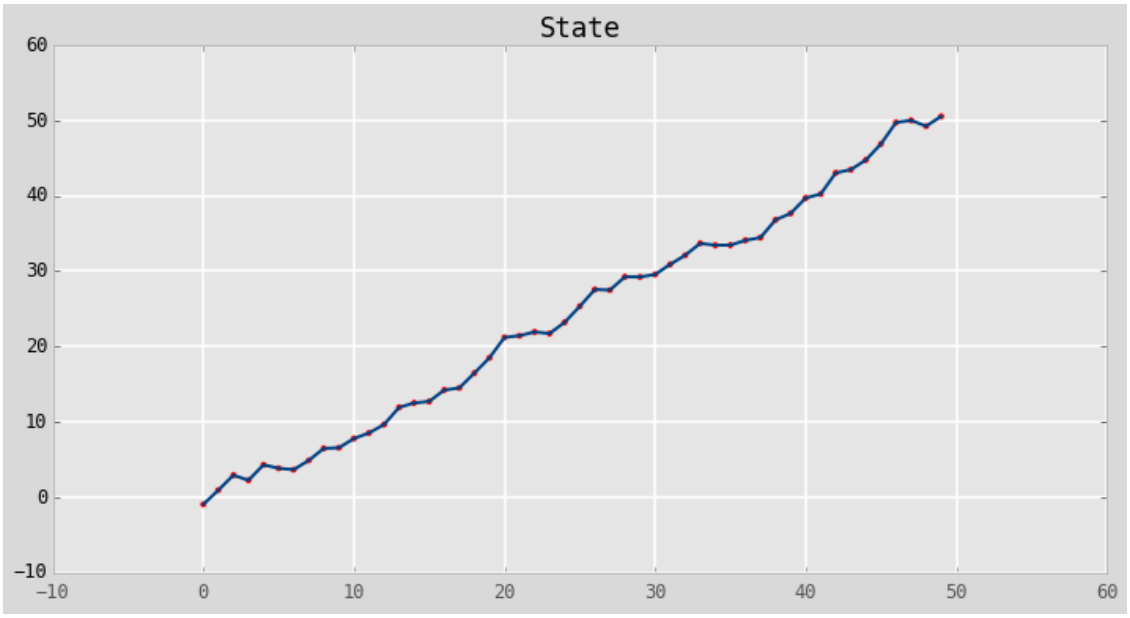
Now, let's implement the same thing using the kalman filter. I will implement it as a function that returns a KalmanFilter object so that you can run the analysis code several times with the KalmanFilter initialized to the same starting conditions each time.

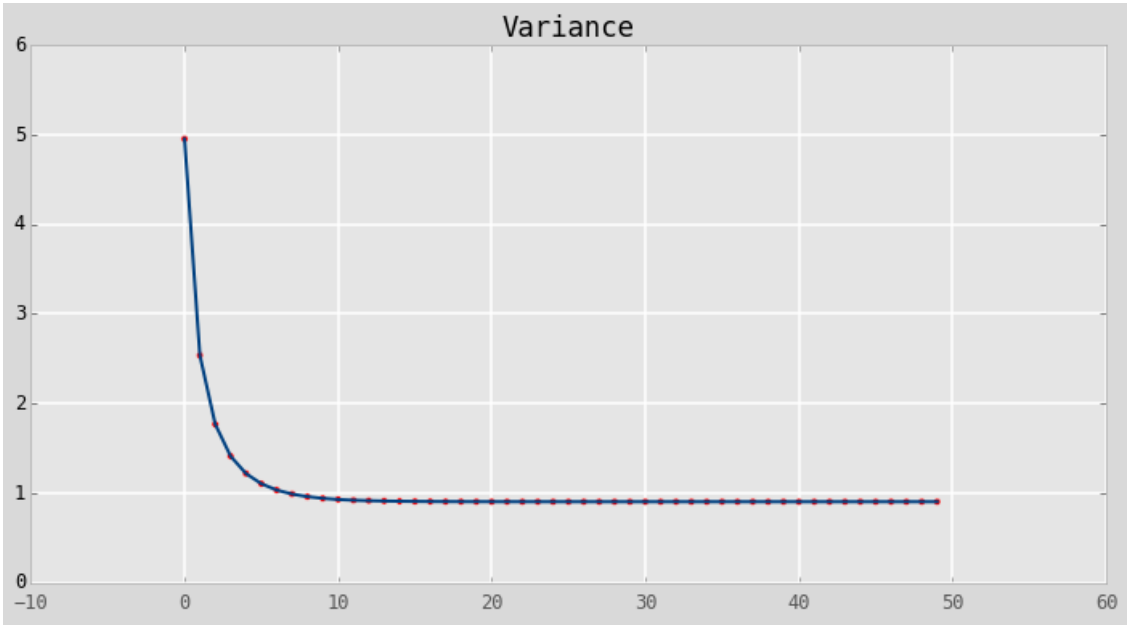
```
In [30]: from filterpy.kalman import KalmanFilter

         def mkf_filter(R, Q):
             f = KalmanFilter(dim_x=1, dim_z=1, dim_u=1)
             f.P = 500.
             f.H = np.array([[1.]])
             f.F = np.array([[1.]])
             f.B = np.array([[1.]])
             f.Q = Q
             f.R = R

             return f
```

Finally, let's compare the two. I will plot the data from the 1-D Kalman filter as a blue line, and the output of the filter from this chapter as red dots. I wrote it as a function so you can easily modify the parameters and regenerate the plots.

```
In [31]: def plot_kf_compare(x0, p0, R, Q, move):
             # storage for filter output
             x1 = []
             x2 = []

             p1 = []
```

```
    p2 = []

    # initialize the filters
    f = mkf_filter(R, Q)
    f.x[0,0] = 0.
    f.P[0,0] = p0
    pos = (x0, p0)
    for i in range(50):
        z = i*move + randn()
        pos = update(pos[0], pos[1], z, R)
        f.update(z)

        x1.append(pos[0])
        x2.append(f.x[0,0])

        p1.append(pos[1])
        p2.append(f.P[0,0])

        u = move + randn()
        pos = predict(pos[0], pos[1], u, Q)
        f.predict(u=u)

    plt.scatter(range(len(x2)), x2, c='r')
    plt.title('State')
    plt.plot(x1)
    plt.figure()
    plt.plot(p1)
    plt.scatter(range(len(x2)), p2, c='r')
    plt.title('Variance')
    plt.show()

plot_kf_compare(x0=0., p0=500., R=5., Q=.2, move=1.)
```





Discussion As you can see, both filters produce the same results. Feel free to vary the initial guess, the measurement noise, and the process noise; so long as you make the same changes to both filters the output should be the same. This is a solid demonstration, albeit not a rigorous proof, that both filters in fact implement the same math for the 1-D case.

7.10 Converting the Multivariate Equations to the Univariate Case

As it turns out the Kalman filter equations are quite easy to deal with in one dimension, so let's do the mathematical proof.

> **Important** This section will provide you with a strong intuition into what the Kalman filter equations are actually doing. I strong recommend reading this section carefully as it should make this material much easier to understand. It is not merely a proof of correctness that you would normally want to skip past!

Let'start with the predict step, which is slightly easier. Here are the multivariate equations.

$$\mathbf{x}^- := \mathbf{Fx} + \mathbf{Bu}$$
$$\mathbf{P} := \mathbf{FPF}^T + \mathbf{Q}$$

The state $mathbfx$ only has one variable, so it is a 1×1 matrix. Our motion $\mathbf{u}$ is also be a 1×1 matrix. Therefore, $\mathbf{F}$ and $\mathbf{B}$ must also be 1×1 matrices. That means that they are all scalars, and we can write

$$x = Fx + Bu$$

Here the variables are not bold, denoting that they are just variables.

Our state transition is simple - the next state is the same as this state, so $F = 1$. The same holds for the motion transition, so, $B = 1$. Thus we have

$$x = x + u$$

which is equivelant to the Gaussian equation from the last chapter

$$\mu = \mu_1 + \mu_2$$

Hopefully the general process is clear, so now I will go a bit faster on the rest. Our other equation for the predict step is

$$\mathbf{P} := \mathbf{FPF}^T + \mathbf{Q}$$

Again, since our state only has one variable $\mathbf{P}$ and $\mathbf{Q}$ must also be 1×1 matrix, which we can treat as scalars, yielding

$$P := FPF^T + Q$$

We already know $F = 1$. The transpose of a scalar is the scalar, so $F^T = 1$. This yields

$$P := P + Q$$

which is equivalent to the Gaussian equation of

$$\sigma^2 = \sigma_1^2 + \sigma_2^2$$

Here our our multivariate Kalman filter equations for the update step.

$$\begin{aligned}
\mathbf{y} &:= \mathbf{z} - \mathbf{Hx} \\
\mathbf{K} &:= \mathbf{PH}^T(\mathbf{HPH}^T + \mathbf{R})^{-1} \\
\mathbf{x} &:= \mathbf{x}^- + \mathbf{Ky} \\
\mathbf{P} &:= (\mathbf{I} - \mathbf{KH})\mathbf{P}
\end{aligned}$$

As above, all of the matrices become scalars. H defines how we convert from a position to a measurement. Both are positions, so there is no conversion, and thus $H = 1$. Let's substitute in our known values and convert to scalar in one step. One final thing you need to know - division is scalar's analogous operation for matrix inversion, so we will convert the matrix inversion to division.

$$\begin{aligned}
y &:= z - x \\
K &:= P/(P + R) \\
x &:= x + Ky \\
P &:= (1 - K)P
\end{aligned}$$

Before we continue with the proof, I want you to look at those equations to recognize what a simple concept these equations implement. The residual y is nothing more than the measurement minus the previous state. The gain K is scaled based on how certain we are about the last prediction vs how certain we are about the measurement. We choose a new state x based on the old value of x plus the scaled value of the residual. Finally, we update the uncertainty based on how certain we are about the measurement. Algorithmically this should sound exactly like what we did in the last chapter.

So let's finish off the algebra to prove that. It's straightforward, and not at all necessary for you to learn unless you are interested. Feel free to skim past if you like - it will not help you with Kalman filtering.

Recall that the univariate equations for the update step are:

$$\begin{aligned}
\mu &= \frac{\sigma_1^2\mu_2 + \sigma_2^2\mu_1}{\sigma_1^2 + \sigma_2^2}, \\
\sigma^2 &= \frac{1}{\frac{1}{\sigma_1^2} + \frac{1}{\sigma_2^2}}
\end{aligned}$$

Here we will say that μ_1 is the state x, and μ_2 is the measurement z. That is entirely arbitrary, we could have chosen the opposite assigment. Thus it follows that that σ_1^2 is the state uncertainty P, and σ_2^2 is the measurement noise R. Let's substitute those in.

$$\mu = \frac{Pz + Rx}{P + R}\sigma^2 = \frac{1}{\frac{1}{P} + \frac{1}{R}}$$

I will handle μ first. The corresponding equation in the multivariate case is

$$
\begin{aligned}
x &= x + Ky \\
&= x + \frac{P}{P+R}(z-x) \\
&= \frac{P+R}{P+R}x + \frac{Pz-Px}{P+R} \\
&= \frac{Px+Rx+Pz-Px}{P+R} \\
&= \frac{Pz+Rx}{P+R} \quad \blacksquare
\end{aligned}
$$

Now let's look at σ^2. The corresponding equation in the multivarate case is

$$
\begin{aligned}
P &= (1-K)P \\
&= (1 - \frac{P}{P+R})P \\
&= (\frac{P+R}{P+R} - \frac{P}{P+R})P \\
&= (\frac{P+R-P}{P+R})P \\
&= \frac{RP}{P+R} \\
&= \frac{1}{\frac{P+R}{RP}} \\
&= \frac{1}{\frac{R}{RP} + \frac{P}{RP}} \\
&= \frac{1}{\frac{1}{P} + \frac{1}{R}} \quad \blacksquare
\end{aligned}
$$

So we have proven that the multivariate equations are equivalent to the univariate equations when we only have one state variable. I'll close this section by recognizing one quibble - I hand waved my assertion that $H = 1$ and $F = 1$. In general we know this is not true. For example, a digital thermometer may provide measurement in volts, and we need to convert that to temperature, and we use H to do that conversion. I left that issue out of the last chapter to keep the explanation as simple and streamlined as possible. It is very straightforward to add that generalization to the equations of the last chapter, redo the algebra above, and still have the same results. In practice we do not use the equations in the last chapter to perform Kalman filtering due to the material in the next section which demonstrates how much better the Kalman filter performs when we include unobserved variables. So I prefer to leave the equations from the last chapter in their simplest form so that they economically represent our central ideas without any extra complications.

Exercise: Compare to a Filter That Incorporates Velocity The last example did not use one of the fundamental insights of this chapter, unobserved variables. In this example velocity would the the unobserved variable. Write a Kalman filter that uses the

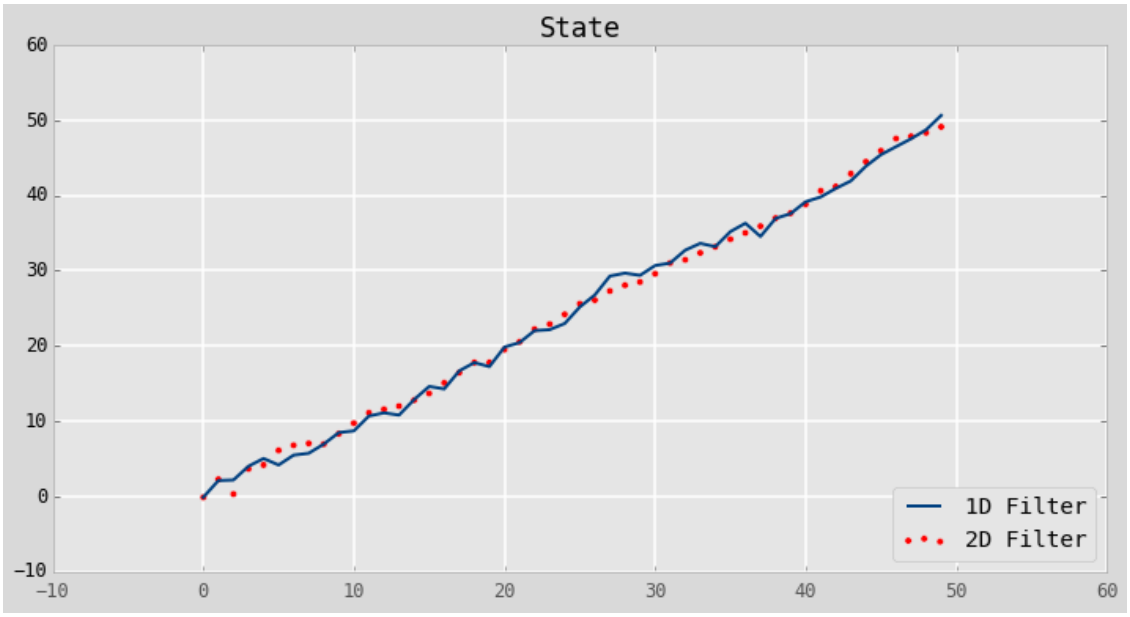
state $\mathbf{x} = \begin{bmatrix} x & \dot{x} \end{bmatrix}^T$ and compare it against the filter in the last exercise which used the state $\mathbf{x} = \begin{bmatrix} x \end{bmatrix}$.

```
In [32]: # your code here
```

Solution We've already implemented a Kalman filter for position and velocity, so I will provide the code without much comment, and then plot the result.

```
In [33]: def pos_vel_filter(R,Q):
             f = KalmanFilter(dim_x=2, dim_z=1)
             f.R = R
             f.Q = Q

             f.F = np.array([[1,1],
                             [0,1]])  # state transition matrix
             f.H = np.array([[1,0]])  # Measurement function
             return f

         def plot_compare_pos_vel(x0, p0, R, Q, move):
             # storage for filter output
             x1 = []
             x2 = []

             # initialize the filters
             f1 = mkf_filter(R, Q)
             f1.x[0,0] = 0.
             f1.P[0,0] = p0

             f2 = pos_vel_filter(R, Q)
             f2.x[0,0] = 0.
             f2.x[1,0] = 1.
             f2.P *= p0

             for i in range(50):
                 u = move + randn()
                 f1.predict(u=u)
                 f2.predict(u=u)

                 z = i*move + randn()
                 f1.update(z)
                 f2.update(z)

                 x1.append(f1.x[0,0])
                 x2.append(f2.x[0,0])
```

```
    plt.plot(x1, label='1D Filter')
    plt.scatter(range(len(x2)), x2, c='r', label='2D Filter')
    plt.title('State')
    plt.legend(loc=4)
    plt.show()

plot_compare_pos_vel(x0=0., p0=500., R=5., Q=.2, move=1.)
```



Discussion The output of the filter that incorporates velocity into the state produces much better output than the filter that only tracks position - the output is much closer to a straight line. We've already discussed why unobserved variables increase the precision of the filter, so I will not repeat that explanation here. But the last exercise and this one is intended to trigger a train of thought:

1. The equations in this chapter are mathematically equivalient to the equations in the last chapter when we are only tracking one state variable.

2. Therefore, the simple Bayesian reasoning we used in the last chapter applies to this chapter as well.

3. Therefore, the equations in this chapter might 'look ugly', but they really are just implementing multiplying and addition of Gaussians.

   The above might not seem worth emphasizing, but as we continue in the book the mathematical demands will increase significantly. It is easy to get lost in a thicket of linear algebra equations when you read a book or paper on optimal

estimation. Any time you start getting lost, just go back to the basics of the predict/update cycle based on residuals between measurements and predictions and the meaning of the math will usually be much clearer. The math *looks* daunting, and can sometimes be very hard to solve analytically, but the concepts are quite simple.

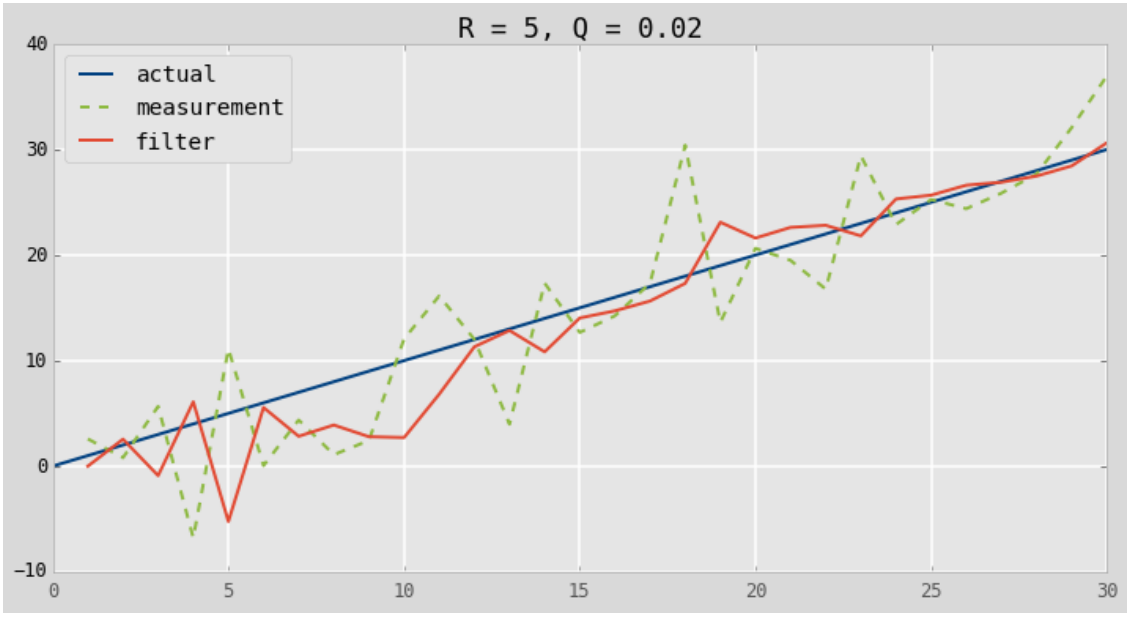
7.11 Adjusting the Filter

Your results will vary slightly depending on what numbers your random generator creates for the noise component of the noise, but the filter in the last section should track the actual position quite well. Typically as the filter starts up the first several predictions are quite bad, and varies a lot. But as the filter builds its state the estimates become much better.

Let's start varying our parameters to see the effect of various changes. This is a *very normal* thing to be doing with Kalman filters. It is difficult, and often impossible to exactly model our sensors. An imperfect model means imperfect output from our filter. Engineers spend a lot of time tuning Kalman filters so that they perform well with real world sensors. We will spend time now to learn the effect of these changes. As you learn the effect of each change you will develop an intuition for how to design a Kalman filter. As I wrote earlier, designing a Kalman filter is as much art as science. The science is, roughly, designing the $\mathbf{H}$ and $\mathbf{F}$ matrices - they develop in an obvious manner based on the physics of the system we are modeling. The art comes in modeling the sensors and selecting appropriate values for the rest of our variables.

Let's look at the effects of the noise parameters $\mathbf{R}$ and $\mathbf{Q}$. I will only run the filter for twenty steps to ensure we can see see the difference between the measurements and filter output. I will start by holding $\mathbf{R}$ to 5 and vary $\mathbf{Q}$.

```
In [34]: dog = DogSensor(velocity=1, noise=30)
         zs = [dog.sense() for t in range(30)]

         plot_track (data=zs, R=5, Q=10,count=30, plot_P=False, title='R = 5, Q = 10')
         plot_track (data=zs, R=5, Q=.02,count=30, plot_P=False, title='R = 5, Q = 0.02'
```



The filter in the first plot should follow the noisy measurement almost exactly. In the second plot the filter should vary from the measurement quite a bit, and be much closer to a straight line than in the first graph.

In the Kalman filter $\mathbf{R}$ is the *measurement noise* and $\mathbf{Q}$ is the *process uncertainty*. $\mathbf{R}$ is the same in both plots, so ignore it for the moment. Why does $\mathbf{Q}$ affect the plots this way?

Let's remind ourselves of what the term *process uncertainty* means. Consider the problem of tracking a ball. We can accurately model its behavior in static air with math, but if there is any wind our model will diverge from reality.

In the first case we set $\mathbf{Q} = 10$, which is quite large. In physical terms this is telling the filter "I don't trust my motion prediction step". Strictly speaking, we are telling the filter there is a lot of external noise that we are not modeling with $\mathbf{F}$, but the upshot of that is to not trust the motion prediction step. So the filter will be computing velocity ($\dot{x}$), but then mostly ignoring it because we are telling the filter that the computation is extremely suspect. Therefore the filter has nothing to use but the measurements, and thus it follows the measurements closely.

In the second case we set $\mathbf{Q} = 0.02$, which is quite small. In physical terms we are telling the filter "trust the motion computation, it is really good!". Again, more strictly this actually says there is very small amounts of process noise, so the motion computation will be accurate. So the filter ends up ignoring some of the measurement as it jumps up and down, because the variation in the measurement does not match our trustworthy velocity prediction.

AUTHOR'S NOTE: move covariance matrix coverage here, then do R, then Q. Order as below is confusing.

7.11.1 Designing Q

But what does "quite large" and "quite small" mean, and what should $\mathbf{Q}$ contain? The numbers in the $\mathbf{Q}$ matrix are not arbitrary, but the variances of the process noise. This means that they have the same units as the rest of the system. So, suppose the noise of our sensor has a standard deviation of $0.5m$, and the rest of our system is specified in meters as well. Variance is the standard deviation squared, so if $\sigma = 0.5$, then $\sigma^2 = 0.25$.

If we have m state variables then $\mathbf{Q}$ will be an $m \times m$ matrix. $\mathbf{Q}$ is a covariance matrix for the state variables, so it will contain the variances and covariances for the process noise for each state variable.

Let's make this concrete. Assume our state variables are $x = \begin{bmatrix} x & \dot{x} \end{bmatrix}^T$. (**note**: it is customary to use this transpose form of writing an matrix in text. It is how we denote that x is a column matrix without taking up a lot of line space). Then $\mathbf{Q}$ will contain:

$$Q = \begin{bmatrix} \sigma_x^2 & \sigma_{x\dot{x}} \\ \sigma_{\dot{x}x} & \sigma_{\dot{x}}^2 \end{bmatrix}$$

But again, what does this *mean*? This is a one dimensional problem, where our variables are x and $\dot{x}$. Assume we are tracking a person walking in 1D, so x is their position, and $\dot{x}$ is their velocity. We have no state variable for $\ddot{x}$, so we are assuming acelleration is zero, and thus their velocity is constant. No one walks with constant velocity, even if they are trying to do so. The *process noise* specifies how much variance there is in each state variable due to the changes in velocity that inevitably happen.

You will very typically see Q expressed in this form (indeed, this is what the code immediately above does):

$$\begin{bmatrix} 0 & 0 \\ 0 & 0.1 \end{bmatrix}$$

Why all zeros but in the last row and column. This is a useful approximation that we can use for **Q** under certain circumstances. Think about the person. As they accelerate, that will also alter their velocity, and eventually their position. But if the acceleration is small compared to our time sample rate, then the changes to distance will small. This follows from the Newtonian equations:

$$v = a\Delta t$$
$$d = \frac{a}{2}\Delta t^2$$

If t is small and a is small than the contribution of $\frac{a}{2}\Delta t^2$ will be extremely small. In this case it is safe to set all of the terms in **Q** to 0 except the variance for the last term.

On the other hand, let's suppose this is not the case. How should Q be designed? Our design of the system is:

$$X_{n+1} = \Phi X_n + U_n$$

where ΦX_n is our state transition, which computes $\mathbf{x}$ at time $n+1$ using Newtonian equations, and U_n is the white noise associated with the process. For a walking human, based on the equations above we get

$$U_n = \begin{bmatrix} \frac{a\Delta t^2}{2} \\ \Delta t \end{bmatrix}$$

So white noise has the variance U_n and a mean of 0, which we notate as $w \sim \mathcal{N}(0, Q)$.

Finding an analytic value for **Q** in a simple problem like this is not difficult, but it quickly becomes difficult to impossible as the number of state variables increase. So in this chapter we will use the simplification that only the variance of the last term is important. In the Kalman filter math chapter we will discuss finding an analytic solution for **Q**, and then present C. F. van Loan's extremely useful numerical technique for finding **Q**, which is what you will typically use in practice.

author's note: text needs to move to kalman math chapter. leaving here for now

7.11.2 Designing R

Now let's leave **Q** = 0.1, but bump **R** up to 1000. This is telling the filter that the measurement noise is very large.

```
In [35]: plot_track (data=zs, R=1000, Q=0.1,count=30, plot_P=False, title='R = 1000, Q =
```

The filter output should be much closer to the green line, especially after 10-20 cycles. If you are running this in Ipython Notebook, I strongly urge you to run this many times in a row (click inside the code box, and press CTRL-Enter). Most times the filter tracks almost exactly with the actual position, randomly going slightly above and below the green line, but sometimes it stays well over or under the green line for a long time. What is happening in the latter case?

The filter is strongly preferring the motion update to the measurement, so if the prediction is off it takes a lot of measurements to correct it. It will eventually correct because the velocity is a hidden variable - it is computed from the measurements, but it will take awhile.

To some extent you can get similar looking output by varying either $\mathbf{R}$ or $\mathbf{Q}$, but I urge you to not 'magically' alter these until you get output that you like. Always think about the physical implications of these assignments, and vary $\mathbf{R}$ and/or $\mathbf{Q}$ based on your knowledge of the system you are filtering.

7.12 A Detailed Examination of the Covariance Matrix

So far I have not given a lot of coverage of the covariance matrix. $\mathbf{P}$, the covariance matrix is nothing more than the variance of our state - such as the position of our dog. It has many elements in it, but don't be daunted; we will learn how to interpret a very large 9×9 covariance matrix, or even larger.

Recall the beginning of the chapter, where we provided the equation for the covariance matrix. It read:

$$\mathbf{P} = \begin{pmatrix} \sigma_1^2 & \sigma_{12} & \cdots & \sigma_{1n} \\ \sigma_{21} & \sigma_2^2 & \cdots & \sigma_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ \sigma_{n1} & \sigma_{n2} & \cdots & \sigma_n^2 \end{pmatrix}$$

(I have substituted $\mathbf{P}$ for Σ because of the nomenclature used by the Kalman filter literature).

The diagonal contains the variance of each of our state variables. So, if our state variables are

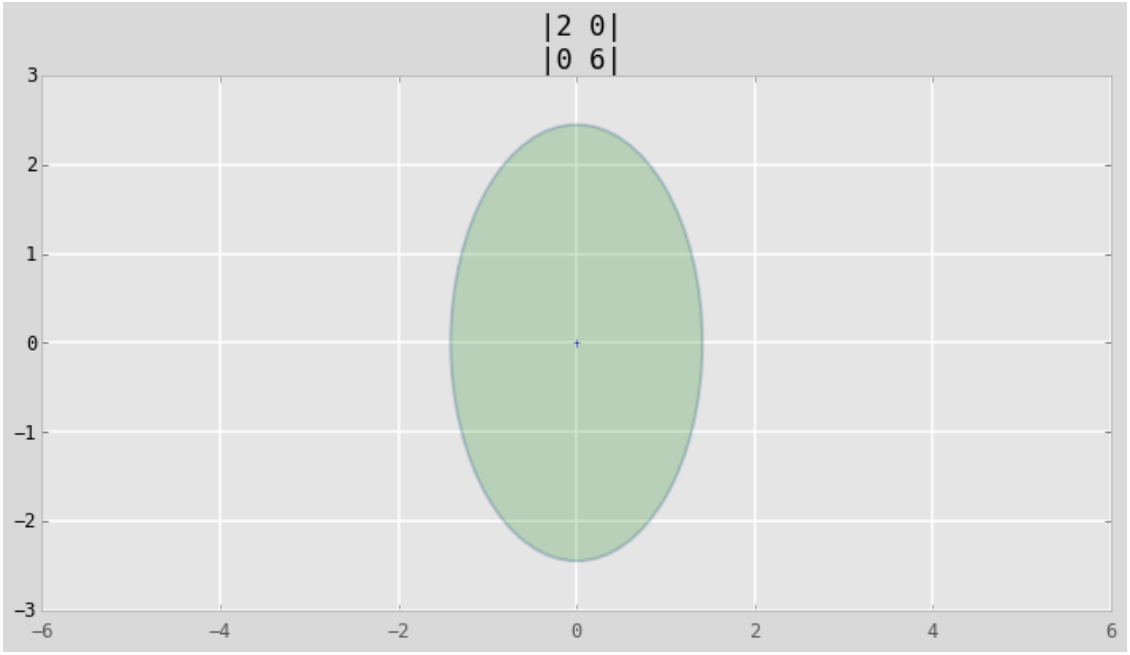
$$\mathbf{x} = \begin{pmatrix} x \\ \dot{x} \end{pmatrix}$$

and the covariance matrix happens to be

$$\mathbf{P} = \begin{pmatrix} 2 & 0 \\ 0 & 6 \end{pmatrix}$$

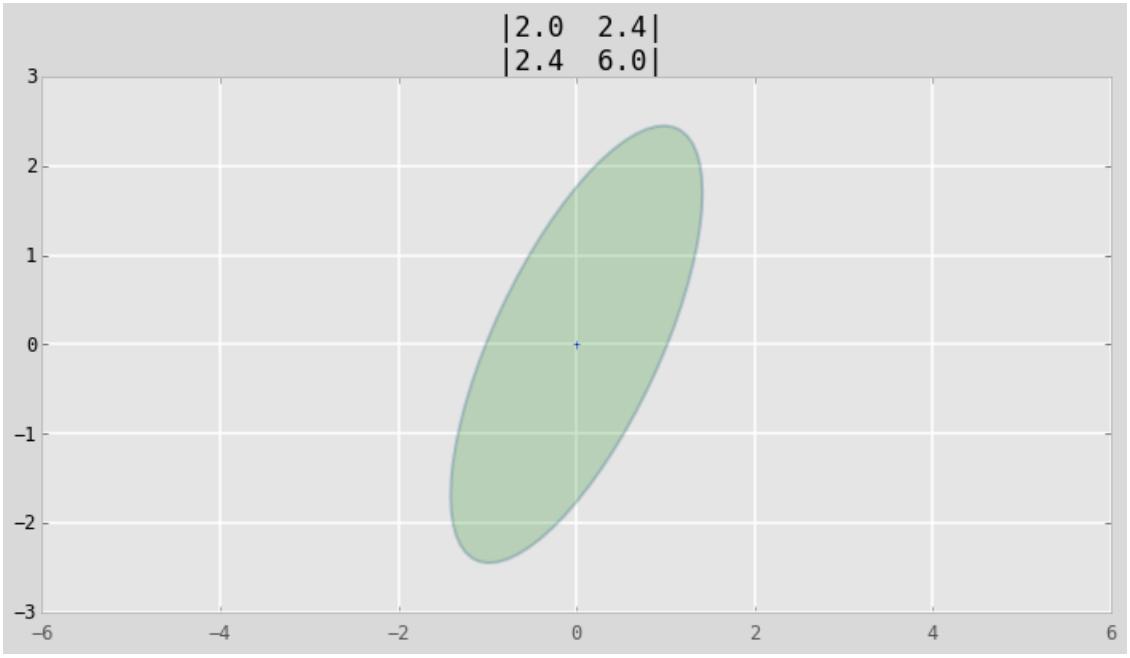
we know that the variance of x is 2, and the variance of $\dot{x}$ is 6. The off diagonal elements are all 0, so we also know that x and $\dot{x}$ are not correlated. Recall the ellipses that we drew of the covariance matrices. Let's look at the ellipse for the matrix.

```
In [36]: P = np.array([[2,0],[0,6]])
         stats.plot_covariance_ellipse ((0,0), P,  facecolor='g', alpha=0.2,
                                        title='|2 0|\n|0 6|')
```



Of course it is unlikely that the position and velocity of an object remain uncorrelated for long. Let's look at a more typical covariance matrix

```
In [37]: P = np.array([[2,2.4],[2.4,6]])
         stats.plot_covariance_ellipse ((0,0), P,  facecolor='g', alpha=0.2,
                                        title ='|2.0  2.4|\n|2.4  6.0|')
```



Here the ellipse is slanted, signifying that x and $\dot{x}$ are correlated (and, of course, dependent - all correlated variables are dependent). You may or may not have noticed that the off diagonal elements were set to the same value, 2.4. This was not an accident. Let's look at the equation for the covariance for the case where the number of dimensions is two.

$$\mathbf{P} = \begin{pmatrix} \sigma_1^2 & p\sigma_1\sigma_2 \\ p\sigma_2\sigma_1 & \sigma_2^2 \end{pmatrix}$$

Look at the computation for the off diagonal elements.

$$\mathbf{P}_{0,1} = p\sigma_1\sigma_2$$
$$\mathbf{P}_{1,0} = p\sigma_2\sigma_1.$$

If we re-arrange terms we get

$$\mathbf{P}_{0,1} = p\sigma_1\sigma_2$$
$$\mathbf{P}_{1,0} = p\sigma_1\sigma_1, \text{ yielding}$$
$$\mathbf{P}_{0,1} = P_{1,0}$$

In general, we can state that $\mathbf{P}_{i,j} = \mathbf{P}_{j,i}$.

So for my example I multiplied the diagonals, 2 and 6, to get 12, and then scaled that with the arbitrarily chosen $p = .2$ to get 2.4.

Let's get back to concrete terms. Let's start by revisiting plotting a track. I will hard code the data and noise to avoid being at the mercy of the random number generator, which might generate data that does not illustrate what I want to talk about. I will start by using the same parameters as a chart above: `R=5`, `Q=.02`, and `P=500`.

```
In [38]: # guarantee the noise is the same each time so I can be sure of
         # what the graphs look like.
         zs = [-6.947, 12.467, 6.899, 2.643, 6.980, 5.820, 5.788, 10.614, 5.210,
               14.338, 11.401, 19.138, 14.169, 19.572, 25.471, 13.099, 27.090,
               12.209, 14.274, 21.302, 14.678, 28.655, 15.914, 28.506, 23.181,
               18.981, 28.197, 39.412, 27.640, 31.465, 34.903, 28.420, 33.889,
               46.123, 31.355, 30.473, 49.861, 41.310, 42.526, 38.183, 41.383,
               41.919, 52.372, 42.048, 48.522, 44.681, 32.989, 37.288, 49.141,
               54.235, 62.974, 61.742, 54.863, 52.831, 61.122, 61.187, 58.441,
               47.769, 56.855, 53.693, 61.534, 70.665, 60.355, 65.095, 63.386]

         plot_track (data=zs, R=5, Q=.02, P=500., count=len(zs), plot_P=False, title='P=
```

Looking at the output we see a very large spike in the filter output at the beginning. If you look at the data (dotted red line) you will see a corresponding, smaller spike in the beginning of the data. We set `P=500`, which corresponds to $\mathrm{P} = \left[\begin{smallmatrix} 500 & 0 \\ 0 & 500 \end{smallmatrix}\right]$. We now have enough information to understand what this means, and how the Kalman filter treats it. The 500 in the upper left hand corner corresponds to σ_x^2; therefore we are saying the standard deviation of `x` is $\sqrt{500}$, or roughly 22.36 meters, assuming our measurements are in meters. If we recall how standard deviations work, roughly 99% of the samples occur withing 3σ, therefore `P=500` is telling the Kalman filter that the initial estimate could be up to 67 meters

off. That is a pretty large error, so when the measurement spikes the Kalman filter distrusts its own estimate and jumps wildly to try to incorporate the measurement. Then, as the filter evolves $\mathbf{P}$ quickly converges to a more realistic value.

Now let us see the effect of a smaller initial value for `P`.

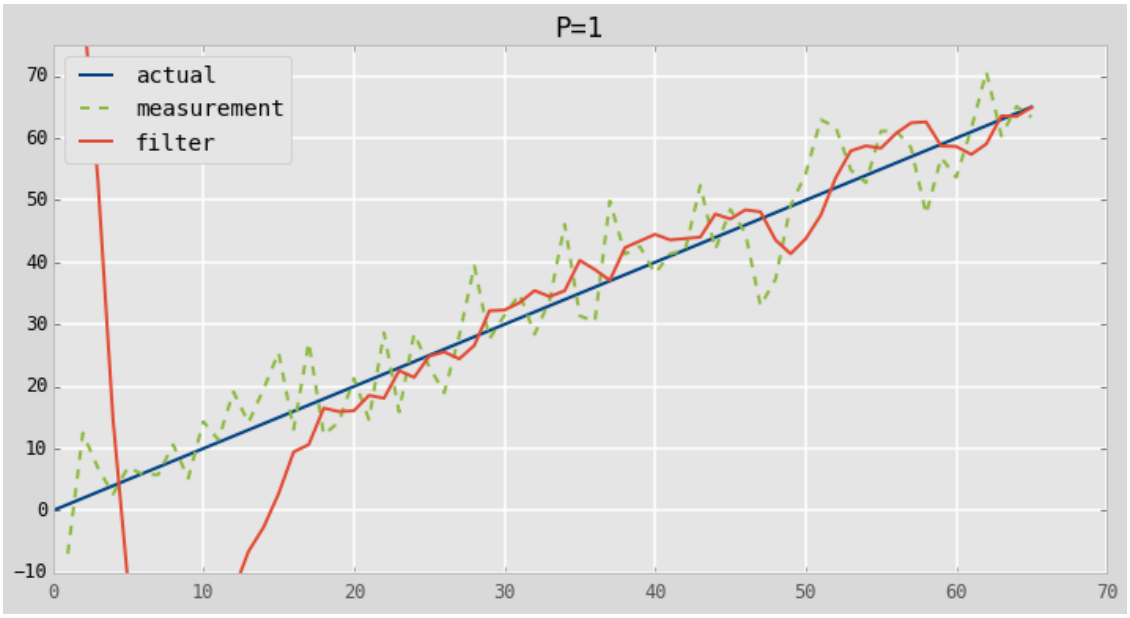
```
In [39]: plot_track (data=zs, R=5, Q=.02, P=1., count=len(zs), plot_P=False, title='P=1'
```

This plot does not have the spike that the former plot did; the filter starts tracking the measurements and doesn't take any time to 'settle' to the signal.

Do not conclude from this that the 'magic' is to just use a small P. Yes, this will avoid having the Kalman filter take time to accurately track the signal, but if we are truly uncertain about the initial measurements this can cause the filter to generate very bad results. If we are tracking a living object we are probably very uncertain about where it is before we start tracking it. On the other hand, if we are filtering the output of a thermometer, we are just as certain about the first measurement as the 1000th. For your Kalman filter to perform well you must set P to a value that truly reflects your knowledge about the data.

Let's see the result of a bad initial estimate coupled with a very small P We will set our initial estimate at 100m (whereas the dog starts at 0m), but set P=1.

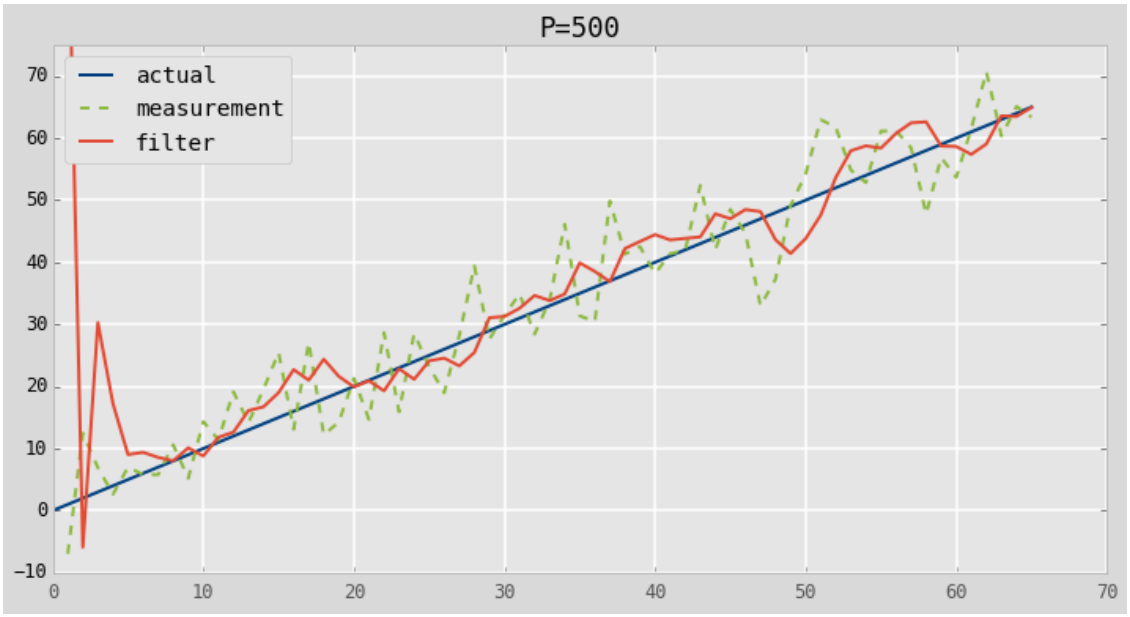
```
In [40]: x = np.array([[100,0]]).T
         plot_track(data=zs, R=5, Q=.02, P=1., initial_x=x,count=len(zs),
                    plot_P=False, title='P=1')
```



We can see that the initial estimates are terrible, up to around step 15 to 20. This is because we told the Kalman filter that we strongly believe in our initial estimate of 100m.

Now, let's provide a more reasonable value for P and see the difference.

```
In [41]: x = np.array([[100,0]]).T
         plot_track(data=zs, R=5, Q=.02, P=500., initial_x=x,count=len(zs),
                    plot_P=False, title='P=500')
```



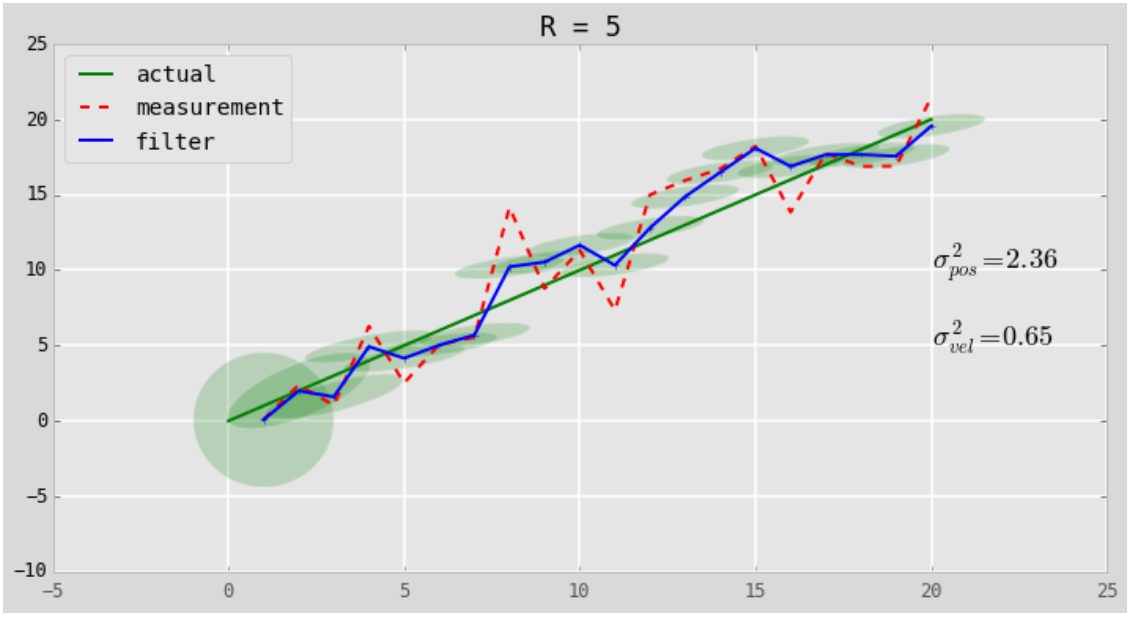
In this case the Kalman filter is very uncertain about the initial state, so it converges onto the signal much faster. It is producing good output after only 5 to 6 evolutions. With the theory we have developed so far this is about as good as we can do. However, this scenario is a bit artificial; if we do not know where the object is when we start tracking we do not initialize the filter to some arbitrary value, such as 0 or 100. Instead, we would normally take the first measurement, use that to initialize the Kalman filter, and proceed from there. But this is an engineering decision. You really need to understand the domain in which you are working and initialize your filter on the best available information. For example, suppose we were trying to track horses in a horse race. The initial measurements might be very bad, and provide you with a position far from the starting gate. We know that the horse must of started at the starting gate; initializing the filter to the initial measurement would lead to suboptimal results. In this scenario we would want to always initialize the Kalman filter with the starting gate position.

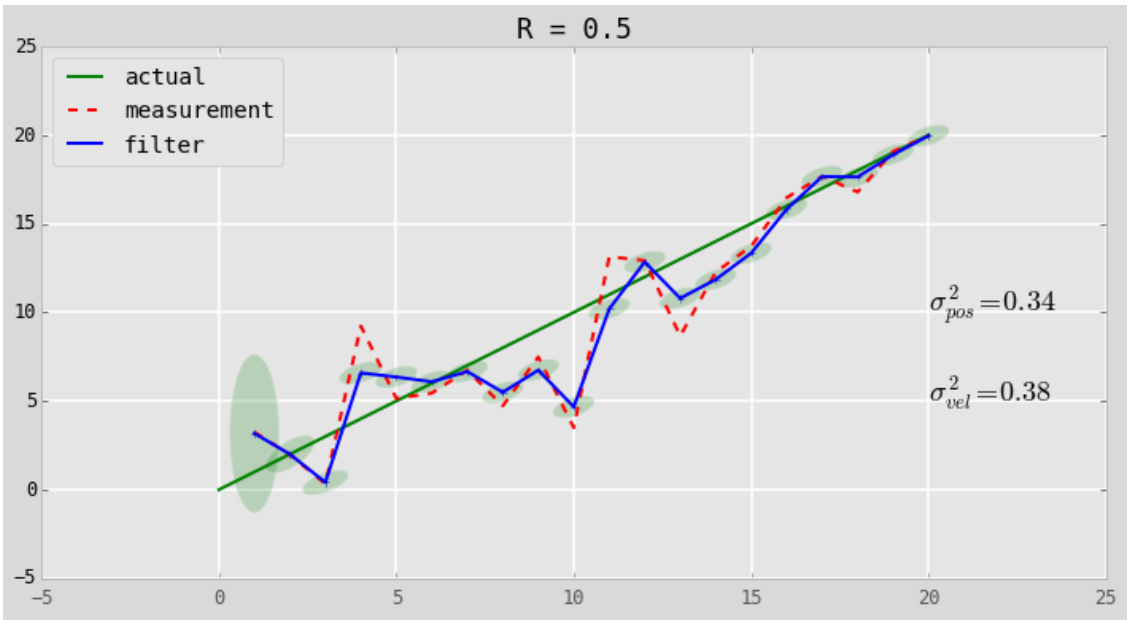
If we have the luxury of not needing to perform the filtering in real time, as the data comes in, we can take advantage of other techniques. We can 'eyeball' the data and see that the initial measurements are giving us reasonable values for the dog's position because we can see all of the data at once. A `fixed lag smoother` will look N steps ahead before computing the state, and other filters will do things like first run forwards, than backwards over the data. This will be the subject of later chapters. It is worthwhile to keep in mind that whenever possible we should prefer this sort of batch processing because it takes advantage of all available information. It does incur cost of additional processing time and increased storage due to the requirement to store some or all of the measurements. And, of course, batch processing does not work if we need real time results, such as when using GPS in our car.

Lets do another Kalman filter for our dog, and this time plot the covariance ellipses on the same plot as the position.

```
In [42]: def plot_track_ellipses(noise, count, R, Q=0, P=20., plot_P=True, title='Kalman
             dog = DogSensor(velocity=1, noise=noise)
             f = dog_tracking_filter(R=R, Q=Q, cov=P)

             ps = []
             zs = []
             cov = []
             for t in range (count):
                 z = dog.sense()
                 f.update (z)
                 ps.append (f.x[0,0])
                 cov.append(f.P)
                 zs.append(z)
                 f.predict()

             p0, = plt.plot([0,count],[0,count],'g', label='actual')
             p1, = plt.plot(range(1,count+1),zs,c='r', linestyle='dashed', label='measur
             p2, = plt.plot(range(1,count+1),ps, c='b', label='filter')
```

```
    plt.legend(loc='best')
    plt.title(title)

    for i,p in enumerate(cov):
        stats.plot_covariance_ellipse ((i+1, ps[i]), cov=p, axis_equal=False,
                                       facecolor='g', edgecolor=None, alpha=0.2

        if i == len(cov)-1:
            s = ('$\sigma^2_{pos} = %.2f$' % p[0,0])
            plt.text (20,10,s,fontsize=18)
            s = ('$\sigma^2_{vel} = %.2f$' % p[1,1])
            plt.text (20,5,s,fontsize=18)
    #plt.xlim((-10,30))
    #plt.ylim((-10,40))
    plt.show()


plot_track_ellipses (noise=5, R=5, Q=.2, count=20, title='R = 5')
plot_track_ellipses (noise=5, R=.5, Q=.2, count=20, title='R = 0.5')
```





The output on these is a bit messy, but you should be able to see what is happening. In both plots we are drawing the covariance matrix for each point. We start with the covariance $\mathbf{P} = \begin{pmatrix} 50 & 0 \\ 0 & 50 \end{pmatrix}$, which signifies a lot of uncertainty about our initial belief. After we receive the first measurement the Kalman filter updates this belief, and so the variance is no longer as large. In the top plot the first ellipse (the one on the far left) should be a slightly squashed ellipse. As the filter continues processing the measurements the covariance ellipse quickly shifts shape until it settles down to being a long, narrow ellipse tilted in the direction of movement.

Think about what this means physically. The x-axis of the ellipse denotes our uncertainty in position, and the y-axis our uncertainty in velocity. So, an ellipse that is taller than it is wide signifies that we are more uncertain about the velocity than the position. Conversely, a wide, narrow ellipse shows high uncertainty in position and low uncertainty in velocity. Finally, the amount of tilt shows the amount of correlation between the two variables.

The first plot, with $\mathbf{R} = 5$, finishes up with an ellipse that is wider than it is tall. If that is not clear I have printed out the variances for the last ellipse in the lower right hand corner. The variance for position is 3.85, and the variance for velocity is 3.0.

In contrast, the second plot, with $\mathbf{R} = 0.5$, has a final ellipse that is taller than wide. The ellipses in the second plot are all much smaller than the ellipses in the first plot. This stands to reason because a small $\mathbf{R}$ implies a small amount of noise in our measurements. Small noise means accurate predictions, and thus a strong belief in our position.

7.13 Question: Explain Ellipse Differences

Why are the ellipses for $\mathbf{R} = 5$ shorter, and more tilted than the ellipses for $\mathbf{R} = 0.5$. Hint: think about this in the context of what these ellipses mean physically, not in terms of the

math. If you aren't sure about the answer,change **R** to truly large and small numbers such as 100 and 0.1, observe the changes, and think about what this means.

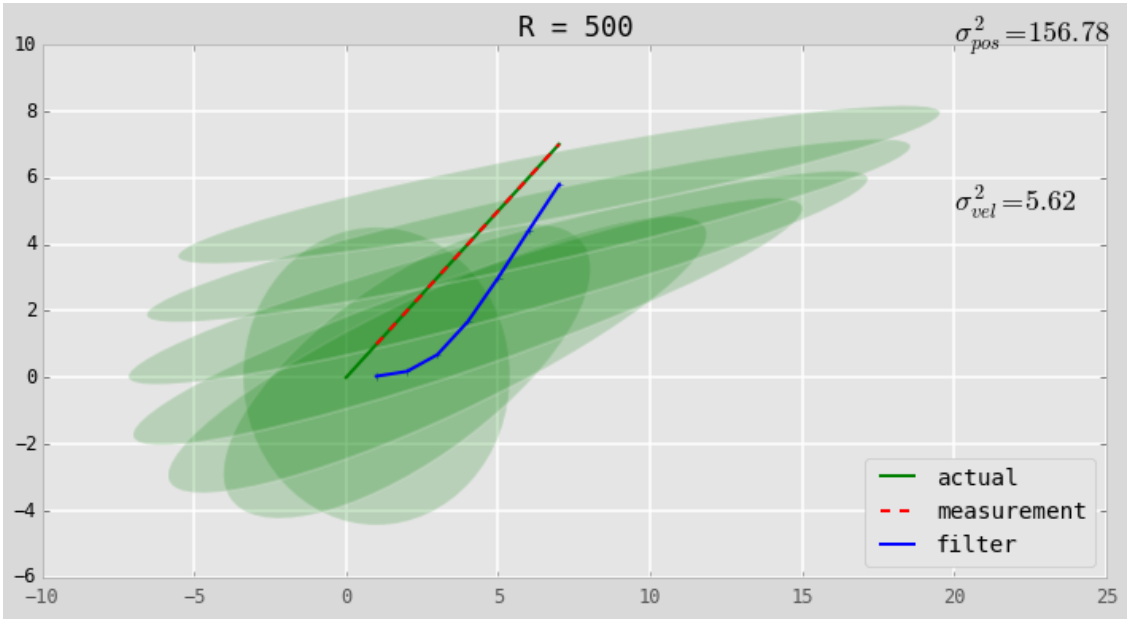
7.13.1 Solution

The x axis is for position, and y is velocity. An ellipse that is vertical, or nearly so, says there is no correlation between position and velocity, and an ellipse that is diagonal says that there is a lot of correlation. Phrased that way, it sounds unlikely - either they are correlated or not. But this is a measure of the *output of the filter*, not a description of the actual, physical world. When **R** is very large we are telling the filter that there is a lot of noise in the measurements. In that case the Kalman gain **K** is set to favor the prediction over the measurement, and the prediction comes from the velocity state variable. So, there is a large correlation between x and $\dot{x}$. Conversely, if **R** is small, we are telling the filter that the measurement is very trustworthy, and **K** is set to favor the measurement over the prediction. Why would the filter want to use the prediction if the measurement is nearly perfect? If the filter is not using much from the prediction there will be very little correlation reported.

This is a critical point to understand!. The Kalman filter is just a mathematical model for a real world system. A report of little correlation *does not mean* there is no correlation in the physical system, just that there was no *linear* correlation in the mathematical model. It's just a report of how much measurement vs prediction was incorporated into the model.

Let's bring that point home with a truly large measurement error. We will set $\mathbf{R} = 500$. Think about what the plot will look like before scrolling down. To emphasize the issue, I will set the amount of noise injected into the measurements to 0, so the measurement will exactly equal the actual position.

```
In [43]: plot_track_ellipses (noise=0, R=500, Q=.2, count=7, title='R = 500')
```



I hope the result was what you were expecting. The ellipse quickly became very wide and not very tall. It did this because the Kalman filter mostly used the prediction vs the measurement to produce the filtered result. We can also see how the filter output is slow to acquire the track. The Kalman filter assumes that the measurements are extremely noisy, and so it is very slow to update its estimate for $\dot{x}$.

Keep looking at these plots until you grasp how to interpret the covariance matrix $\mathbf{P}$. When you start dealing with a, say, 9×9 matrix it may seem overwhelming - there are 81 numbers to interpret. Just break it down - the diagonal contains the variance for each state variable, and all off diagonal elements are the product of two variances and a scaling factor p. You will not be able to plot a 9×9 matrix on the screen because it would require living in 10-D space, so you have to develop your intution and understanding in this simple, 2-D case.

> **sidebar**: when plotting covariance ellipses, make sure to always use *plt.axis('equal')* in your code. If the axis use different scales the ellipses will be drawn distorted. For example, the ellipse may be drawn as being taller than it is wide, but it may actually be wider than tall.

7.14 Walking Through the KalmanFilter Code (Optional)

** author's note: this code is somewhat old. This section needs to be edited **

The kalman filter code that we are using is implemented in my Python library `filterpy`. If you are interested in the full implementation of the filter you should look in `filterpy\kalman\kalman_filter.py`. In the following I will present a simplified implementation of the same code. The code in the library handles issues that are beyond the scope of this chapter, such as numerical stability and support for the extended Kalman filter, subject of a later chapter.

The code is implemented as the class `KalmanFilter`. Some Python programmers are not a fan of object oriented (OO) Python, and eschew classes. I do not intend to enter into that battle other than to say that I have often seen OO abused. Here I use the class to encapsulate the data that is pertinent to the filter so that you do not have to store and pass around a half dozen variables everywhere.

The method `__init__()` is used by Python to create the object. Here is the method

```
def __init__(self, dim_x, dim_z):
    """ Create a Kalman filter. You are responsible for setting the
    various state variables to reasonable values; the defaults below will
    not give you a functional filter.

    Parameters
    ----------
```

```
    dim_x : int
        Number of state variables for the Kalman filter. For example, if
        you are tracking the position and velocity of an object in two
        dimensions, dim_x would be 4.

        This is used to set the default size of P, Q, and u

    dim_z : int
        Number of of measurement inputs. For example, if the sensor
        provides you with position in (x,y), dim_z would be 2.
    """

    self.dim_x = dim_x
    self.dim_z = dim_z

    self.x = np.zeros((dim_x,1)) # state
    self.P = np.eye(dim_x)       # uncertainty covariance
    self.Q = np.eye(dim_x)       # process uncertainty
    self.u = 0                   # control input vector
    self.B = np.zeros((dim_x,1))
    self.F = 0                   # state transition matrix
    self.H = 0                   # Measurement function
    self.R = np.eye(dim_z)       # state uncertainty

    # identity matrix. Do not alter this.
    self._I = np.eye(dim_x)
```

More than anything this method exists to document for you what the variable names are in the filter. To do anything useful with this filter you will have to modify most of these values. Some are set to useful values. For example, `R` is set to an identity matrix; if you want the diagonals of `R` to be 10. you may write (as we did earlier in this chapter) `my_filter.R += 10.`.

The names used for each variable matches the math symbology used in this chapter. Thus, `self.P` is the covariance matrix, `self.x` is the state, and so on.

The predict function implements the predict step of the Kalman equations, which are

$$\hat{\mathbf{x}} = \mathbf{Fx} + \mathbf{Bu}$$
$$\mathbf{P} = \mathbf{FPF}^T + \mathbf{Q}$$

The corresponding code is

```
def predict(self):
    self.x = self.F.dot(self.x) + self.B.dot(self.u)
    self.P = self.F.dot(self.P).dot(self.F.T) + self.Q
```

I haven't discussed the use of numpy much until now, but this method illustrates the power of that package. We use numpy's `array` class to store our data and perform the linear

algebra for our filters. `array` implements matrix multiplication using the `.dot()` method; if you use `*` you will get element-wise multiplication. As a heavy user of linear algebra this design is somewhat distressing as I use matrix multiplication far more often than element-wise multiplication. However, this design is due to historical developments in the library and we must live with it. The Python community has recognized this problem, and in Python 3.5 we will have the `@` operator to implement matrix multiplication.

With that in mind, the Python code `self.F.dot(self.x)` implements the math expression $\mathbf{Fx}$.

Numpy's `array` implements matrix transposition by using the `.T` property. Therefore, `F.T` is the python implementation of $\mathbf{F}^T$.

The `update()` method implements the update equations of the Kalman filter, which are

$$\begin{aligned}
\tilde{\mathbf{y}} &= \mathbf{z} - \mathbf{H}\hat{\mathbf{x}} \\
\mathbf{K} &= \mathbf{P}\mathbf{H}^T(\mathbf{H}\mathbf{P}\mathbf{H}^T + \mathbf{R})^{-1} \\
\hat{\mathbf{x}} &= \hat{\mathbf{x}} + \mathbf{K}\tilde{\mathbf{y}} \\
\mathbf{P} &= (\mathbf{I} - \mathbf{K}\mathbf{H})\mathbf{P}
\end{aligned}$$

The corresponding code is:

```
def update(self, Z, R=None):
    """
    Add a new measurement (Z) to the kalman filter. If Z is None, nothing
    is changed.

    Optionally provide R to override the measurement noise for this
    one call, otherwise  self.R will be used.

    self.residual, self.S, and self.K are stored in case you want to
    inspect these variables. Strictly speaking they are not part of the
    output of the Kalman filter, however, it is often useful to know
    what these values are in various scenarios.
    """

    if Z is None:
        return

    if R is None:
        R = self.R
    elif np.isscalar(R):
        R = np.eye(self.dim_z) * R

    # error (residual) between measurement and prediction
    self.residual = Z - self.H.dot(self.x)

    # project system uncertainty into measurement space
```

```
    self.S = self.H.dot(self.P).dot(self.H.T) + R

    # map system uncertainty into kalman gain
    self.K = self.P.dot(self.H.T).dot(linalg.inv(self.S))

    # predict new x with residual scaled by the kalman gain
    self.x = self.x + self.K.dot(self.residual)

    KH = self.K.dot(self.H)
    I_KH = self._I - KH
    self.P = (I_KH.dot(self.P.dot(I_KH.T)) +
              self.K.dot(self.R.dot(self.K.T)))
```

There are a few more complications in this piece of code compared to `predict()` but it should still be quite clear.

The first complication are the lines:

```
    if Z is None:
        return
```

This just lets you deal with missing data in a natural way. It is typical to use `None` to indicate the absence of data. If there is no data for an update we skip the update equations. This bit of code means you can write something like:

```
z = read_sensor()    # may return None if no data
my_kf.update(z)
```

instead of: z = read_sensor() if z is not None: my_kf.update(z)

Reasonable people will argue whether my choice is cleaner, or obscures the fact that we do not update if the measurement is `None`. Having written a lot of avionics code my proclivity is always to do the safe thing. If we pass 'None' into the function I do not want an exception to occur; instead, I want the reasonable thing to happen, which is to just return without doing anything. If you feel that my choice obscures that fact, go ahead and write the explicit `if` statement prior to calling `update()` and get the best of both worlds.

The next bit of code lets you optionally pass in a value to override `R`. It is common for the sensor noise to vary over time; if it does you can pass in the value as the optional parameter `R`.

```
    if R is None:
        R = self.R
    elif np.isscalar(R):
        R = np.eye(self.dim_z) * R
```

This code will use self.R if you do not provide a value for `R`. If you did provide a value, it will check if you provided a scalar (number); if so it constructs a matrix of the correct dimension for you. Otherwise it assumes that you passed in a matrix of the correct dimension.

The rest of the code implements the Kalman filter equations, with one exception. Instead of implementing

$$\mathbf{P} = (\mathbf{I} - \mathbf{KH})\mathbf{P}$$

it implements the somewhat more complicated form

$$\mathbf{P} = (\mathbf{I} - \mathbf{KH})\mathbf{P}(\mathbf{I} - \mathbf{KRK})^T + \mathbf{KRK}^T$$

.

The reason for this altered equation is that it is more numerically stable than the former equation, at the cost of being a bit more expensive to compute. It is not always possible to find the optimal value for K, in which case the former equation will not produce good results because it assumes optimality. The longer reformulation used in the code is derived from more general math that does not assume optimality, and hence provides good results for non-optimal filters (such as when we can not correctly model our measurement error).

Various texts differ as to whether this form of the equation should always be used, or only used when you know you need it. I choose to expend a bit more processing power to ensure stability; if your hardware is very constrained and you are able to prove that the simpler equation is correct for your problem then you might choose to use it instead. Personally, I find that a risky approach and do not recommend it to non-experts. Brown's *Introduction to Random Signals and Applied Kalman Filtering* [3] discusses this issue in some detail, if you are interested.

7.15 References

- [1] http://docs.scipy.org/doc/scipy/reference/tutorial/stats.htmly
- [2] https://en.wikipedia.org/wiki/Kalman_filter
- [3] Brown, Robert Grover. *Introduction to Random Signals and Applied Kalman Filtering* John Wiley & Sons, Inc. 2012
- [4] `filterpy` library. Roger Labbe. https://github.com/rlabbe/filterpy

Chapter 8

Kalman Filter Math

If you've gotten this far I hope that you are thinking that the Kalman filter's fearsome reputation is somewhat undeserved. Sure, I hand waved some equations away, but I hope implementation has been fairly straightforward for you. The underlying concept is quite straightforward - take two measurements, or a measurement and a prediction, and choose the output to be somewhere between the two. If you believe the measurement more your guess will be closer to the measurement, and if you believe the prediction is more accurate your guess will lie closer it it. That's not rocket science (little joke - it is exactly this math that got Apollo to the moon and back!).

Well, to be honest I have been choosing my problems carefully. For any arbitrary problem finding some of the matrices that we need to feed into the Kalman filter equations can be quite difficult. I haven't been *too tricky*, though. Equations like Newton's equations of motion can be trivially computed for Kalman filter applications, and they make up the bulk of the kind of problems that we want to solve. If you are a hobbyist, you can safely pass by this chapter for now, and perhaps forever. Some of the later chapters will assume the material in this chapter, but much of the work will still be accessible to you.

But, I urge everyone to at least read the first section, and to skim the rest. It is not much harder than what you have done - the difficulty comes in finding closed form expressions for specific problems, not understanding the math in this chapter.

8.1 Modeling a Linear System that Has Noise

We need to start by understanding the underlying equations and assumptions that the Kalman filter uses. We are trying to model real world phenomena, so what do we have to consider?

First, each physical system has a process. For example, a car traveling at a certain velocity goes so far in a fixed amount of time, and it's velocity varies as a function of it's acceleration. We describe that behavior with the well known Newtonian equations we learned in high school.

$$v = at$$
$$d = \frac{1}{2}at_2 + v_0t + d_0$$

But, of course we know this is not all that is happening. First, we do not have perfect measures of things like the velocity and acceleration - there is always noise in the measurements, and we have to model that. Second, no car travels on a perfect road. There are bumps that cause the car to slow down, there is wind drag, there are hills that raise and lower the speed. If we do not have explicit knowledge of these factors we lump them all together under the term "process noise".

Trying to model off of those factors explicitly and exactly is impossible for anything but the most trivial problem. I could try to modify Newton's equations for things like bumps in the road, the behavior of the car's suspension system, heck, the effects of hitting bugs with the windshield, but the job would never be done - there would always be more effects to add. What is worse, each of those models would in themselves be a simplification - do I assume the wind is constant, that the drag of the car is the same for all angles of the wind, that the suspension act as perfect springs, and so on?

So control theory makes a mathematically correct simplification. We acknowledge that there are many factors that influence the system that we either do not know or that we don't want to have to model. At any time t we say that the actual value (say, the position of our car) is the predicted value plus some unknown process noise:

$$x(t) = x_{pred}(t) + noise(t)$$

This is not meant to imply that $noise(t)$ is a function that we can derive analytically or that it is well behaved. If there is a bump in the road at $t = 10$ then the noise factor will just incorporate that effect. Again, this is not implying that we model, compute, or even know the value of *noise(t)*, it is merely a statement of fact - we can *always* describe the actual value as the predicted value plus some other value.

Let's express this in linear algebra. Using the same notation from previous chapters, we can say that our model of the system (without noise) is:

$$f(x) = Fx$$

That is, we have a set of linear equations that describe our system. For our car, F will be the coefficients for Newton's equations of motion.

Now we need to model the noise. We will just call that w, and add it to the equation.

$$f(x) = Fx + w$$

Finally, we need to consider inputs into the system. We are dealing with linear problems here, so we will assume that there is some input u into the system, and that we have some linear model that defines how that input changes the system. For example, if you press down on the accelerator in your car the car will accelerate. We will need a matrix G to convert u into the effect on the system. We just add that into our equation:

$$f(x) = Fx + Gu + w$$

And that's it. That is the equation that Kalman set out to solve, and he found a way to compute an optimal solution if we assume certain properties of w.

8.2 Walking Through the Kalman Filter Equations

I promised that you would not have to understand how to derive Kalman filter equations, and that is true. However, I do think it is worth walking through the equations one by one and becoming familiar with the variables. If this is your first time through the material feel free to skip ahead to the next section. However, you will eventually want to work through this material, so why not now? You will need to have passing familiarity with these equations to read material written about the Kalman filter, as they all presuppose that you are familiar with the equations. I will reiterate them here for easy reference.

Predict Step

$$\mathbf{x}' = \mathbf{Fx} + \mathbf{Gu} \tag{1}$$

$$\mathbf{P} = \mathbf{FPF}^T + \mathbf{Q} \tag{2}$$

Update Step

$$\gamma = \mathbf{z} - \mathbf{Hx} \tag{3}$$

$$\mathbf{K} = \mathbf{PH}^T(\mathbf{HPH}^T + \mathbf{R})^{-1} \tag{4}$$

$$\mathbf{x} = \mathbf{x}' + \mathbf{K}\gamma \tag{5}$$

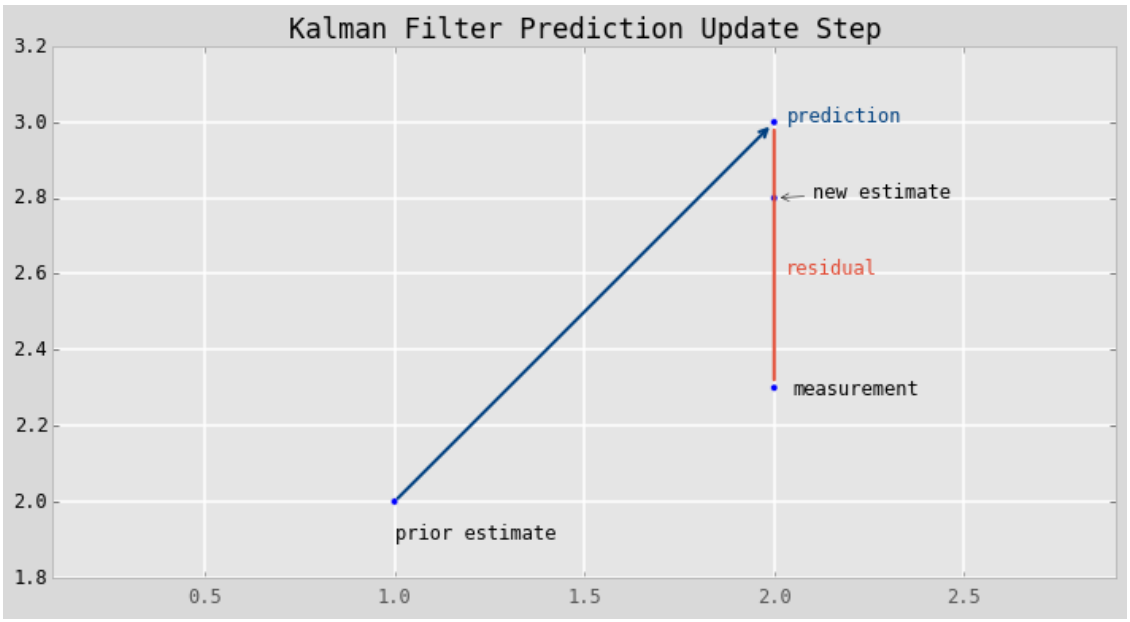
$$\mathbf{P} = (\mathbf{I} - \mathbf{KH})\mathbf{P} \tag{6}$$

I will start with the measurement step, as that is what we started with in the one dimensional Kalman filter case. Our first equation is

$$\gamma = \mathbf{z} - \mathbf{Hx} \tag{3}$$

On the right we have $\mathbf{Hx}$. That should be recognizable as the measurement function. Multiplying $\mathbf{H}$ with $\mathbf{x}$ puts $\mathbf{x}$ into *measurement space*; in other words, the same basis and units as the sensor's measurements. The variable $\mathbf{z}$ is just the measurement; it is typical, but not universal to use $\mathbf{z}$ to denote measurements in the literature ($\mathbf{y}$ is also sometimes used). Do you remember this chart?

```
In [2]: sys.path.insert(0,'../Chapter06_Multivariate_Kalman_Filter')
        import mkf_internal
        mkf_internal.show_residual_chart()
```



The blue prediction line is the output of $\mathbf{Hx}$, and the dot labeled "measurement" is $\mathbf{z}$. Therefore, $\gamma = \mathbf{z} - \mathbf{Hx}$ is how we compute the residual, drawn in red. So γ is the residual.

The next line is the formidable:

$$\mathbf{K} = \mathbf{PH}^T(\mathbf{HPH}^T + \mathbf{R})^{-1} \tag{4}$$

Unfortunately it is a fair amount of linear algebra to derive this. The derivation can be quite elegant, and I urge you to look it up if you have the mathematical education to follow it. But $\mathbf{K}$ is just the *Kalman gain* - the ratio of how much measurement vs prediction we should use to create the new estimate. $\mathbf{R}$ is the *measurement noise*, and $\mathbf{P}$ is our *uncertainty covariance matrix*.

So let's work through this expression by expression. Start with $\mathbf{HPH}^T$. The linear equation $\mathbf{ABA}^T$ can be thought of as changing the basis of $\mathbf{B}$ to $\mathbf{A}$. So $\mathbf{HPH}^T$ is taking the covariance $\mathbf{P}$ and putting it in measurement ($\mathbf{H}$) space. Then, once in measurement space, we can add the measurement noise $\mathbf{R}$ to it. Hence, the expression for the uncertainty in the measurement is:

$$(\mathbf{HPH}^T + \mathbf{R})^{-1}$$

Taking the inverse is linear algebra's way of doing $\frac{1}{x}$. So if you accept my admittedly hand wavey explanation it can be seen to be computing:

$$gain_{measurement\,space} = \frac{uncertainty_{prediction}}{uncertainty_{measurement}}$$

In other words, the *Kalman gain* equation is doing nothing more than computing a ratio based on how much we trust the prediction vs the measurement. If we are confident in our measurements and unconfident in our predictions $\mathbf{K}$ will favor the measurement, and vice

versa. The equation is complicated because we are doing this in multiple dimensions via matrices, but the concept is simple - scale by a ratio.

Without going into the derivation of $\mathbf{K}$, I'll say that this equation is the result of finding a value of $\mathbf{K}$ that optimizes the *mean-square estimation error*. It does this by finding the minimal values for $\mathbf{P}$ along it's diagonal. Recall that the diagonal of P is just the variance for each state variable. So, this equation for $\mathbf{K}$ ensures that the Kalman filter output is optimal. To put this in concrete terms, for our dog tracking problem this means that the estimates for both position and velocity will be optimal - a value of $\mathbf{K}$ that made the position extremely accurate but the velocity very inaccurate would be rejected in favor of a $\mathbf{K}$ that made both position and velocity just somewhat accurate.

Our next line is:

$$\mathbf{x} = \mathbf{x}' + \mathbf{K}\gamma \tag{5}$$

This just multiplies the residual by the Kalman gain, and adds it to the state variable. In other words, this is the computation of our new estimate.

Finally, we have:

$$\mathbf{P} = (\mathbf{I} - \mathbf{KH})\mathbf{P} \tag{6}$$

I is the identity matrix, and is the way we represent 1 in multiple dimensions. H is our measurement function, and is a constant. So, simplified, this is simply $P = (1 - cK)P$. K is our ratio of how much prediction vs measurement we use. So, if K is large then $(1 - cK)$ is small, and P will be made smaller than it was. If K is small, then $(1 - cK)$ is large, and P will be made larger than it was. So we adjust the size of our uncertainty by some factor of the *Kalman gain*. I would like to draw your attention back to the g-h filter, which included this Python code:

```
# update filter
w = w * (1-scale_factor) + z * scale_factor
```

This multidimensional Kalman filter equation is partially implementing this calculation for the variance instead of the state variable.

Now we have the measurement steps. The first equation is

$$\mathbf{x}' = \mathbf{Fx} + \mathbf{Gu} \tag{1}$$

This is just our state transition equation which we have already discussed. $\mathbf{Fx}$ multiplies $\mathbf{x}$ with the state transition matrix to compute the next state. G and u add in the contribution of the control input $\mathbf{u}$, if any.

The final equation is:

$$\mathbf{P} = \mathbf{FPF}^T + \mathbf{Q} \tag{2}$$

$\mathbf{FPF}^T$ is the way we put $\mathbf{P}$ into the process space using linear algebra so that we can add in the process noise $\mathbf{Q}$ to it.

8.3 Design of the Process Noise Matrix

In [2]:

Chapter 9

Designing Kalman Filters

9.1 Introduction

In this chapter we will work through the design of several Kalman filters to gain experience and confidence with the various equations and techniques.

For our first multidimensional problem we will track a robot in a 2D space, such as a field. We will start with a simple noisy sensor that outputs noisy (x, y) coordinates which we will need to filter to generate a 2D track. Once we have mastered this concept, we will extend the problem significantly with more sensors and then adding control inputs. blah blah

9.2 Tracking a Robot

This first attempt at tracking a robot will closely resemble the 1-D dog tracking problem of previous chapters. This will allow us to 'get our feet wet' with Kalman filtering. So, instead of a sensor that outputs position in a hallway, we now have a sensor that supplies a noisy measurement of position in a 2-D space, such as an open field. That is, at each time T it will provide an (x, y) coordinate pair specifying the measurement of the sensor's position in the field.

Implementation of code to interact with real sensors is beyond the scope of this book, so as before we will program simple simulations in Python to represent the sensors. We will develop several of these sensors as we go, each with more complications, so as I program them I will just append a number to the function name. `pos_sensor1()` is the first sensor we write, and so on.

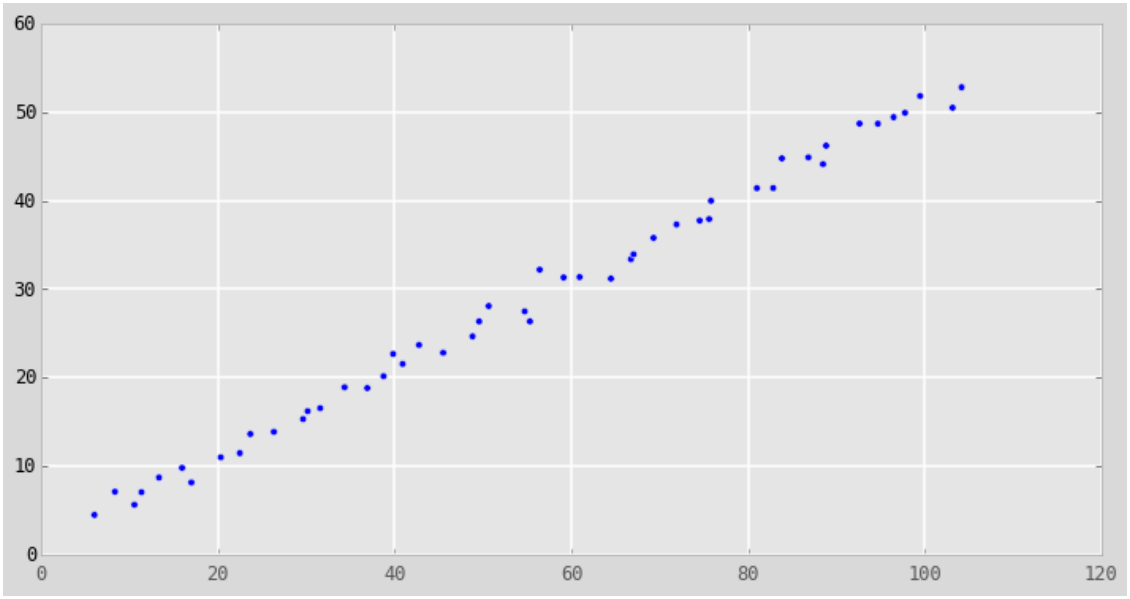
So let's start with a very simple sensor, one that travels in a straight line. It takes as input the last position, velocity, and how much noise we want, and returns the new position.

```
In [2]: import numpy.random as random
        import copy
        class PosSensor1(object):
            def __init__(self, pos = [0,0], vel = (0,0), noise_scale = 1.):
                self.vel = vel
```

```
            self.noise_scale = noise_scale
            self.pos = copy.deepcopy(pos)

        def read(self):
            self.pos[0] += self.vel[0]
            self.pos[1] += self.vel[1]

            return [self.pos[0] + random.randn() * self.noise_scale,
                    self.pos[1] + random.randn() * self.noise_scale]
```

A quick test to verify that it works as we expect.

```
In [3]: pos = [4,3]
        s = PosSensor1 (pos, (2,1), 1)

        for i in range (50):
            pos = s.read()
            plt.scatter(pos[0], pos[1])
        plt.show()
```



That looks correct. The slope is 1/2, as we would expect with a velocity of (2,1), and the data seems to start at near (6,4).

Step 1: Choose the State Variables As always, the first step is to choose our state variables. We are tracking in two dimensions and have a sensor that gives us a reading in each of those two dimensions, so we know that we have the two *observed variables* x and y. If we created our Kalman filter using only those two variables the performance would not

be very good because we would be ignoring the information velocity can provide to us. We will want to incorporate velocity into our equations as well. I will represent this as

$$\mathbf{x} = \begin{bmatrix} x \\ v_x \\ y \\ v_y \end{bmatrix}$$

There is nothing special about this organization. I could have listed the (xy) coordinates first followed by the velocities, and/or I could done this as a row matrix instead of a column matrix. For example, I could have chosen:

$$\mathbf{x} = \begin{bmatrix} x & y & v_x & v_y \end{bmatrix}$$

All that matters is that the rest of my derivation uses this same scheme. However, it is typical to use column matrices for state variables, and I prefer it, so that is what we will use.

It might be a good time to pause and address how you identify the unobserved variables. This particular example is somewhat obvious because we already worked through the 1D case in the previous chapters. Would it be so obvious if we were filtering market data, population data from a biology experiment, and so on? Probably not. There is no easy answer to this question. The first thing to ask yourself is what is the interpretation of the first and second derivatives of the data from the sensors. We do that because obtaining the first and second derivatives is mathematically trivial if you are reading from the sensors using a fixed time step. The first derivative is just the difference between two successive readings. In our tracking case the first derivative has an obvious physical interpretation: the difference between two successive positions is velocity.

Beyond this you can start looking at how you might combine the data from two or more different sensors to produce more information. This opens up the field of *sensor fusion*, and we will be covering examples of this in later sections. For now, recognize that choosing the appropriate state variables is paramount to getting the best possible performance from your filter.

Step 2: Design State Transition Function Our next step is to design the state transition function. Recall that the state transition function is implemented as a matrix **F** that we multipy with the previous state of our system to get the next state, like so.

$$\mathbf{x}' = \mathbf{F}\mathbf{x}$$

I will not belabor this as it is very similar to the 1-D case we did in the previous chapter. Our state equations for position and velocity would be:

$$\begin{aligned} x' &= (1 * x) + (\Delta t * v_x) + (0 * y) + (0 * v_y) \\ v_x &= (0 * x) + (1 * v_x) + (0 * y) + (0 * v_y) \\ y' &= (0 * x) + (0 * v_x) + (1 * y) + (\Delta t * v_y) \\ v_y &= (0 * x) + (0 * v_x) + (0 * y) + (1 * v_y) \end{aligned}$$

Laying it out that way shows us both the values and row-column organization required for **F**. In linear algebra, we would write this as:

$$\begin{bmatrix} x \\ v_x \\ y \\ v_y \end{bmatrix}' = \begin{bmatrix} 1 & \Delta t & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & \Delta t \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ v_x \\ y \\ v_y \end{bmatrix}$$

So, let's do this in Python. It is very simple; the only thing new here is setting `dim_z` to 2. We will see why it is set to 2 in step 4.

```
In [4]: from filterpy.kalman import KalmanFilter
        import numpy as np

        f1 = KalmanFilter(dim_x=4, dim_z=2)
        dt = 1.   # time step

        f1.F = np.array ([[1, dt, 0,  0],
                          [0,  1, 0,  0],
                          [0,  0, 1, dt],
                          [0,  0, 0,  1]])
```

Step 3: Design the Motion Function We have no control inputs to our robot (yet!), so this step is trivial - set the motion input **u** to zero. This is done for us by the class when it is created so we can skip this step, but for completeness we will be explicit.

```
In [5]: f1.u = 0.
```

Step 4: Design the Measurement Function The measurement function defines how we go from the state variables to the measurements using the equation $\mathbf{z} = \mathbf{Hx}$. At first this is a bit counterintuitive, after all, we use the Kalman filter to go from measurements to state. But the update step needs to compute the residual between the current measurement and the measurement represented by the prediction step. Therefore **H** is multiplied by the state **x** to produce a measurement **z**.

In this case we have measurements for (x,y), so **z** must be of dimension 2×1. Our state variable is size 4×1. We can deduce the required size for **H** by recalling that multiplying a matrix of size $m \times n$ by $n \times p$ yields a matrix of size $m \times p$. Thus,

$$\begin{aligned}(2 \times 1) &= (a \times b)(4 \times 1) \\ &= (a \times 4)(4 \times 1) \\ &= (2 \times 4)(4 \times 1)\end{aligned}$$

So, **H** is of size 2×4.

Filling in the values for **H** is easy in this case because the measurement is the position of the robot, which is the x and y variables of the state **x**. Let's make this just slightly more interesting by deciding we want to change units. So we will assume that the measurements

are returned in feet, and that we desire to work in meters. Converting from feet to meters is a simple as multiplying by 0.3048. However, we are converting from state (meters) to measurements (feet) so we need to divide by 0.3048. So

$$\mathbf{H} = \begin{bmatrix} \frac{1}{0.3048} & 0 & 0 & 0 \\ 0 & 0 & \frac{1}{0.3048} & 0 \end{bmatrix}$$

which corresponds to these linear equations

$$z'_x = (\frac{x}{0.3048}) + (0 * v_x) + (0 * y) + (0 * v_y)$$
$$z'_y = (0 * x) + (0 * v_x) + (\frac{y}{0.3048}) + (0 * v_y)$$

To be clear about my intentions here, this is a pretty simple problem, and we could have easily found the equations directly without going through the dimensional analysis that I did above. In fact, an earlier draft did just that. But it is useful to remember that the equations of the Kalman filter imply a specific dimensionality for all of the matrices, and when I start to get lost as to how to design something it is often extremely useful to look at the matrix dimensions. Not sure how to design **H**? Here is the Python that implements this:

```
In [6]: f1.H = np.array ([[1/0.3048, 0, 0, 0],
                          [0, 0, 1/0.3048, 0]])
        print(f1.H)
```

```
[[ 3.2808399  0.         0.         0.       ]
 [ 0.         0.         3.2808399  0.       ]]
```

Step 5: Design the Measurement Noise Matrix In this step we need to mathematically model the noise in our sensor. For now we will make the simple assumption that the x and y variables are independent Gaussian processes. That is, the noise in x is not in any way dependent on the noise in y, and the noise is normally distributed about the mean. For now let's set the variance for x and y to be 5 for each. They are independent, so there is no covariance, and our off diagonals will be 0. This gives us:

$$\mathbf{R} = \begin{bmatrix} 5 & 0 \\ 0 & 5 \end{bmatrix}$$

It is a 2×2 matrix because we have 2 sensor inputs, and covariance matrices are always of size $n \times n$ for n variables. In Python we write:

```
In [7]: f1.R = np.array([[5,0],
                         [0, 5]])
        print (f1.R)
```

```
[[ 5.  0.]
 [ 0.  5.]]
```

Step 6: Design the Process Noise Matrix Finally, we design the process noise. We don't yet have a good way to model process noise, so for now we will assume there is a small amount of process noise, say 0.1 for each state variable. Later we will tackle this admittedly difficult topic in more detail. We have 4 state variables, so we need a 4×4 covariance matrix:

$$\mathbf{Q} = \begin{bmatrix} 0.1 & 0 & 0 & 0 \\ 0 & 0.1 & 0 & 0 \\ 0 & 0 & 0.1 & 0 \\ 0 & 0 & 0 & 0.1 \end{bmatrix}$$

In Python I will use the numpy eye helper function to create an identity matrix for us, and multipy it by 0.1 to get the desired result.

```
In [8]: f1.Q = np.eye(4) * 0.1
        print(f1.Q)
```

```
[[ 0.1  0.   0.   0. ]
 [ 0.   0.1  0.   0. ]
 [ 0.   0.   0.1  0. ]
 [ 0.   0.   0.   0.1]]
```

Step 7: Design Initial Conditions For our simple problem we will set the initial position at (0,0) with a velocity of (0,0). Since that is a pure guess, we will set the covariance matrix **P** to a large value.

$$\mathbf{x} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \mathbf{P} = \begin{bmatrix} 500 & 0 & 0 & 0 \\ 0 & 500 & 0 & 0 \\ 0 & 0 & 500 & 0 \\ 0 & 0 & 0 & 500 \end{bmatrix}$$

In Python we implement that with

```
In [9]: f1.x = np.array([[0,0,0,0]]).T
        f1.P = np.eye(4) * 500.
        print(f1.x)
        print()
        print (f1.P)
```

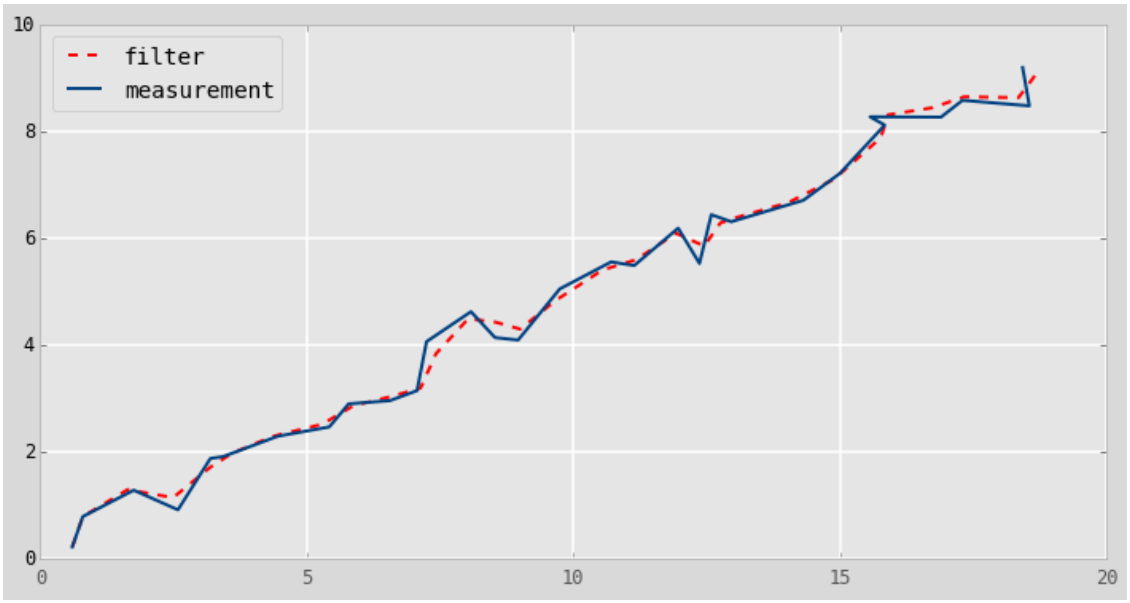
```
[[ 0.]
 [ 0.]
 [ 0.]
 [ 0.]]

[[ 500.    0.    0.    0.]
 [   0.  500.    0.    0.]
 [   0.    0.  500.    0.]
 [   0.    0.    0.  500.]]
```

9.3 Implement the Filter Code

Design is complete, now we just have to write the Python code to run our filter, and output the data in the format of our choice. To keep the code clear, let's just print a plot of the track. We will run the code for 30 iterations.

```
In [10]: f1 = KalmanFilter(dim_x=4, dim_z=2)
         dt = 1.0   # time step

         f1.F = np.array ([[1, dt, 0,  0],
                           [0,  1, 0,  0],
                           [0,  0, 1, dt],
                           [0,  0, 0,  1]])
         f1.u = 0.
         f1.H = np.array ([[1/0.3048, 0, 0, 0],
                           [0, 0, 1/0.3048, 0]])

         f1.R = np.eye(2) * 5
         f1.Q = np.eye(4) * .1

         f1.x = np.array([[0,0,0,0]]).T
         f1.P = np.eye(4) * 500.

         # initialize storage and other variables for the run
         count = 30
         xs, ys = [],[]
         pxs, pys = [],[]

         s = PosSensor1 ([0,0], (2,1), 1.)

         for i in range(count):
             pos = s.read()
             z = np.array([[pos[0]],[pos[1]]])

             f1.predict ()
             f1.update (z)

             xs.append (f1.x[0,0])
             ys.append (f1.x[2,0])
             pxs.append (pos[0]*.3048)
             pys.append(pos[1]*.3048)

         p1, = plt.plot (xs, ys, 'r--')
         p2, = plt.plot (pxs, pys)
         plt.legend([p1,p2], ['filter', 'measurement'], 2)
```

```
plt.show()
```

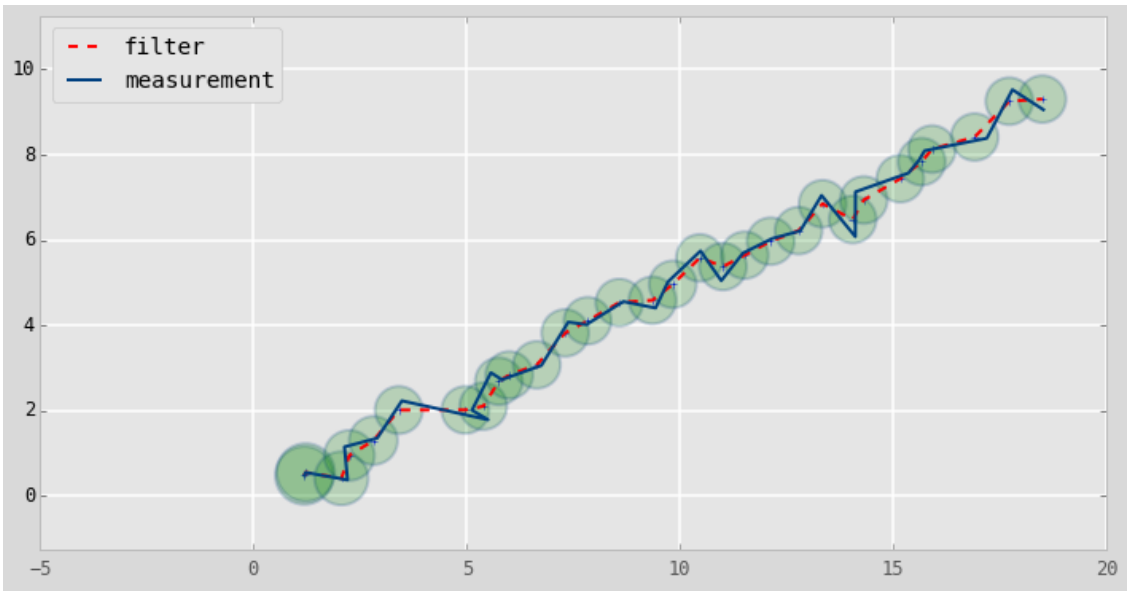


I encourage you to play with this, setting **Q** and **R** to various values. However, we did a fair amount of that sort of thing in the last chapters, and we have a lot of material to cover, so I will move on to more complicated cases where we will also have a chance to experience changing these values.

Now I will run the same Kalman filter with the same settings, but also plot the covariance ellipse for x and y. First, the code without explanation, so we can see the output. I print the last covariance to see what it looks like. But before you scroll down to look at the results, what do you think it will look like? You have enough information to figure this out but this is still new to you, so don't be discouraged if you get it wrong.

```
In [27]: import stats

         f1 = KalmanFilter(dim_x=4, dim_z=2)
         dt = 1.0   # time step

         f1.F = np.array ([[1, dt, 0,  0],
                           [0,  1, 0,  0],
                           [0,  0, 1, dt],
                           [0,  0, 0,  1]])
         f1.u = 0.
         f1.H = np.array ([[1/0.3048, 0, 0, 0],
                           [0, 0, 1/0.3048, 0]])

         f1.R = np.eye(2) * 5
         f1.Q = np.eye(4) * .1
```

```
f1.x = np.array([[0,0,0,0]]).T
f1.P = np.eye(4) * 500.

# initialize storage and other variables for the run
count = 30
xs, ys = [],[]
pxs, pys = [],[]

s = PosSensor1 ([0,0], (2,1), 1.)

for i in range(count):
    pos = s.read()
    z = np.array([[pos[0]],[pos[1]]])

    f1.predict ()
    f1.update (z)

    xs.append (f1.x[0,0])
    ys.append (f1.x[2,0])
    pxs.append (pos[0]*.3048)
    pys.append(pos[1]*.3048)

    # plot covariance of x and y
    cov = np.array([[f1.P[0,0], f1.P[2,0]],
                    [f1.P[0,2], f1.P[2,2]]])

    #e = stats.sigma_ellipse (cov=cov, x=f1.x[0,0], y=f1.x[2,0])
    #stats.plot_sigma_ellipse(ellipse=e)
    stats.plot_covariance_ellipse((f1.x[0,0], f1.x[2,0]), cov=cov,
                                  facecolor='g', alpha=0.2)


p1, = plt.plot (xs, ys, 'r--')
p2, = plt.plot (pxs, pys)
plt.legend([p1,p2], ['filter', 'measurement'], 2)
plt.show()
print("final P is:")
print(f1.P)
```




```
final P is:
[[ 0.30660483  0.12566239  0.          0.        ]
 [ 0.12566239  0.24399092  0.          0.        ]
 [ 0.          0.          0.30660483  0.12566239]
 [ 0.          0.          0.12566239  0.24399092]]
```

Did you correctly predict what the covariance matrix and plots would look like? Perhaps you were expecting a tilted ellipse, as in the last chapters. If so, recall that in those chapters we were not plotting x against y, but x against $\dot{x}$. *x is correlated* to $\dot{x}$, but x is not correlated or dependent on y. Therefore our ellipses are not tilted. Furthermore, the noise for both x and y are modeled to have the same value, 5, in $\mathbf{R}$. If we were to set R to, for example,

$$\mathbf{R} = \begin{bmatrix} 10 & 0 \\ 0 & 5 \end{bmatrix}$$

we would be telling the Kalman filter that there is more noise in x than y, and our ellipses would be longer than they are tall.

The final P tells us everything we need to know about the correlation between the state variables. If we look at the diagonal alone we see the variance for each variable. In other words $\mathbf{P}_{0,0}$ is the variance for x, $\mathbf{P}_{1,1}$ is the variance for $\dot{x}$, $\mathbf{P}_{2,2}$ is the variance for y, and $\mathbf{P}_{3,3}$ is the variance for $\dot{y}$. We can extract the diagonal of a matrix using *numpy.diag()*.

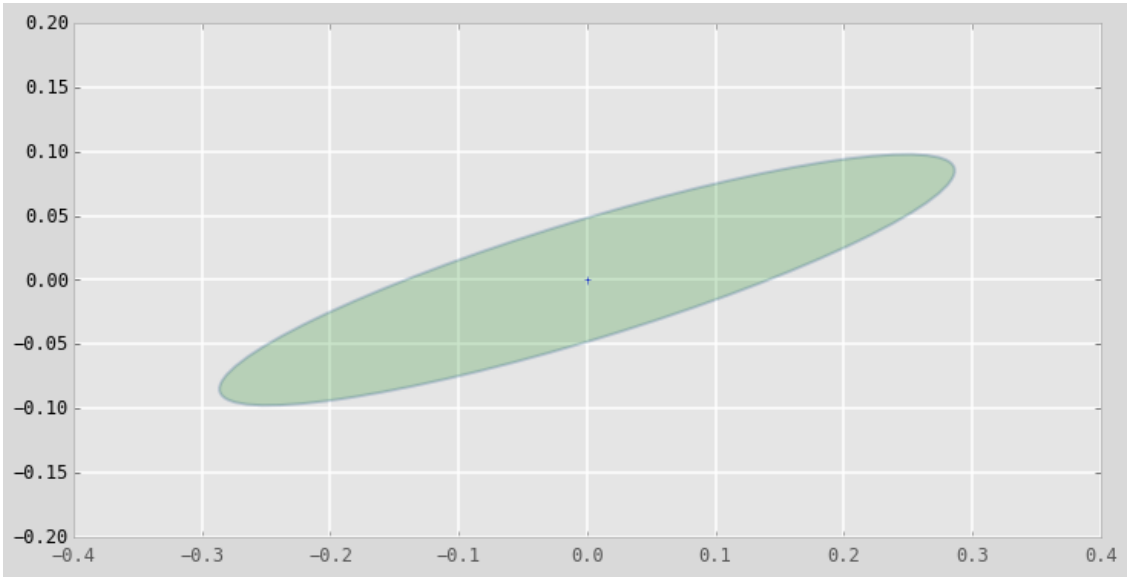
```
In [12]: print(np.diag(f1.P))
```

```
[ 0.30660483  0.24399092  0.30660483  0.24399092]
```

The covariance matrix contains four 2×2 matrices that you should be able to easily pick out. This is due to the correlation of x to $\dot{x}$, and of y to $\dot{y}$. The upper left hand side shows the covariance of x to $\dot{x}$. Let's extract and print, and plot it.

```
In [26]: c = f1.P[0:2,0:2]
         print(c)
         stats.plot_covariance_ellipse((0,0), cov=c, facecolor='g', alpha=0.2)
```

```
[[ 0.08204134  0.02434904]
 [ 0.02434904  0.00955614]]
```



The covariance contains the data for x and $\dot{x}$ in the upper left because of how it is organized. Recall that entries $\mathbf{P}_{i,j}$ and $\mathbf{P}_{j,i}$ contain $p\sigma_1\sigma_2$.

Finally, let's look at the lower left side of $\mathbf{P}$, which is all 0s. Why 0s? Consider $\mathbf{P}_{3,0}$. That stores the term $p\sigma_3\sigma_0$, which is the covariance between $\dot{y}$ and x. These are independent, so the term will be 0. The rest of the terms are for similarly independent variables.

9.4 Tracking a Ball

Now let's turn our attention to a situation where the physics of the object that we are tracking is constrained. A ball thrown in a vacuum must obey Newtonian laws. In a constant gravitational field it will travel in a parabola. I will assume you are familiar with the derivation of the formula:

$$y = \frac{g}{2}t^2 + v_{y0}t + y_0$$
$$x = v_{x0}t + x_0$$

where g is the gravitional constant, t is time, v_{x0} and v_{y0} are the initial velocities in the x and y plane. If the ball is thrown with an initial velocity of v at angle θ above the horizon, we can compute v_{x0} and v_{y0} as

$$v_{x0} = v\cos\theta$$
$$v_{y0} = v\sin\theta$$

Because we don't have real data we will start by writing a simulator for a ball. As always, we add a noise term independent of time so we can simulate noise sensors.

In [14]:
```
from math import radians, sin, cos
import math

def rk4(y, x, dx, f):
    """computes 4th order Runge-Kutta for dy/dx.
    y is the initial value for y
    x is the initial value for x
    dx is the difference in x (e.g. the time step)
    f is a callable function (y, x) that you supply to compute dy/dx for
      the specified values.
    """

    k1 = dx * f(y, x)
    k2 = dx * f(y + 0.5*k1, x + 0.5*dx)
    k3 = dx * f(y + 0.5*k2, x + 0.5*dx)
    k4 = dx * f(y + k3, x + dx)

    return y + (k1 + 2*k2 + 2*k3 + k4) / 6.

def fx(x,t):
    return fx.vel

def fy(y,t):
    return fy.vel - 9.8*t


class BallTrajectory2D(object):
    def __init__(self, x0, y0, velocity, theta_deg=0., g=9.8, noise=[0.0,0.0]):
        self.x = x0
        self.y = y0
        self.t = 0

        theta = math.radians(theta_deg)

        fx.vel = math.cos(theta) * velocity
        fy.vel = math.sin(theta) * velocity

        self.g = g
        self.noise = noise
```

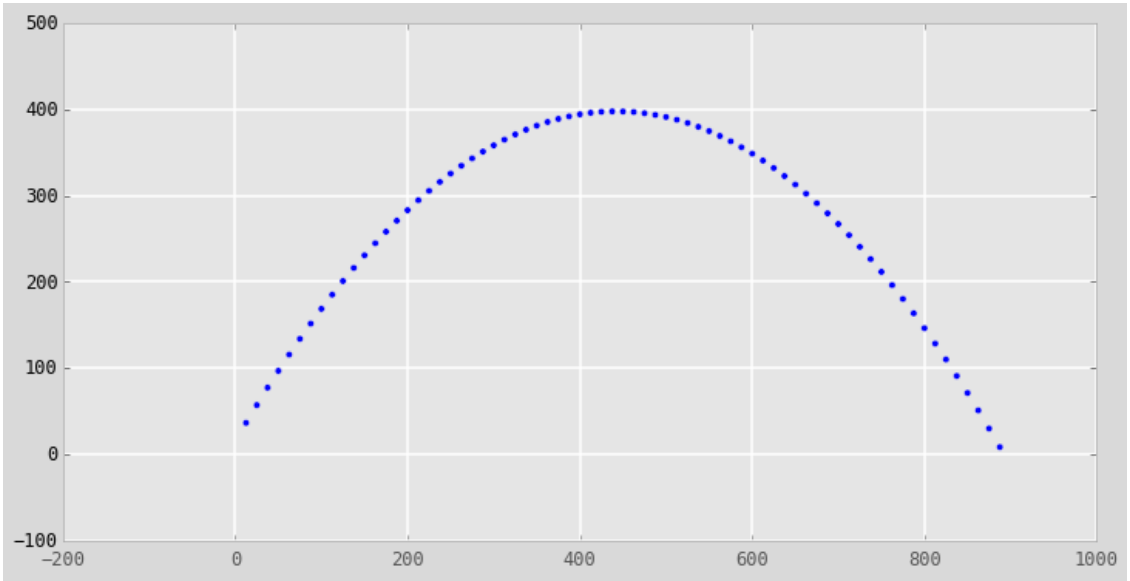
```
        def step (self, dt):
            self.x = rk4 (self.x, self.t, dt, fx)
            self.y = rk4 (self.y, self.t, dt, fy)
            self.t += dt
            return (self.x +random.randn()*self.noise[0], self.y+random.randn()*sel
```

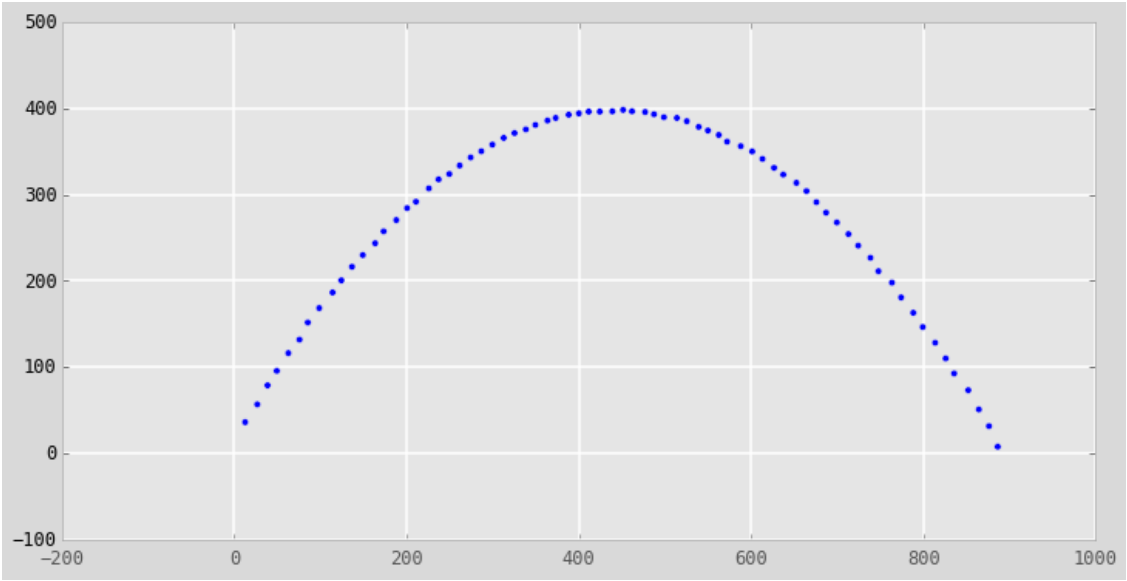
So to create a trajectory starting at (0,15) with a velocity of $60\frac{m}{s}$ and an angle of 65° we would write:

```
traj = BallTrajectory2D (x0=0, y0=15, velocity=100, theta_deg=60)
```

and then call `traj.position(t)` for each time step. Let's test this

```
In [15]: def test_ball_vacuum(noise):
             y = 15
             x = 0
             ball = BallTrajectory2D(x0=x, y0=y, theta_deg=60., velocity=100., noise=noi
             t = 0
             dt = 0.25
             while y >= 0:
                 x,y = ball.step(dt)
                 t += dt
                 if y >= 0:
                     plt.scatter(x,y)

             plt.axis('equal')
             plt.show()

         test_ball_vacuum([0,0]) # plot ideal ball position
         test_ball_vacuum([1,1]) # plot with noise
```





This looks reasonable, so let's continue (excercise for the reader: validate this simulation more robustly).

Step 1: Choose the State Variables We might think to use the same state variables as used for tracking the dog. However, this will not work. Recall that the Kalman filter state transition must be written as $\mathbf{x}' = \mathbf{Fx}$, which means we must calculate the current state from the previous state. Our assumption is that the ball is traveling in a vacuum, so the velocity in x is a constant, and the acceleration in y is solely due to the gravitational constant g. We can discretize the Newtonian equations using the well known Euler method in terms of Δt are:

$$
\begin{aligned}
x_t &= v_{x(t-1)}\Delta t \\
v_{xt} &= vx_{t-1} \\
y_t &= -\frac{g}{2}\Delta t^2 + vy_{t-1}\Delta t + y_{t-1} \\
v_{yt} &= -g\Delta t + v_{y(t-1)}
\end{aligned}
$$

> **sidebar**: *Euler's method integrates a differential equation stepwise by assuming the slope (derivative) is constant at time t. In this case the derivative of the position is velocity. At each time step Δt we assume a constant velocity, compute the new position, and then update the velocity for the next time step. There are more accurate methods, such as Runge-Kutta available to us, but because we are updating the state with a measurement in each step Euler's method is very accurate.*

This implies that we need to incorporate acceleration for y into the Kalman filter, but not for x. This suggests the following state variables.

$$\mathbf{x} = \begin{bmatrix} x \\ \dot{x} \\ y \\ \dot{y} \\ \ddot{y} \end{bmatrix}$$

Step 2: Design State Transition Function Our next step is to design the state transistion function. Recall that the state transistion function is implemented as a matrix $\mathbf{F}$ that we multipy with the previous state of our system to get the next state$\mathbf{x}' = \mathbf{F}\mathbf{x}$.

I will not belabor this as it is very similar to the 1-D case we did in the previous chapter. Our state equations for position and velocity would be:

$$\begin{aligned}
x' &= (1 * x) + (\Delta t * v_x) + (0 * y) + (0 * v_y) + (0 * a_y) \\
v_x &= (0 * x) + (1 * v_x) + (0 * y) + (0 * v_y) + (0 * a_y) \\
y' &= (0 * x) + (0 * v_x) + (1 * y) + (\Delta t * v_y) + (\frac{1}{2}\Delta t^2 * a_y) \\
v_y &= (0 * x) + (0 * v_x) + (0 * y) + (1 * v_y) + (\Delta t * a_y) \\
a_y &= (0 * x) + (0 * v_x) + (0 * y) + (0 * v_y) + (1 * a_y)
\end{aligned}$$

Note that none of the terms include g, the gravitational constant. This is because the state variable $\ddot{y}$ will be initialized with g, or -9.81. Thus the function $\mathbf{F}$ will propagate g through the equations correctly.

In matrix form we write this as:

$$\mathbf{F} = \begin{bmatrix} 1 & \Delta t & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & \Delta t & \frac{1}{2}\Delta t^2 \\ 0 & 0 & 0 & 1 & \Delta t \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

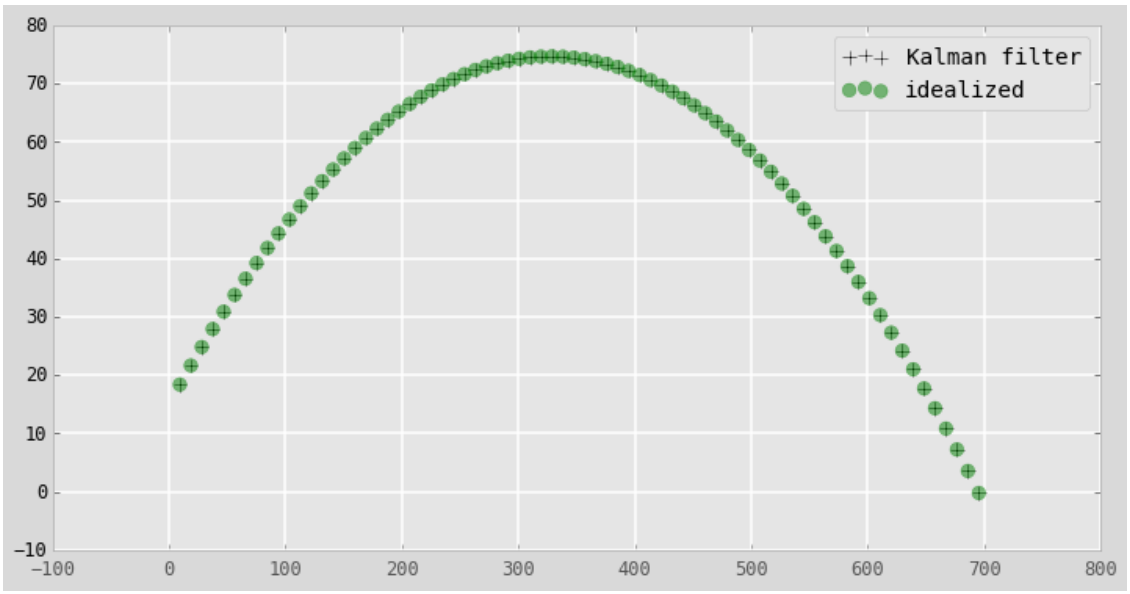
Interlude: Test State Transition The Kalman filter class provides us with useful defaults for all of the class variables, so let's take advantage of that and test the state transistion function before continuing. Here we construct a filter as specified in Step 2 above. We compute the initial velocity in x and y using trigonometry, and then set the initial condition for x.

```
In [16]: from math import sin,cos,radians

         def ball_kf(x, y, omega, v0, dt):

             g = 9.8 # gravitational constant

             f1 = KalmanFilter(dim_x=5, dim_z=2)
```

```
    ay = .5*dt**2

    f1.F = np.array ([[1, dt,  0,  0,  0],    # x   = x0+dx*dt
                      [0,  1,  0,  0,  0],    # dx  = dx
                      [0,  0,  1, dt, ay],    # y   = y0 +dy*dt+1/2*g*dt^2
                      [0,  0,  0,  1, dt],    # dy  = dy0 + ddy*dt
                      [0,  0,  0,  0, 1]])    # ddy = -g.

    # compute velocity in x and y
    omega = radians(omega)
    vx = cos(omega) * v0
    vy = sin(omega) * v0

    f1.Q *= 0.

    f1.x = np.array([[x, vx, y, vy, -g]]).T

    return f1
```

Now we can test the filter by calling predict until $y = 0$, which corresponds to the ball hitting the ground. We will graph the output against the idealized computation of the ball's position. If the model is correct, the Kalman filter prediction should match the ideal model very closely. We will draw the ideal position with a green circle, and the Kalman filter's output with '+' marks.

```
In [17]: y = 15.
         x = 0.
         theta = 20. # launch angle
         v0 = 100.
         dt = 0.1   # time step

         ball = BallTrajectory2D(x0=x, y0=y, theta_deg=theta, velocity=v0, noise=[0,0])
         f1 = ball_kf(x,y,theta,v0,dt)
         t = 0
         while f1.x[2,0] > 0:
             t += dt
             f1.predict()
             x,y = ball.step(dt)
             p1 = plt.scatter(f1.x[0,0], f1.x[2,0], color='black', marker='+', s=75)
             p2 = plt.scatter(x, y,                 color='green', marker='o', s=75, alp

         plt.legend([p1,p2], ['Kalman filter', 'idealized'])
         plt.show()
```



As we can see, the Kalman filter agrees with the physics model very closely. If you are interested in pursuing this further, try altering the initial velocity, the size of dt, and θ, and plot the error at each step. However, the important point is to test your design as soon as possible; if the design of the state transistion is wrong all subsequent effort may be wasted. More importantly, it can be extremely difficult to tease out an error in the state transition function when the filter incorporates measurment updates.

Step 3: Design the Motion Function We have no control inputs to the ball flight, so this step is trivial - set the motion transition function $\mathbf{B} = 0$. This is done for us by the class when it is created so we can skip this step.

Step 4: Design the Measurement Function The measurement function defines how we go from the state variables to the measurements using the equation $\mathbf{z} = \mathbf{Hx}$. We will assume that we have a sensor that provides us with the position of the ball in (x,y), but cannot measure velocities or accelerations. Therefore our function must be:

$$\begin{bmatrix} z_x \\ z_y \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \end{bmatrix} * \begin{bmatrix} x \\ \dot{x} \\ y \\ \dot{y} \\ \ddot{y} \end{bmatrix}$$

where

$$\mathbf{H} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \end{bmatrix}$$

Step 5: Design the Measurement Noise Matrix As with the robot, we will assume that the error is independent in x and y. In this case we will start by assuming that the measurement error in x and y are 0.5 meters. Hence,

$$\mathbf{R} = \begin{bmatrix} 0.5 & 0 \\ 0 & 0.5 \end{bmatrix}$$

Step 6: Design the Process Noise Matrix Finally, we design the process noise. As with the robot tracking example, we don't yet have a good way to model process noise. However, we are assuming a ball moving in a vacuum, so there should be no process noise. For now we will assume the process noise is 0 for each state variable. This is a bit silly - if we were in a perfect vacuum then our predictions would be perfect, and we would have no need for a Kalman filter. We will soon alter this example to be more realistic by incorporating air drag and ball spin.

We have 5 state variables, so we need a 5×5 covariance matrix:

$$\mathbf{Q} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Step 7: Design the Initial Conditions We already performed this step when we tested the state transistion function. Recall that we computed the initial velocity for x and y using trigonometry, and set the value of $\mathbf{x}$ with:

```
omega = radians(omega)
vx = cos(omega) * v0
vy = sin(omega) * v0

f1.x = np.mat([x, vx, y, vy, -g]).T
```

With all the steps done we are ready to implement our filter and test it. First, the implementation:

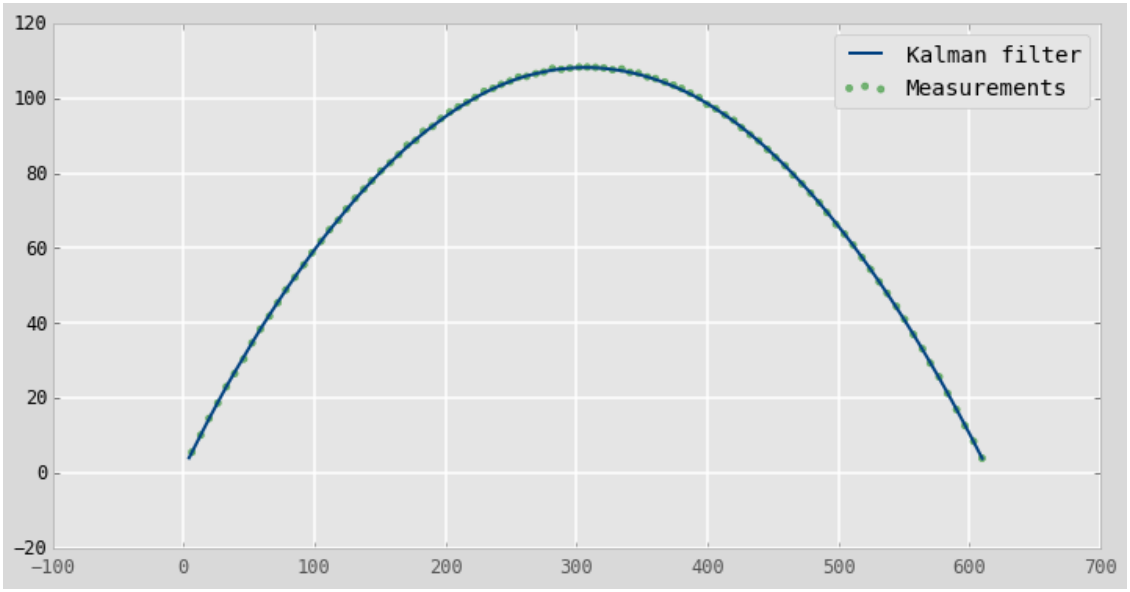
```
In [18]: from math import sin,cos,radians

         def ball_kf(x, y, omega, v0, dt, r=0.5, q=0.):

             g = 9.8 # gravitational constant
             f1 = KalmanFilter(dim_x=5, dim_z=2)

             ay = .5*dt**2
             f1.F = np.mat ([[1, dt,  0,  0,  0],    # x   = x0+dx*dt
                             [0,  1,  0,  0,  0],    # dx  = dx
                             [0,  0,  1, dt, ay],    # y   = y0 +dy*dt+1/2*g*dt^2
```

```
                        [0,  0,  0,  1, dt],   # dy  = dy0 + ddy*dt
                        [0,  0,  0,  0, 1]])   # ddy = -g.

    f1.H = np.mat([
                [1, 0, 0, 0, 0],
                [0, 0, 1, 0, 0]])

    f1.R *= r
    f1.Q *= q

    omega = radians(omega)
    vx = cos(omega) * v0
    vy = sin(omega) * v0

    f1.x = np.mat([x,vx,y,vy,-9.8]).T

    return f1
```

Now we will test the filter by generating measurements for the ball using the ball simulation class.

In [19]:
```
y = 1.
x = 0.
theta = 35. # launch angle
v0 = 80.
dt = 1/10.   # time step

ball = BallTrajectory2D(x0=x, y0=y, theta_deg=theta, velocity=v0, noise=[.2,.2]
f1 = ball_kf(x,y,theta,v0,dt)

t = 0
xs = []
ys = []
while f1.x[2,0] > 0:
    t += dt
    x,y = ball.step(dt)
    z = np.mat([[x,y]]).T

    f1.update(z)
    xs.append(f1.x[0,0])
    ys.append(f1.x[2,0])

    f1.predict()

    p1 = plt.scatter(x, y, color='green', marker='.', s=75, alpha=0.5)
```

```
p2, = plt.plot (xs, ys,lw=2)
plt.legend([p2,p1], ['Kalman filter', 'Measurements'])
plt.show()
```



We see that the Kalman filter reasonably tracks the ball. However, as already explained, this is a silly example; we can predict trajectories in a vacuum with arbitrary precision; using a Kalman filter in this example is a needless complication.

9.5 Tracking a Ball in Air

We are now ready to design a practical Kalman filter application. For this problem we assume that we are tracking a ball traveling through the Earth's atmosphere. The path of the ball is influenced by wind, drag, and the rotation of the ball. We will assume that our sensor is a camera; code that we will not implement will perform some type of image processing to detect the position of the ball. This is typically called *blob detection* in computer vision. However, image processing code is not perfect; in any given frame it is possible to either detect no blob or to detect spurious blobs that do not correspond to the ball. Finally, we will not assume that we know the starting position, angle, or rotation of the ball; the tracking code will have to initiate tracking based on the measurements that are provided. The main simplification that we are making here is a 2D world; we assume that the ball is always traveling orthogonal to the plane of the camera's sensor. We have to make that simplification at this point because we have not yet discussed how we might extract 3D information from a camera, which necessarily provides only 2D data.

9.5.1 Implementing Air Drag

Our first step is to implement the math for a ball moving through air. There are several treatments available. A robust solution takes into account issues such as ball roughness (which affects drag non-linearly depending on velocity), the Magnus effect (spin causes one side of the ball to have higher velocity relative to the air vs the opposite side, so the coefficient of drag differs on opposite sides), the effect of lift, humidity, air density, and so on. I assume the reader is not interested in the details of ball physics, and so will restrict this treatment to the effect of air drag on a non-spinning baseball. I will use the math developed by Nicholas Giordano and Hisao Nakanishi in *Computational Physics* [1997].

Important: Before I continue, let me point out that you will not have to understand this next piece of physics to proceed with the Kalman filter. My goal is to create a reasonably accurate behavior of a baseball in the real world, so that we can test how our Kalman filter performs with real-world behavior. In real world applications it is usually impossible to completely model the physics of a real world system, and we make do with a process model that incorporates the large scale behaviors. We then tune the measurement noise and process noise until the filter works well with our data. There is a real risk to this; it is easy to finely tune a Kalman filter so it works perfectly with your test data, but performs badly when presented with slightly different data. This is perhaps the hardest part of designing a Kalman filter, and why it gets referred to with terms such as 'black art'.

I dislike books that implement things without explanation, so I will now develop the physics for a ball moving through air. Move on past the implementation of the simulation if you are not interested.

A ball moving through air encounters wind resistance. This imparts a force on the wall, called *drag*, which alters the flight of the ball. In Giordano this is denoted as

$$F_{drag} = -B_2v^2$$

where B_2 is a coefficient derived experimentally, and v is the velocity of the object. F_{drag} can be factored into x and y components with

$$F_{drag,x} = -B_2vv_xF_{drag,y} = -B_2vv_y$$

If m is the mass of the ball, we can use $F = ma$ to compute the acceleration as

$$a_x = -\frac{B_2}{m}vv_xa_y = -\frac{B_2}{m}vv_y$$

Giordano provides the following function for $\frac{B_2}{m}$, which takes air density, the cross section of a baseball, and its roughness into account. Understand that this is an approximation based on wind tunnel tests and several simplifying assumptions. It is in SI units: velocity is in meters/sec and time is in seconds.

$$\frac{B_2}{m} = 0.0039 + \frac{0.0058}{1 + \exp\left[(v - 35)/5\right]}$$

Starting with this Euler discretation of the ball path in a vacuum:

$$\begin{aligned} x &= v_x \Delta t \\ y &= v_y \Delta t \\ v_x &= v_x \\ v_y &= v_y - 9.8\Delta t \end{aligned}$$

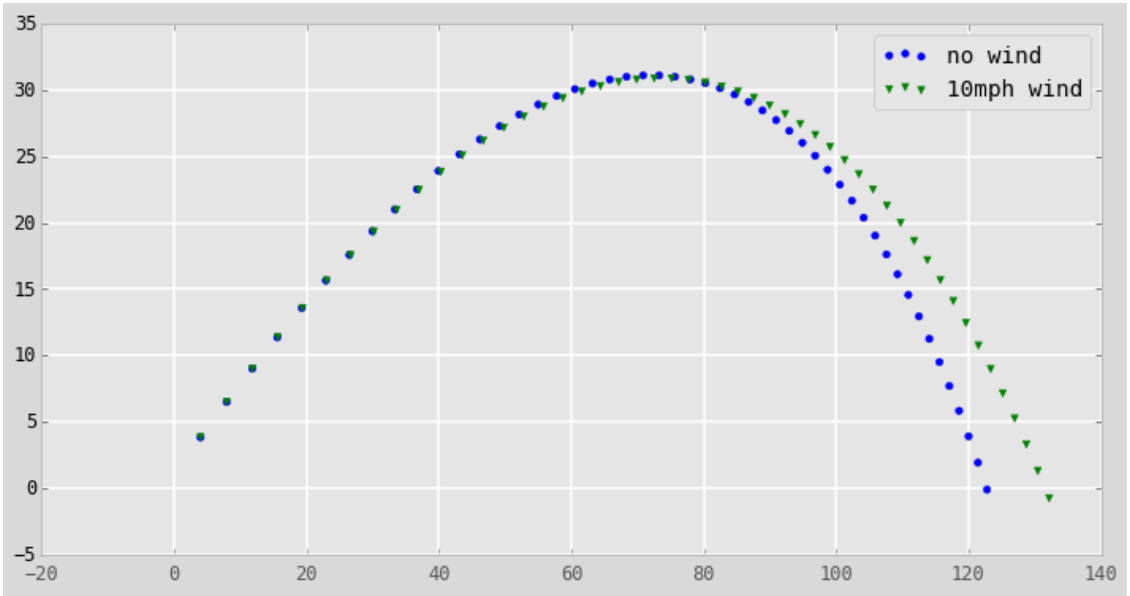
We can incorporate this force (acceleration) into our equations by incorporating $accel * \Delta t$ into the velocity update equations. We should subtract this component because drag will reduce the velocity. The code to do this is quite straightforward, we just need to break out the Force into x and y components.

I will not belabor this issue further because the computational physics is beyond the scope of this book. Recognize that a higher fidelity simulation would require incorporating things like altitude, temperature, ball spin, and several other factors. My intent here is to impart some real-world behavior into our simulation to test how our simpler prediction model used by the Kalman filter reacts to this behavior. Your process model will never exactly model what happens in the world, and a large factor in designing a good Kalman filter is carefully testing how it performs against real world data.

The code below computes the behavior of a baseball in air, at sea level, in the presence of wind. I plot the same initial hit with no wind, and then with a tail wind at 10 mph. Baseball statistics are universally done in US units, and we will follow suit here (http://en.wikipedia.org/wiki/United_States_customary_units). Note that the velocity of 110 mph is a typical exit speed for a baseball for a home run hit.

```
In [20]: from math import sqrt, exp, cos, sin, radians

         def mph_to_mps(x):
             return x * .447

         def drag_force(velocity):
             """ Returns the force on a baseball due to air drag at
             the specified velocity. Units are SI"""

             return (0.0039 + 0.0058 / (1. + exp((velocity-35.)/5.))) * velocity

         v = mph_to_mps(110.)
         y = 1
         x = 0
         dt = .1
         theta = radians(35)

         def solve(x, y, vel, v_wind, launch_angle):
             xs = []
             ys = []
             v_x = vel*cos(launch_angle)
```

```
    v_y = vel*sin(launch_angle)
    while y >= 0:
        # Euler equations for x and y
        x += v_x*dt
        y += v_y*dt

        # force due to air drag
        velocity = sqrt ((v_x-v_wind)**2 + v_y**2)
        F = drag_force(velocity)

        # euler's equations for vx and vy
        v_x = v_x - F*(v_x-v_wind)*dt
        v_y = v_y - 9.8*dt - F*v_y*dt

        xs.append(x)
        ys.append(y)

    return xs, ys

x,y = solve(x=0, y=1, vel=v, v_wind=0, launch_angle=theta)
p1 = plt.scatter(x, y, color='blue')

x,y = solve(x=0, y=1,vel=v, v_wind=mph_to_mps(10), launch_angle=theta)
p2 = plt.scatter(x, y, color='green', marker="v")
plt.legend([p1,p2], ['no wind', '10mph wind'])
plt.show()
```



We can easily see the difference between the trajectory in a vacuum and in the air. I used the same initial velocity and launch angle in the ball in a vacuum section above. We computed that the ball in a vacuum would travel over 240 meters (nearly 800 ft). In the air, the distance is just over 120 meters, or roughly 400 ft. 400ft is a realistic distance for a well hit home run ball, so we can be confident that our simulation is reasonably accurate.

Without further ado we will create a ball simulation that uses the math above to create a more realistic ball trajectory. I will note that the nonlinear behavior of drag means that there is no analytic solution to the ball position at any point in time, so we need to compute the position step-wise. I use Euler's method to propagate the solution; use of a more accurate technique such as Runge-Kutta is left as an exercise for the reader. That modest complication is unnecessary for what we are doing because the accuracy difference between the techniques will be small for the time steps we will be using.

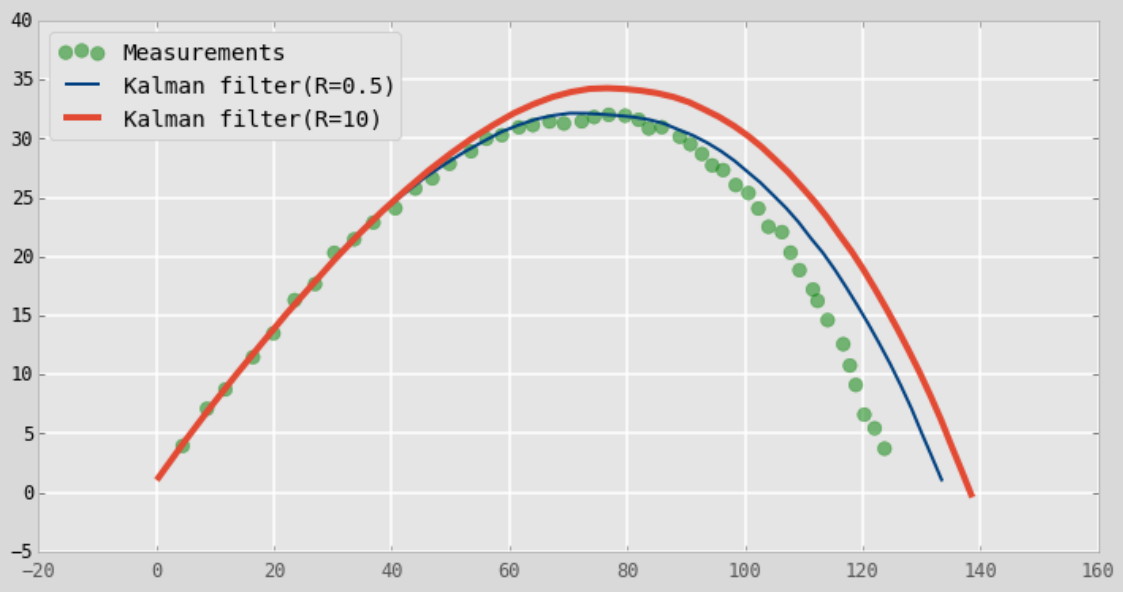
```
In [21]: from math import radians, sin, cos, sqrt, exp

         class BaseballPath(object):
             def __init__(self, x0, y0, launch_angle_deg, velocity_ms, noise=(1.0,1.0)):
                 """ Create 2D baseball path object
                    (x = distance from start point in ground plane, y=height above gro

                 x0,y0            initial position
                 launch_angle_deg angle ball is travelling respective to ground plane
                 velocity_ms      speeed of ball in meters/second
                 noise            amount of noise to add to each reported position in
                 """

                 omega = radians(launch_angle_deg)
                 self.v_x = velocity_ms * cos(omega)
                 self.v_y = velocity_ms * sin(omega)

                 self.x = x0
                 self.y = y0

                 self.noise = noise


             def drag_force (self, velocity):
                 """ Returns the force on a baseball due to air drag at
                 the specified velocity. Units are SI
                 """
                 B_m = 0.0039 + 0.0058 / (1. + exp((velocity-35.)/5.))
                 return B_m * velocity


             def update(self, dt, vel_wind=0.):
```

```
        """ compute the ball position based on the specified time step and
        wind velocity. Returns (x,y) position tuple.
        """

        # Euler equations for x and y
        self.x += self.v_x*dt
        self.y += self.v_y*dt

        # force due to air drag
        v_x_wind = self.v_x - vel_wind
        v = sqrt (v_x_wind**2 + self.v_y**2)
        F = self.drag_force(v)

        # Euler's equations for velocity
        self.v_x = self.v_x - F*v_x_wind*dt
        self.v_y = self.v_y - 9.81*dt - F*self.v_y*dt

        return (self.x + random.randn()*self.noise[0],
                self.y + random.randn()*self.noise[1])
```

Now we can test the Kalman filter against measurements created by this model.

In [22]:
```
y = 1.
x = 0.
theta = 35. # launch angle
v0 = 50.
dt = 1/10.    # time step

ball = BaseballPath(x0=x, y0=y, launch_angle_deg=theta, velocity_ms=v0, noise=[
f1 = ball_kf(x,y,theta,v0,dt,r=1.)
f2 = ball_kf(x,y,theta,v0,dt,r=10.)
t = 0
xs = []
ys = []
xs2 = []
ys2 = []

while f1.x[2,0] > 0:
    t += dt
    x,y = ball.update(dt)
    z = np.mat([[x,y]]).T

    f1.update(z)
    f2.update(z)
    xs.append(f1.x[0,0])
```

```
        ys.append(f1.x[2,0])
        xs2.append(f2.x[0,0])
        ys2.append(f2.x[2,0])
        f1.predict()
        f2.predict()

        p1 = plt.scatter(x, y, color='green', marker='o', s=75, alpha=0.5)

    p2, = plt.plot (xs, ys, lw=2)
    p3, = plt.plot (xs2, ys2, lw=4, c='#e24a33')
    plt.legend([p1,p2, p3],
               ['Measurements', 'Kalman filter(R=0.5)', 'Kalman filter(R=10)'],
               loc='best')
    plt.show()
```



I have plotted the output of two different Kalman filter settings. The measurements are depicted as green circles, a Kalman filter with R=0.5 as a thin blue line, and a Kalman filter with R=10 as a thick red line. These R values are chosen merely to show the effect of measurement noise on the output, they are not intended to imply a correct design.

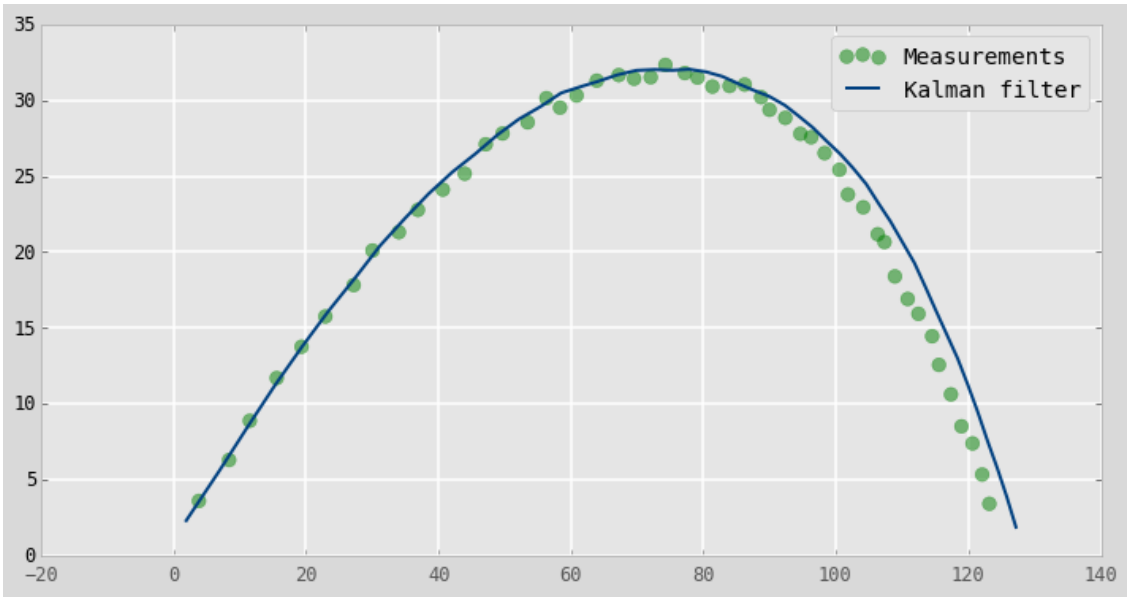
We can see that neither filter does very well. At first both track the measurements well, but as time continues they both diverge. This happens because the state model for air drag is nonlinear and the Kalman filter assumes that it is linear. If you recall our discussion about nonlinearity in the g-h filter chapter we showed why a g-h filter will always lag behind the acceleration of the system. We see the same thing here - the acceleration is negative, so the Kalman filter consistently overshoots the ball position. There is no way for the filter to catch up so long as the acceleration continues, so the filter will continue to diverge.

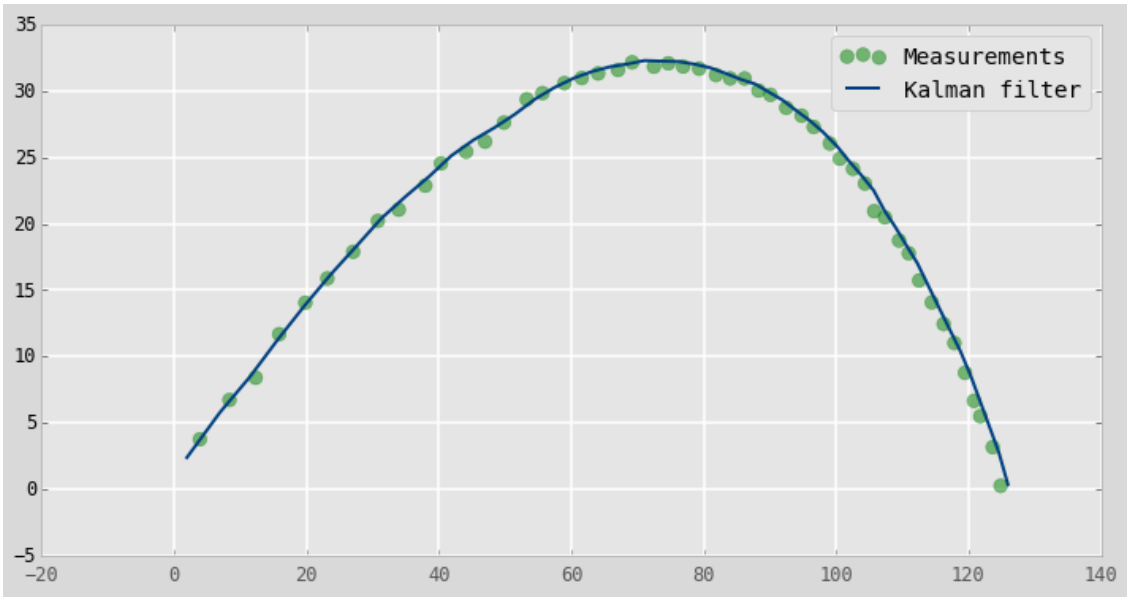
What can we do to improve this? The best approach is to perform the filtering with a nonlinear Kalman filter, and we will do this in subsequent chapters. However, there is also what I will call an 'engineering' solution to this problem as well. Our Kalman filter assumes that the ball is in a vacuum, and thus that there is no process noise. However, since the ball is in air the atmosphere imparts a force on the ball. We can think of this force as process noise. This is not a particularly rigorous thought; for one thing, this force is anything but Gaussian. Secondly, we can compute this force, so throwing our hands up and saying 'it's random' will not lead to an optimal solution. But let's see what happens if we follow this line of thought.

The following code implements the same Kalman filter as before, but with a non-zero process noise. I plot two examples, one with `Q=.1`, and one with `Q=0.01`.

```
In [23]: def plot_ball_with_q(q, r=1., noise=0.3):
             y = 1.
             x = 0.
             theta = 35. # launch angle
             v0 = 50.
             dt = 1/10.   # time step

             ball = BaseballPath(x0=x,
                                 y0=y,
                                 launch_angle_deg=theta,
                                 velocity_ms=v0,
                                 noise=[noise,noise])
             f1 = ball_kf(x,y,theta,v0,dt,r=r, q=q)
             t = 0
             xs = []
             ys = []

             while f1.x[2,0] > 0:
                 t += dt
                 x,y = ball.update(dt)
                 z = np.mat([[x,y]]).T

                 f1.update(z)
                 xs.append(f1.x[0,0])
                 ys.append(f1.x[2,0])
                 f1.predict()


                 p1 = plt.scatter(x, y, color='green', marker='o', s=75, alpha=0.5)

             p2, = plt.plot (xs, ys,lw=2)
             plt.legend([p1,p2], ['Measurements', 'Kalman filter'])
             plt.show()
```

```
plot_ball_with_q(0.01)
plot_ball_with_q(0.1)
```



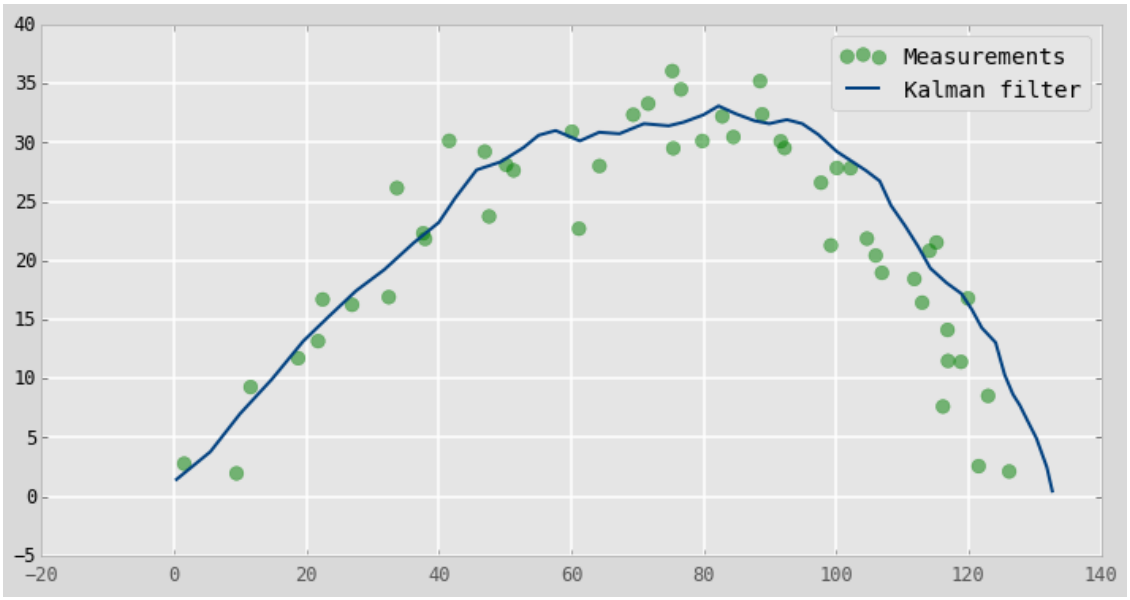


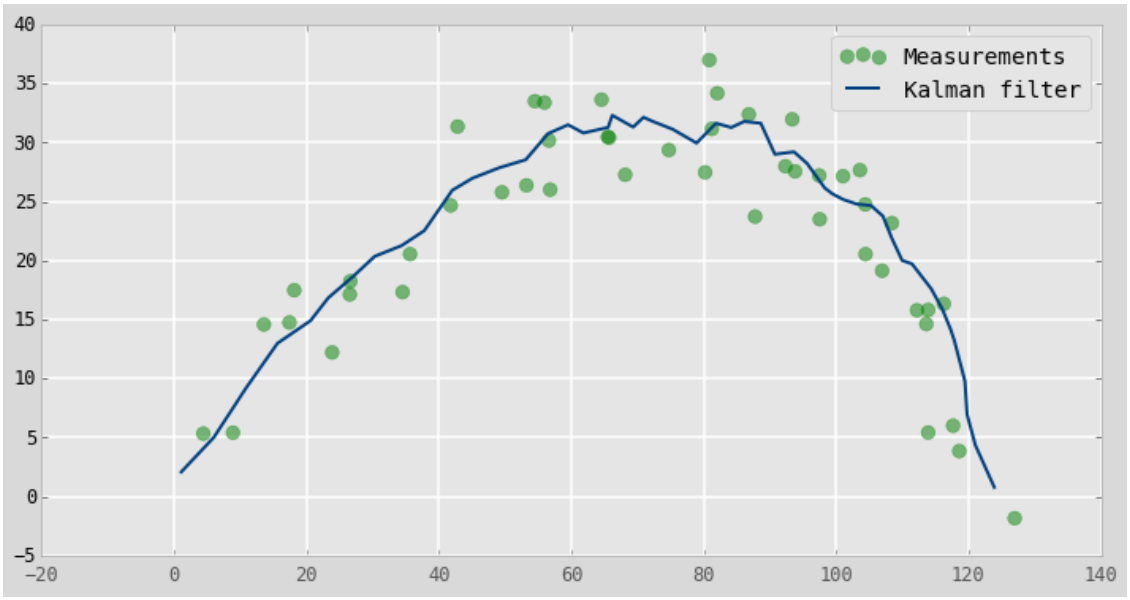
The second filter tracks the measurements fairly well. There appears to be a bit of lag, but very little.

Is this a good technique? Usually not, but it depends. Here the nonlinearity of the force on the ball is fairly constant and regular. Assume we are trying to track an automobile -

the accelerations will vary as the car changes speeds and turns. When we make the process noise higher than the actual noise in the system the filter will opt to weigh the measurements higher. If you don't have a lot of noise in your measurements this might work for you. However, consider this next plot where I have increased the noise in the measurements.

```
In [24]: plot_ball_with_q(0.01, r=3, noise=3.)
         plot_ball_with_q(0.1, r=3, noise=3.)
```





This output is terrible. The filter has no choise but to give more weight to the measurements than the process (prediction step), but when the measurements are noisy the filter output will just track the noise. This inherent limitation of the linear Kalman filter is what lead to the development of nonlinear versions of the filter.

With that said, it is certainly possible to use the process noise to deal with small nonlinearities in your system. This is part of the 'black art' of Kalman filters. Our model of the sensors and of the system are never perfect. Sensors are non-Gaussian and our process model is never perfect. You can mask some of this by setting the measurement errors and process errors higher than their theoretically correct values, but the trade off is a non-optimal solution. Certainly it is better to be non-optimal than to have your Kalman filter diverge. However, as we can see in the graphs above, it is easy for the output of the filter to be very bad. It is also very common to run many simulations and tests and to end up with a filter that performs very well under those conditions. Then, when you use the filter on real data the conditions are slightly different and the filter ends up performing terribly.

For now we will set this problem aside, as we are clearly misapplying the Kalman filter in this example. We will revisit this problem in subsequent chapters to see the effect of using various nonlinear techniques. In some domains you will be able to get away with using a linear Kalman filter for a nonlinear problem, but usually you will have to use one or more of the techniques you will learn in the rest of this book.

9.5.2 Tracking Noisy Data

If we are applying a Kalman filter to a thermometer in an oven in a factory then our task is done once the Kalman filter is designed. The data from the thermometer may be noisy, but there is never doubt that the thermometer is reading the temperature of *some other* oven. Contrast this to our current situation, where we are using computer vision to detect ball blobs from a video camera. For any frame we may detect or may not detect the ball, and we may have one or more spurious blobs - blobs not associated with the ball at all. This can occur because of limitations of the computer vision code, or due to foreign objects in the scene, such as a bird flying through the frame. Also, in the general case we may have no idea where the ball starts from. A ball may be picked up, carried, and thrown from any position, for example. A ball may be launched within view of the camera, or the initial launch might be off screen and the ball merely travels through the scene. There is the possibility of bounces and deflections - the ball can hit the ground and bounce, it can bounce off a wall, a person, or any other object in the scene.

Consider some of the problems that can occur. We could be waiting for a ball to appear, and a blob is detected. We initialize our Kalman filter with that blob, and look at the next frame to detect where the ball is going. Maybe there is no blob in the next frame. Can we conclude that the blob in the previous frame was noise? Or perhaps the blob was valid, but we did not detect the blob in this frame.

author's note: not sure if I want to cover this. If I do, not sure I want to cover this here.

Chapter 10

The Extended Kalman Filter

The Kalman filter that we have developed to this point is extremely good, but it is also limited. Its derivation is in the linear space, and hence it only works for linear problems. Let's be a bit more rigorous here. You can, and we have in this book, apply the Kalman filter to nonlinear problems. For example, in the g-h filter chapter we explored using a g-h filter in a problem with constant acceleration. It 'worked', in that it remained numerically stable and the filtered output did track the input, but there was always a lag. It is easy to prove that there will always be a lag when $\ddot{\mathbf{x}} > 0$. The filter no longer produces an optimal result. If we make our time step arbitrarily small we can still handle many problems, but typically we are using Kalman filters with physical sensors and solving real-time problems. Either fast enough sensors do not exist, are prohibitively expensive, or the computation time required is excessive. It is not a workable solution.

The early adopters of Kalman filters were the radar people, and this fact was not lost on them. Radar is inherently nonlinear. Radars measure the slant range to an object, and we are typically interested in the aircraft's position over the ground. We invoke Pythagoras and get the nonlinear equation:

$$x = \sqrt{slant^2 - altitude^2}$$

So shortly after the Kalman filter was enthusiastically taken up by the radar industry people began working on how to extend the Kalman filter into nonlinear problems. It is still an area of ongoing research, and in the Unscented Kalman filter chapter we will implement a powerful, recent result of that research. But in this chapter we will cover the most common form, the Extended Kalman filter, or EKF. Today, most real world "Kalman filters" are actually EKFs. The Kalman filter in your car's and phone's GPS is an EKF, for example.

10.1 The Problem with Nonlinearity

You may not realize it, but the only math you really know how to do is linear math. Equations of the form

$$A\mathbf{x} = \mathbf{b}$$

.

That may strike you as hyperbole. After all, in this book we have integrated a polynomial to get distance from velocity and time: We know how to integrate a polynomial, for example, and so we are able to find the closed form equation for distance given velocity and time:

$$\int (vt + v_0)\, dt = \frac{a}{2}t^2 + v_0 t + d_0$$

That's nonlinear. But it is also a very special form. You spent a lot of time, probably at least a year, learning how to integrate various terms, and you still can not integrate some arbitrary equation - no one can. We don't know how. If you took freshman Physics you perhaps remember homework involving sliding frictionless blocks on a plane and other toy problems. At the end of the course you were almost entirely unequipped to solve real world problems because the real world is nonlinear, and you were taught linear, closed forms of equations. It made the math tractable, but mostly useless.

The mathematics of the Kalman filter is beautiful in part due to the Gaussian equation being so special. It is nonlinear, but when we add and multipy it using linear algebra we get another Gaussian equation as a result. That is very rare. $\sin x * \sin y$ does not yield a $\sin(\cdot)$ as an output.

If you are not well versed in signals and systems there is a perhaps startling fact that you should be aware of. A linear system is defined as a system whose output is linearly proportional to the sum of all its inputs. A consequence of this is that to be linear if the input is zero than the output must also be zero. Consider an audio amp - if a sing into a microphone, and you start talking, the output should be the sum of our voices (input) scaled by the amplifier gain. But if amplifier outputs a nonzero signal for a zero input the additive relationship no longer holds. This is because you can say $amp(roger) = amp(roger + 0)$ This clearly should give the same output, but if amp(0) is nonzero, then

$$\begin{aligned} amp(roger) &= amp(roger + 0) \\ &= amp(roger) + amp(0) \\ &= amp(roger) + non\_zero\_value \end{aligned}$$

which is clearly nonsense. Hence, an apparently linear equation such as

$$L(f(t)) = f(t) + 1$$

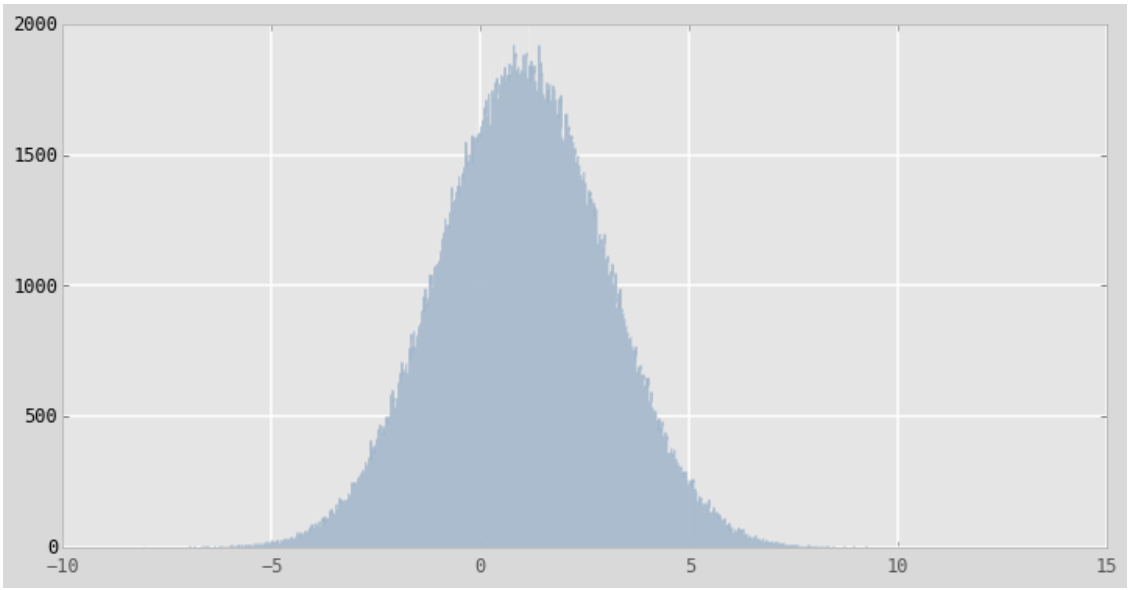
is not linear because $L(0) = 1$! Be careful!

10.2 The Effect of Nonlinear Transfer Functions on Gaussians

Unfortunately Gaussians are not closed under an arbitrary nonlinear function. Recall the equations of the Kalman filter - at each step of its evolution we do things like pass the covariances through our process function to get the new covariance at time k. Our process function was always linear, so the output was always another Gaussian. Let's look at that on a graph. I will take an arbitrary Gaussian and pass it through the function $f(x) = 2x + 1$

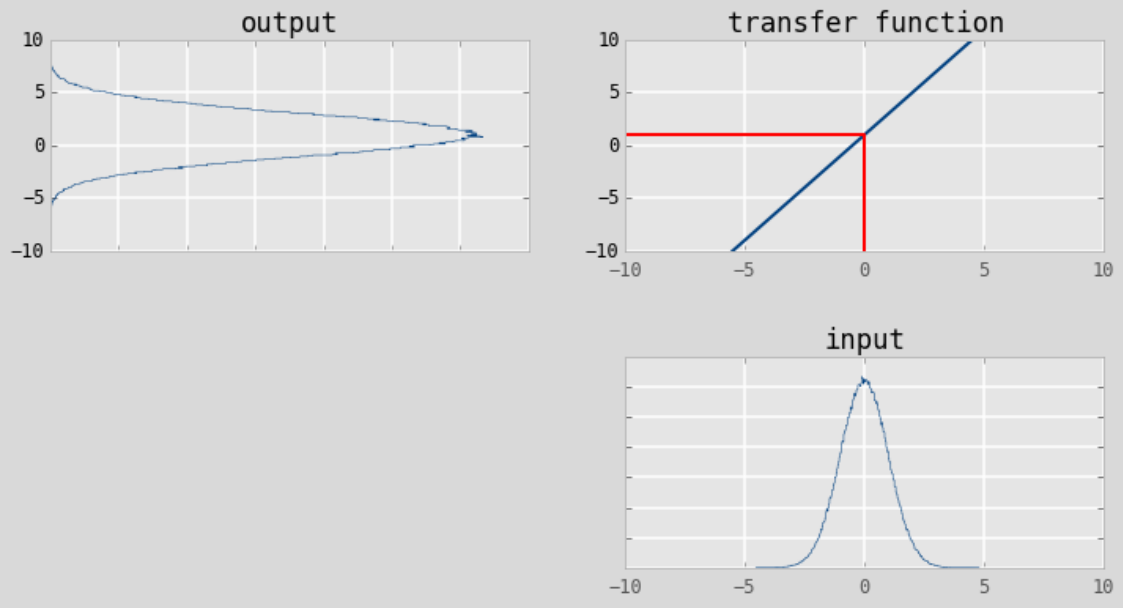
and plot the result. We know how to do this analytically, but lets do this with sampling. I will generate 500,000 points on the Gaussian curve, pass it through the function, and then plot the results. I will do it this way because the next example will be nonlinear, and we will have no way to compute this analytically.

```
In [2]: import numpy as np
        from numpy.random import normal

        data = normal(loc=0.0, scale=1, size=500000)
        ys = 2*data + 1

        plt.hist(ys,1000)
        plt.show()
```



This is an unsuprising result. The result of passing the Gaussian through $f(x) = 2x + 1$ is another Gaussian centered around 1. Let's look at the input, transfer function, and output at once.

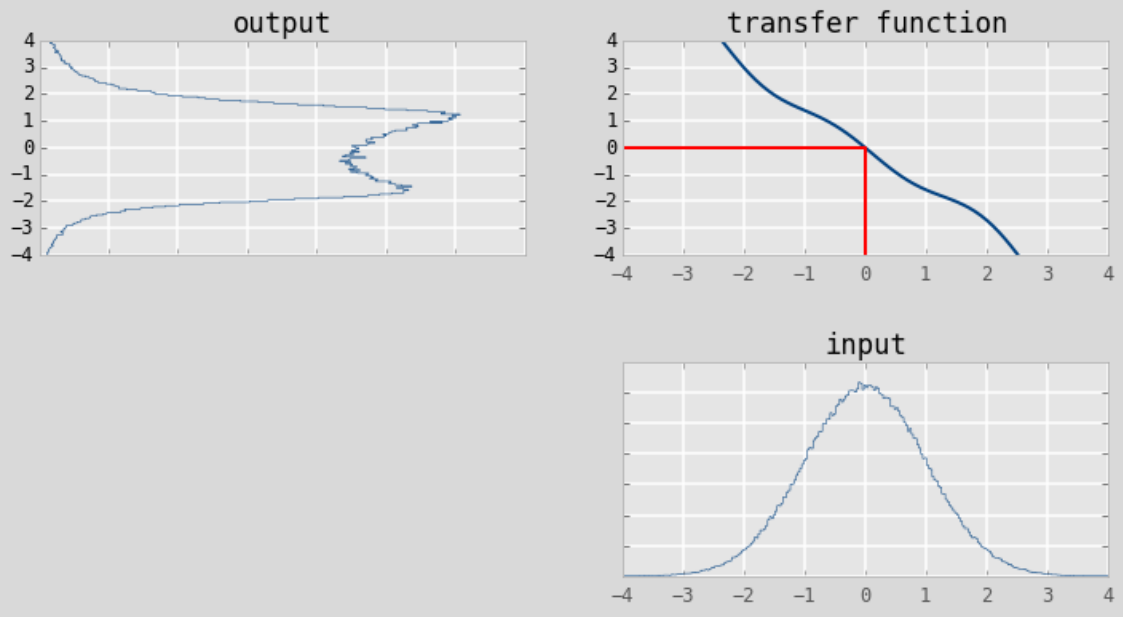
```
In [3]: from nonlinear_plots import plot_transfer_func

        def g(x):
            return 2*x+1

        plot_transfer_func (data, g, lims=(-10,10), num_bins=300)
```



The plot labelled 'input' is the histogram of the original data. This is passed through the transfer function $f(x) = 2x + 1$ which is displayed in the chart to the upper right. The red lines shows how one value, $x = 0$ is passed through the function. Each value from input is passed through in the same way to the output function on the left. The output looks like a Gaussian, and is in fact a Gaussian. We can see that it is altered -the variance in the output is larger than the variance in the input, and the mean has been shifted from 0 to 1, which is what we would expect given the transfer function $f(x) = 2x + 1$ The $2x$ affects the variance, and the $+1$ shifts the mean.

Now let's look at a nonlinear function and see how it affects the probability distribution.

```
In [4]: from nonlinear_plots import plot_transfer_func

        def g(x):
            return (np.cos(4*(x/2+0.7)))*np.sin(0.3*x)-1.6*x

        plot_transfer_func (data, g, lims=(-4,4), num_bins=300)
```



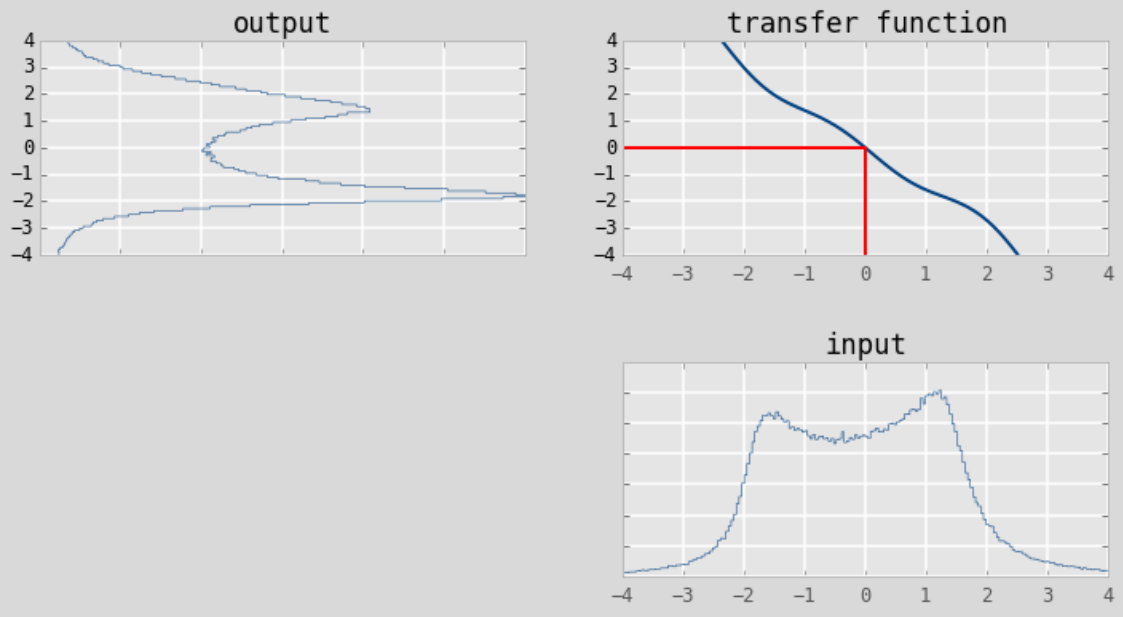
This result may be somewhat suprising to you. The transfer function looks "fairly" linear - it is pretty close to a straight line, but the probability distribution of the output is completely different from a Gaussian. Recall the equations for multiplying two univariate Gaussians:

$$\mu = \frac{\sigma_1^2\mu_2 + \sigma_2^2\mu_1}{\sigma_1^2 + \sigma_2^2}, \sigma = \frac{1}{\frac{1}{\sigma_1^2} + \frac{1}{\sigma_2^2}}$$

These equations do not hold for non-Gaussians, and certainly do not hold for the probability distribution shown in the 'output' chart above.

Think of what this implies for the Kalman filter algorithm of the previous chapter. All of the equations assume that a Gaussian passed through the process function results in another Gaussian. If this is not true then all of the assumptions and guarantees of the Kalman filter do not hold. Let's look at what happens when we pass the output back through the function again, simulating the next step time step of the Kalman filter.

```
In [5]: y=g(data)
        plot_transfer_func (y, g, lims=(-4,4), num_bins=300)
```



As you can see the probability function is futher distorted from the original Gaussian. However, the graph is still somewhat symmetric around 0, let's see what the mean is.

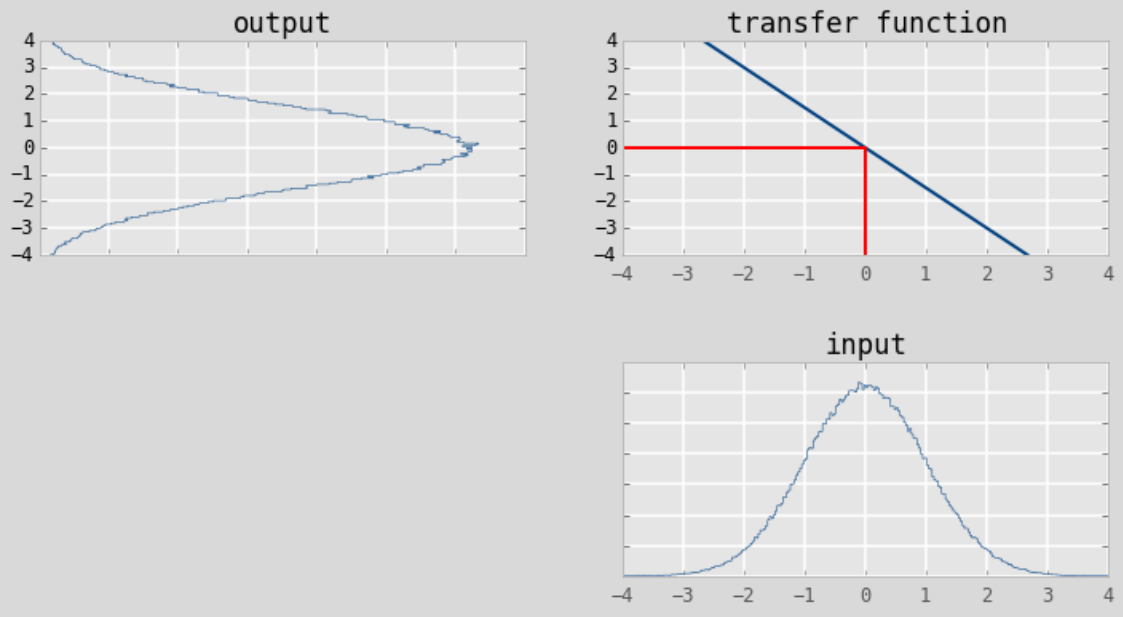
```
In [6]: print ('input  mean, variance: %.4f, %.4f'% (np.average(data), np.std(data)**2))
        print ('output mean, variance: %.4f, %.4f'% (np.average(y), np.std(y)**2))
```

```
input  mean, variance: 0.0006, 1.0019
output mean, variance: -0.0286, 2.2455
```

Let's compare that to the linear function that passes through (-2,3) and (2,-3), which is very close to the nonlinear function we have plotted. Using the equation of a line we have

$$m = \frac{-3-3}{2-(-2)} = -1.5$$

```
In [7]: def h(x): return -1.5*x
        plot_transfer_func (data, h, lims=(-4,4), num_bins=300)
        out = h(data)
        print ('output mean, variance: %.4f, %.4f'% (np.average(out), np.std(out)**2))
```




```
output mean, variance: -0.0009, 2.2544
```

Although the shapes of the output are very different, the mean and variance of each are almost the same. This may lead us to reasoning that perhaps we can ignore this problem if the nonlinear equation is 'close to' linear. To test that, we can iterate several times and then compare the results.

```
In [8]: out = h(data)
        out2 = g(data)

        for i in range(10):
            out = h(out)
            out2 = g(out2)
        print ('linear    output mean, variance: %.4f, %.4f'% (np.average(out), np.std(o
        print ('nonlinear output mean, variance: %.4f, %.4f'% (np.average(out2), np.std(
```

```
linear    output mean, variance: -0.0532, 7496.3696
nonlinear output mean, variance: -1.9719, 26248.5350
```

Unfortunately we can see that the nonlinear version is not stable. We have drifted significantly from the mean of 0, and the variance is half an order of magnitude larger.

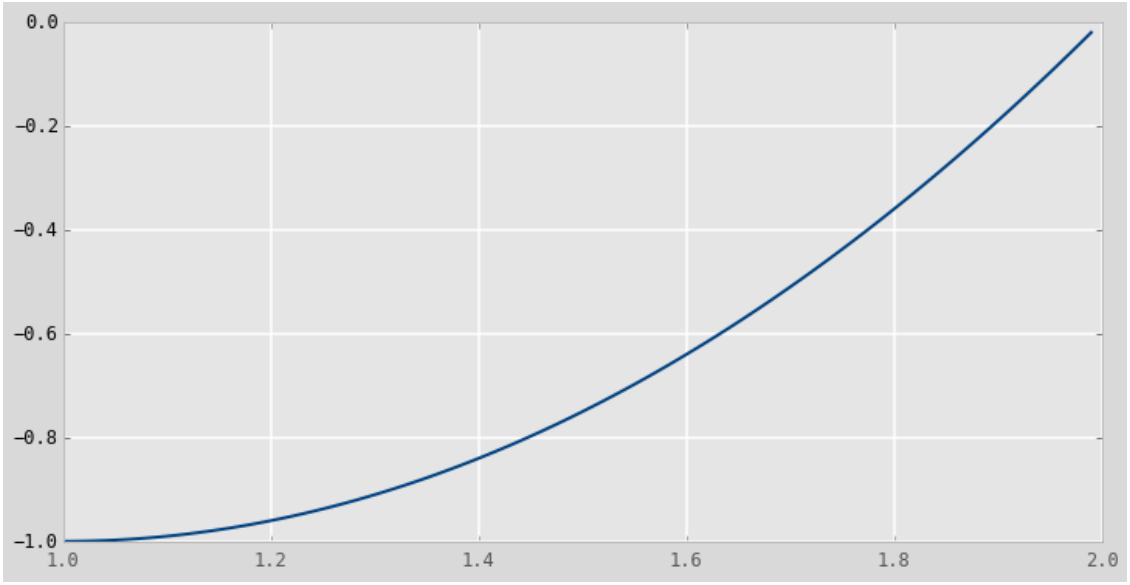
10.3 The Extended Kalman Filter

The extended Kalman filter (EKF) works by linearizing the system model at each update. For example, consider the problem of tracking a cannonball in flight. Obviously it follows

a curved flight path. However, if our update rate is small enough, say 1/10 second, then the trajectory over that time is nearly linear. If we linearize that short segment we will get an answer very close to the actual value, and we can use that value to perform the prediction step of the filter. There are many ways to linearize a set of nonlinear differential equations, and the topic is somewhat beyond the scope of this book. In practice, a Taylor series approximation is frequently used with EKFs, and that is what we will use.

Consider the function $f(x) = x^2 - 2x$, which we have plotted below.

```
In [9]: xs =  np.arange(0,2,0.01)
        ys = [x**2 - 2*x for x in xs]
        plt.plot (xs, ys)
        plt.xlim(1,2)
        plt.show()
```

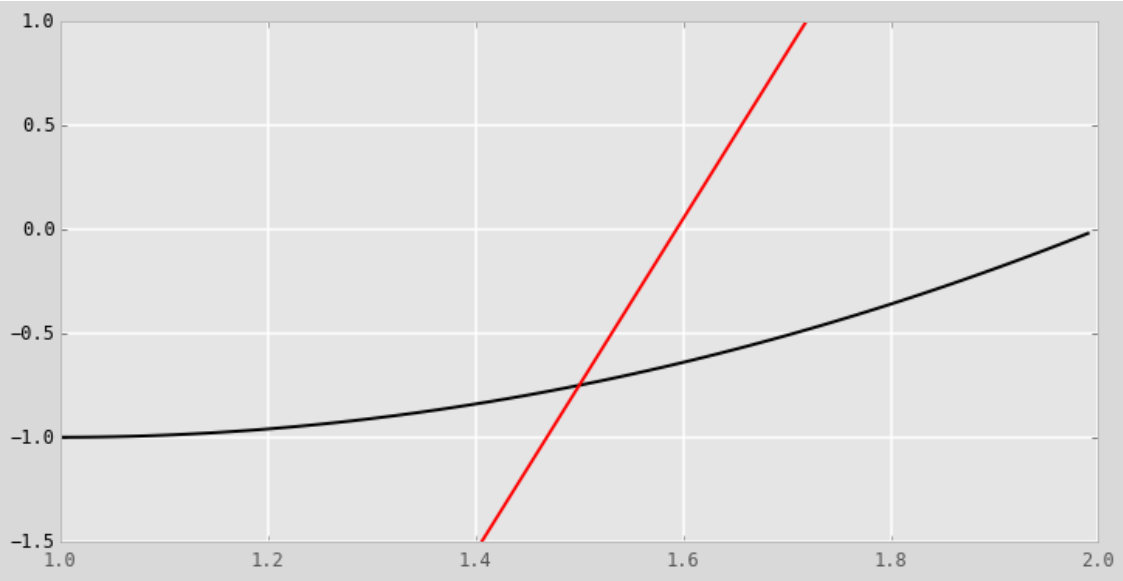


We want a linear appoximation of this function so that we can use it in the Kalman filter. We will see how it is used in the Kalman filter in the next section, so don't worry about that yet. We can see that there is no single linear function (line) that gives a close approximation of this function. However, during each innovation of the Kalman filter we know it's current state, so if we linearize the function at that value we will have a close approximation. For example, suppose our current state is $x = 1.5$. What would be a good linearization for this function?

We can use any linear function that passes through the curve at (1.5,-0.75). For example, consider using f(x)=8x−12.75 as the linearization, as in the plot below.

```
In [10]: def y(x):
             return 8*x - 12.75
         plt.plot (xs, ys,c='k')
```

```
plt.plot ([1.25, 1.75], [y(1.25), y(1.75)], c='r')
plt.xlim(1,2)
plt.ylim([-1.5, 1])
plt.show()
```



This is not a good linearization for $f(x)$. It is exact for $x = 1.5$, but quickly diverges when x varies by a small amount.

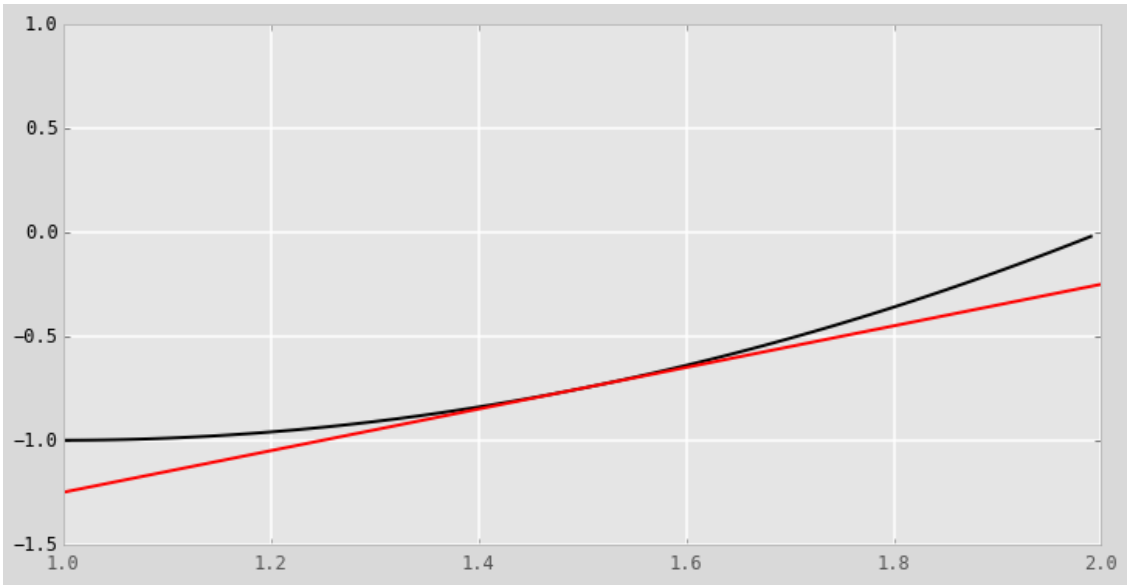
A much better approach is to use the slope of the function at the evaluation point as the linearization. We find the slope by taking the first derivative of the function:

$$f(x) = x^2 - 2x \frac{df}{dx} = 2x - 2$$

,

so the slope at 1.5 is $2 * 1.5 - 2 = 1$. Let's plot that.

```
In [11]: def y(x):
             return x - 2.25

         plt.plot (xs, ys,c='k')
         plt.plot ([1,2], [y(1),y(2)], c='r')
         plt.xlim(1,2)
         plt.ylim([-1.5, 1])
         plt.show()
```



Here we can see that this linearization is much better. It is still exactly correct at $x = 1.5$, but the errors are very small as x varies. Compare the tiny error at $x = 1.4$ vs the very large error at $x = 1.4$ in the previous plot. This does not constitute a formal proof of correctness, but this sort of geometric depiction should be fairly convincing. Certainly it is easy to see that in this case if the line had any other slope the errors would accumulate more quickly.

To implement the extended Kalman filter we will leave the linear equations as they are, and use partial derivatives to evaluate the system matrix **F** and the measurement matrix **H** at the state at time t ($\mathbf{x}_t$). Since **F** also depends on the control input vector **u**m we will need to include that term:

$$F \equiv \left.\frac{\partial f}{\partial x}\right|_{x_t, u_t}$$
$$H \equiv \left.\frac{\partial h}{\partial x}\right|_{x_t}$$

All this means is that at each update step we compute **F** as the partial derivative of our function $f()$ evaluated at x.

We approximate the state transition function **F** by using the Taylor-series expansion

** orphan text This approach has many issues. First, of course, is the fact that the linearization does not produce an exact answer. More importantly, we are not linearizing the actual path, but our filter's estimation of the path. We linearize the estimation because it is statistically likely to be correct; but of course it is not required to be. So if the filter's output is bad that will cause us to linearize an incorrect estimate, which will almost certainly lead to an even worse estimate. In these cases the filter will quickly diverge. This is where the 'black art' of Kalman filter comes in. We are trying to linearize an estimate, and there is no guarantee that the filter will be stable. A vast amount of the literature on Kalman filters is devoted to this problem. Another issue is that we need to linearize the system using

analytic methods. It may be difficult or impossible to find an analytic solution to some problems. In other cases we may be able to find the linearization, but the computation is very expensive. **

In the next chapter we will spend a lot of time on a new development, the unscented Kalman filter(UKF) which avoids many of these problems. I think that as it becomes better known it will supplant the EKF in most applications, though that is still an open question. Certainly research has shown that the UKF performs at least as well as, and often much better than the EKF.

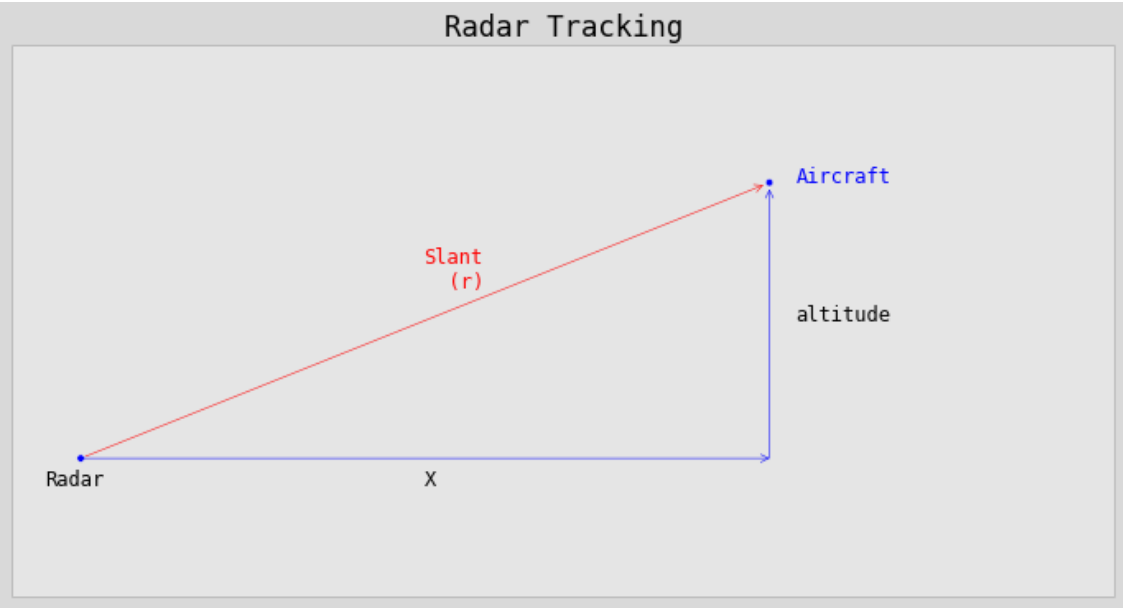
I think the easiest way to understand the EKF is to just start off with an example. Perhaps the reason for some of my mathmatical choices will not be clear, but trust that the end result will be an EKF.

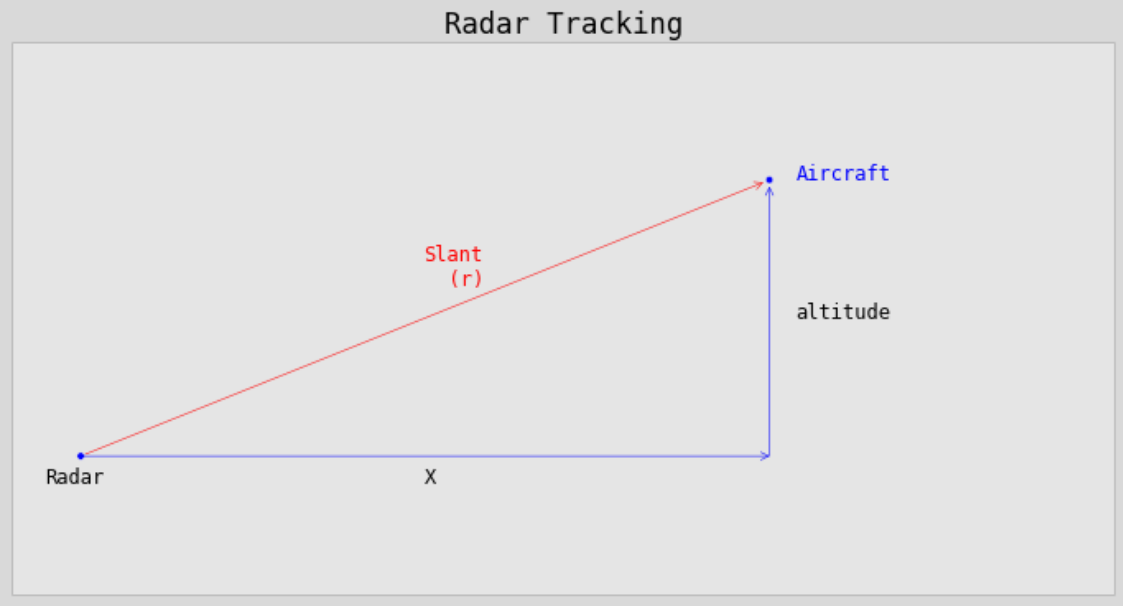
10.3.1 Example: Tracking a Flying Airplane

We will start by simulating tracking an airplane by using ground based radar. Radars work by emitting a beam of radio waves and scanning for a return bounce. Anything in the beam's path will reflects some of the signal back to the radar. By timing how long it takes for the reflected signal to get back to the radar the system can compute the *slant distance* - the straight line distance from the radar installation to the object.

For this example we want to take the slant range measurement from the radar and compute the horizontal position (distance of aircraft from the radar measured over the ground) and altitude of the aircraft, as in the diagram below.

```
In [12]: import ekf_internal
         ekf_internal.show_radar_chart()
```





As discussed in the introduction, our measurement model is the nonlinear function $x = \sqrt{slant^2 - altitude^2}$. Therefore we will need a nonlinear

Predict step:

Linear	**Nonlinear**
$x = Fx$	$x = \underline{f(x)}$
$P = FPF^T + Q$	$P = \overline{FP}F^T + Q$

Update step:

Linear	**Nonlinear**
$K = PH^T(HPH^T + R)^{-1}$	$K = PH^T(HPH^T + R)^{-1}$
$x = x + K(z - Hx)$	$x = x + K(z - \underline{h(x)})$
$P = P(I - KH)$	$P = P(I - KH)$

As we can see there are two minor changes to the Kalman filter equations. The first change replaces the equation $\mathbf{x} = \mathbf{Fx}$ with $\mathbf{x} = f(\mathbf{x})$. In the Kalman filter, $\mathbf{Fx}$ is how we compute the new state based on the old state. However, in a nonlinear system we cannot use linear algebra to compute this transition. So instead we hypothesize a nonlinear function $f()$ which performs this function. Likewise, in the Kalman filter we convert the state to a measurement with the linear function $\mathbf{Hx}$. For the extended Kalman filter we replace this with a nonlinear function $h()$, giving $\mathbf{z}_x = h(\mathbf{x})$.

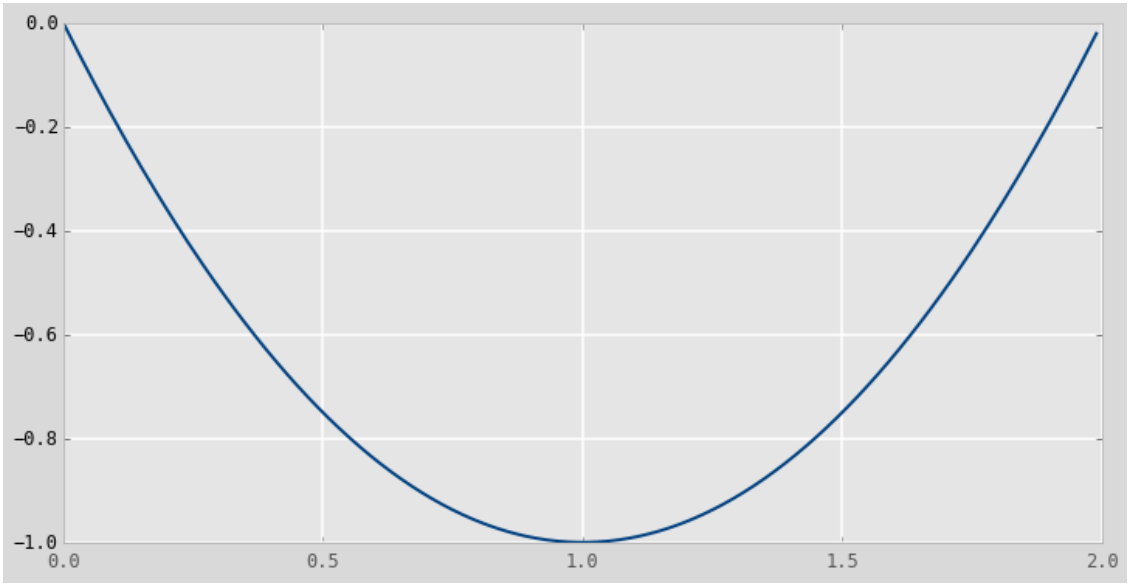
The only question left is how do we implement use $f()$ and $h()$ in the Kalman filter if they are nonlinear? We reach for the single tool that we have available for solving nonlinear equations - we linearize them at the point we want to evaluate the system. For example, consider the function $f(x) = x^2 - 2x$

The rest of the equations are unchanged, so $f()$ and $h()$ must produce a matrix that approximates the values of the matrices $\mathbf{F}$ and $\mathbf{H}$ at the current value for $\mathbf{x}$. We do this by computing the partial derivatives of the state and measurements functions:

$$F \equiv \left.\frac{\partial f}{\partial x}\right|_x, H \equiv \left.\frac{\partial h}{\partial x}\right|_x$$

All this means is that at each update step we compute F as the partial derivative of our function $f()$ evaluated at the point of f.

```
In [13]: xs =  np.arange(0,2,0.01)
         ys = [x**2 - 2*x for x in xs]
         plt.plot (xs, ys)
         plt.show()
```



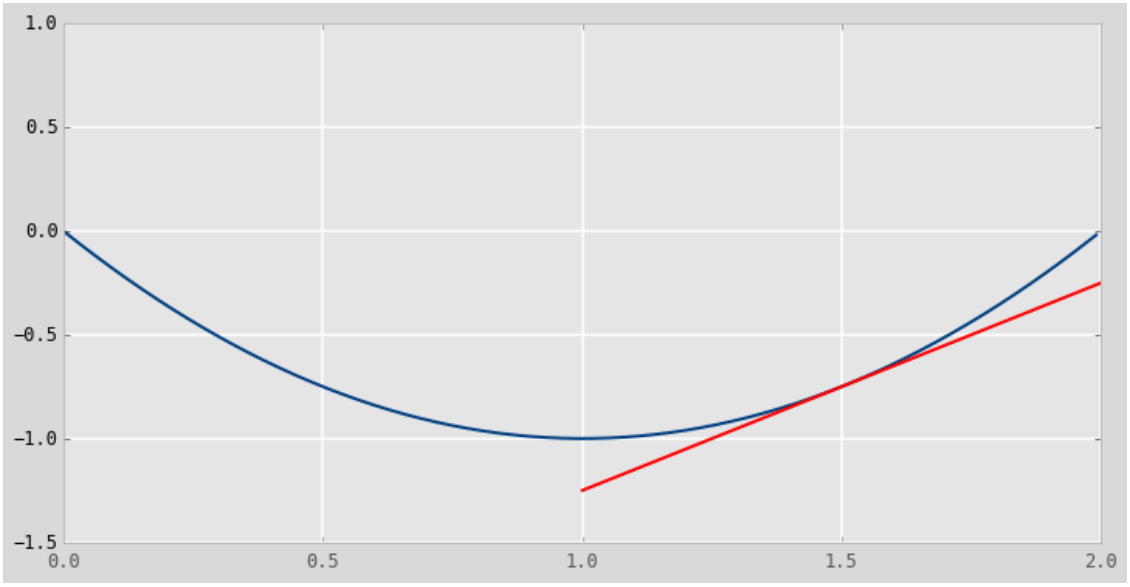
Suppose we want to linearlize this equation so we can evaluate it's value at 1.5. In other words, we want to create a linear function of the form $y_l(x) = ax + b$ such that $y_l(1.5)$ gives the same value as $y(1.5)$. Obviously there is not single linear equation that will do this. But if we linearize $y(x)$ at 1.5, then we will have a perfect answer for $y_l(1.5)$, and a progressively worse answer as our evaluation point gets further away from 1.5.

The simplest way to linearize a function is to take a partial derivative of it. In geometic terms, the derivative of a function at a point is just the slope of the function. Let's just look at that, and then reason about why this is a good choice.

The derivative of $f(x) = x^2 - 2x$ is $\frac{\partial f}{\partial x} = 2x - 2$, so the slope at 1.5 is $2 * 1.5 - 2 = 1$. Let's plot that.

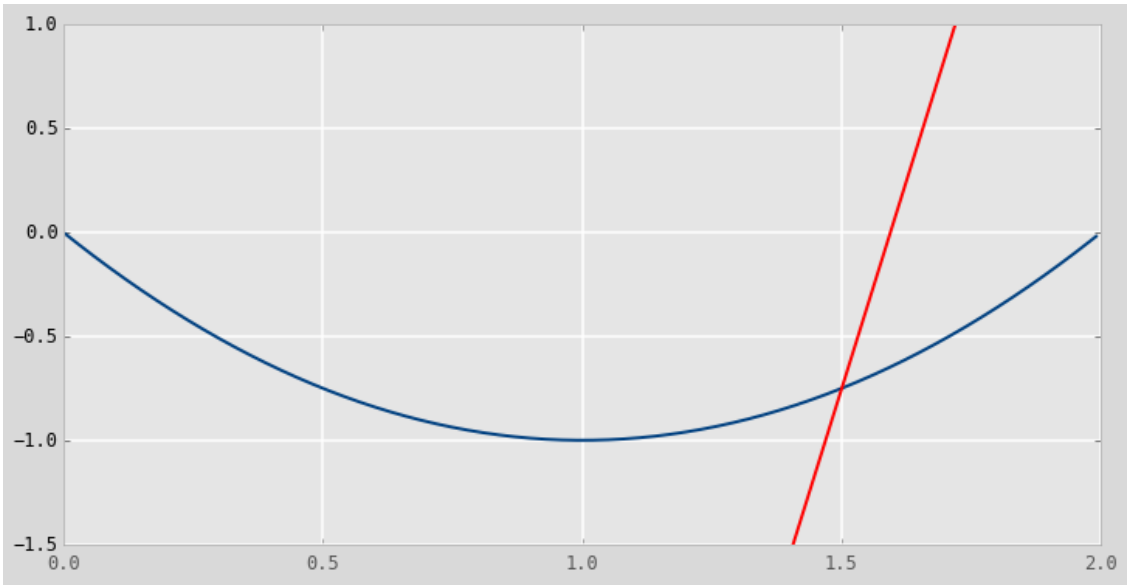
```
In [14]: def y(x):
             return x - 2.25

         plt.plot (xs, ys)
         plt.plot ([1,2], [y(1),y(2)], c='r')
```

```
        plt.ylim([-1.5, 1])

        plt.show()
```



This is a nice visual demonstration of how the slope of the function gives the ideal linear approximation of the function near a point. We could use any linear function such that $f(1.5) = -0.75$, here, but as x varies the value computed by the function would potentially be very far from the functions value. For example, consider using $f(x) = 8x - 12.75$ as the linearization, as in the plot below.

```
In [15]: def y(x):
             return 8*x - 12.75
         plt.plot (xs, ys)
         plt.plot ([1.25, 1.75], [y(1.25), y(1.75)], c='r')
         plt.ylim([-1.5, 1])
         plt.show()
```



We can see that the linearization is exactly correct for $x = 1.5$, but very quickly diverges as x varies from 1.5. This does not constitute a proof that taking the derivative is a good linearization, but it should be fairly convincing.

We will begin by writing a simulation for the radar.

```
In [16]: import random
         import math

         class Radar(object):
             def __init__(self, pos, vel, alt, dt):
                 self.pos = pos
                 self.vel = vel
                 self.alt = alt
                 self.dt = dt

             def get(self):
                 """ Simulate radar range to object at 1K altidue and moving at 100m/s
                 Adds about 5% measurement noise. Returns slant range to the object.
                 Call once for each new measurement at dt time from last call.
                 """

                 # add some process noise to the system
                 vel = self.vel  + 5*random.gauss(0,1)
                 alt = self.alt + 10*random.gauss(0,1)
                 self.pos = self.pos + vel*self.dt

                 # add measurment noise
```

```
err = self.pos * 0.05*random.gauss(0,1)
return math.sqrt(self.pos**2 + alt**2) + err
```

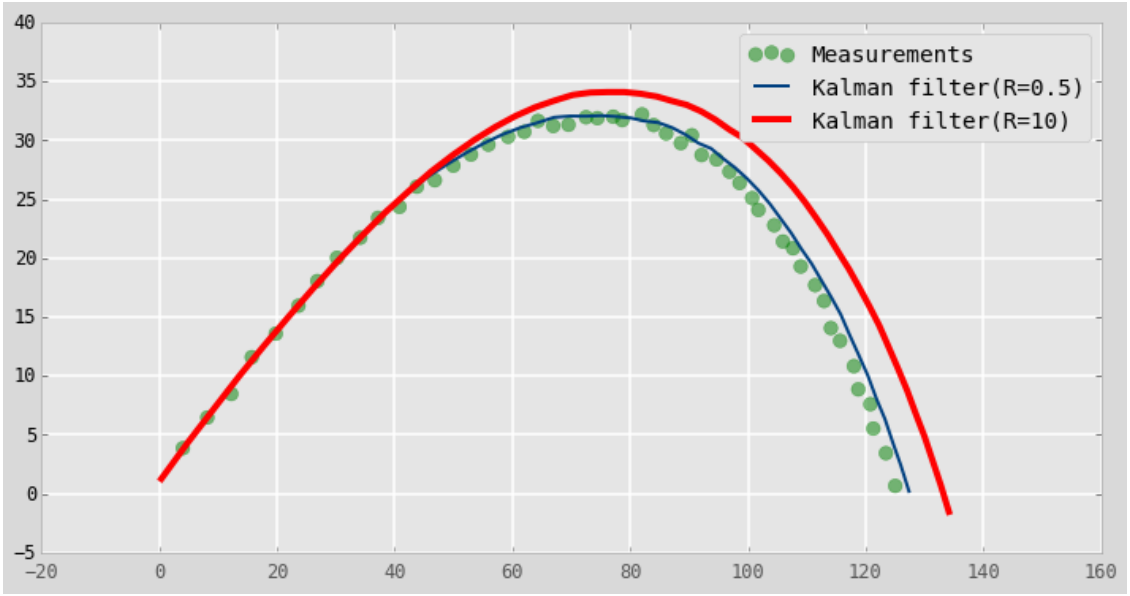
$$F = I + \begin{bmatrix} 0 & 1 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} dt$$

$$\begin{aligned} H &= \begin{bmatrix} \frac{\partial h}{\partial x_{pos}} & \frac{\partial h}{\partial x_{vel}} & \frac{\partial h}{\partial x_{alt}} \end{bmatrix} \\ &= \begin{bmatrix} \frac{x_{pos}}{\sqrt{x_{pos}^2 + x_{alt}^2}} & 0 & \frac{x_{alt}}{\sqrt{x_{pos}^2 + x_{alt}^2}} \end{bmatrix} \end{aligned}$$

10.3.2 Example: A falling Ball

In the **Designing Kalman Filters** chapter I first considered tracking a ball in a vacuum, and then in the atmosphere. The Kalman filter performed very well for vacuum, but diverged from the ball's path in the atmosphere. Let us look at the output; to avoid littering this chapter with code from that chapter I have placed it all in the file 'ekf_internal.py'.

```
In [17]: import ekf_internal
         ekf_internal.plot_ball()
```



We can artifically force the Kalman filter to track the ball by making Q large. That would cause the filter to mistrust its prediction, and scale the kalman gain K to strongly favor the measurments. However, this is not a valid approach. If the Kalman filter is correctly predicting the process we should not 'lie' to the filter by telling it there are process errors that do not exist. We may get away with that for some problems, in some conditions, but in general the Kalman filter's performance will be substandard.

Recall from the **Designing Kalman Filters** chapter that the acceleration is

$$a_x = (0.0039 + \frac{0.0058}{1 + \exp\left[(v-35)/5\right]}) * v * v_x a_y = (0.0039 + \frac{0.0058}{1 + \exp\left[(v-35)/5\right]}) * v * v_y - g$$

These equations will be very unpleasant to work with while we develop this subject, so for now I will retreat to a simpler one dimensional problem using this simplified equation for acceleration that does not take the nonlinearity of the drag coefficient into account:

$$\ddot{x} = \frac{0.0034ge^{-x/20000}\dot{x}^2}{2\beta} - g$$

Here β is the ballistic coefficient, where a high number indicates a low drag.

In [17]:

Chapter 11

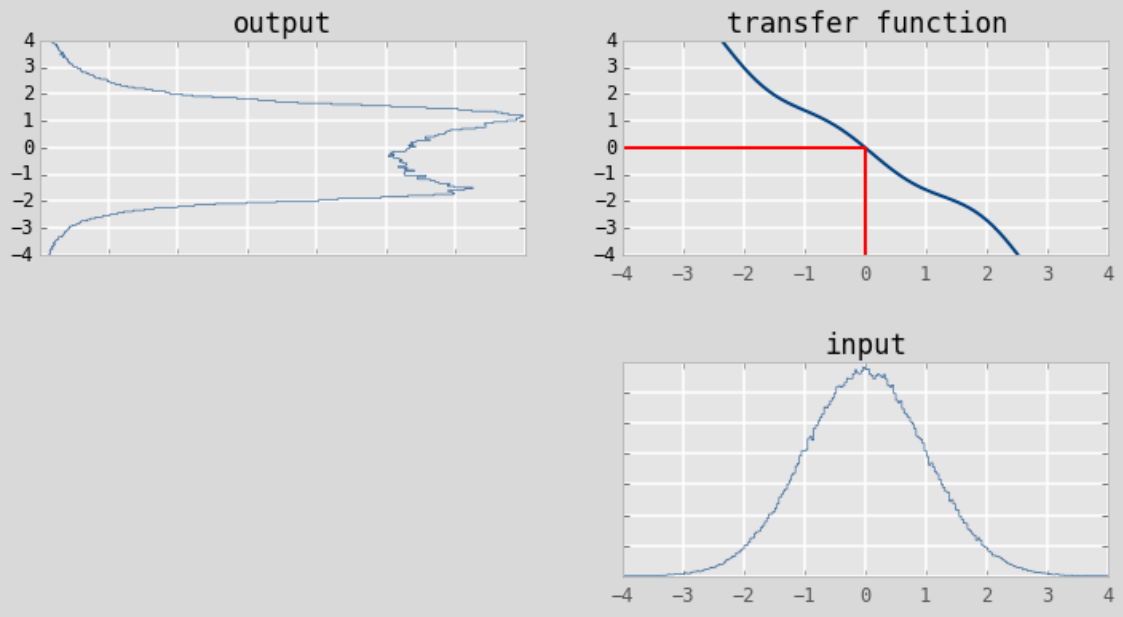
Unscented Kalman Filters

In the previous chapter we developed the Extended Kalman Filter to allow us to use the Kalman filter with nonlinear problems. It is by far the most commonly used Kalman filter. However, it requires that you be able to analytically derive the Jacobian blah blah limp prose.

However, for many problems finding the Jacobian is either very difficult or impossible. Furthermore, being an approximation, the EKF can diverge. For all these reasons there is a need for a different way to approximate the Gaussian being passed through a nonlinear transfer function. In the last chapter I showed you this plot:

author's note - need to add calculation of mean/var to the output.

```
In [2]: from nonlinear_plots import plot_transfer_func
        from numpy.random import normal
        import numpy as np

        data = normal(loc=0.0, scale=1, size=500000)

        def g(x):
            return (np.cos(4*(x/2+0.7)))*np.sin(0.3*x)-1.6*x

        plot_transfer_func (data, g, lims=(-4,4), num_bins=300)
```



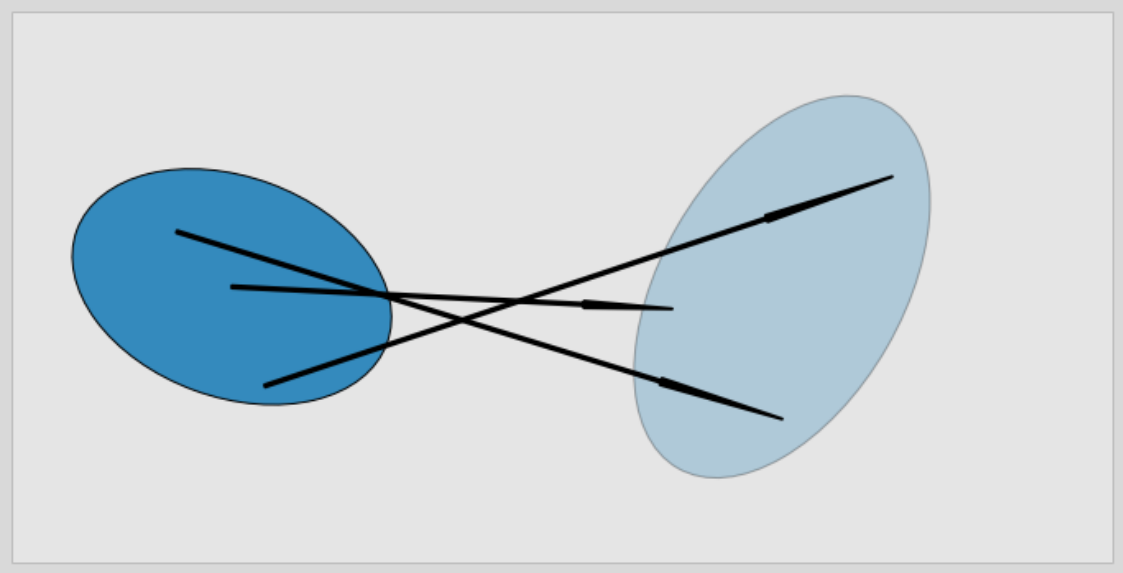
I generated this by taking 500,000 samples from the input, passing it through the nonlinear transform, and building a histogram of the result. From that histogram we can then compute a mean and a variance that we compared to the output of the EKF.

It has perhaps occurred to you that this sampling process constitutes a solution to our problem. This is called a 'monte carlo' approach, and it used by some Kalman filter designs, such as the *Ensemble filter*. Sampling requires no specialized knowledge programming, and does not require a closed form solution. No matter how nonlinear or poorly behaved the transfer function is, as long as we sample with enough points we will build an accurate output distribution.

"Enough points" is the rub. The graph above was created with 500,000 points, and the output is still not smooth. You wouldn't need to use that many points to get a reasonable estimate of the mean and variance, but it will require many points. What's worse, this is only for 1 dimension. In general, the number of points required increases by the power of the number of dimensions. If you need 50 points for 1 dimension, you need 50^2 for two dimensions, 50^3 for three dimensions, and so on. So while this approach does work, it is very computationally expensive. The Unscented Kalman filter uses a somewhat similar technique but reduces the amount of computation needed by a drastic amount.

It is somewhat hard to understand some aspects of this problem by looking at the histogram, so consider this alternative representation, this time for 2 variables/dimensions.

```
In [3]: import ukf_internal
        ukf_internal.show_2d_transform()
```



Here on the left we show an ellipse depicting the 1σ distribution of two variables. The arrows show how three randomly sampled points might be transformed by some arbitrary nonlinear function to a new distribution. The ellipse on the right is drawn semi-transparently to indicate that it is an *estimate* of the mean and variance of this collection of points - if we were to sample, say, a million points the shape of the points might be very far from an ellipse.

11.1 Choosing Sigma Points

So what would be fewest number of sampled points that we can use, and what kinds of constraints does this problem formulation put on the points? We will assume that we have no special knowledge about the nonlinear transform as we want to find a generalized algorithm. For reasons that come clear in the next section, we will call these points *sigma points*.

Let's consider the simplest possible case, and see if it offers any insight. The simplest possible system is *identity* - the transformation does not alter the input. It should be clear that if our algorithm does not work for the identity transformation then the filter will never converge. In other words, if the input is 1 (for a one dimensional system), the output must also be 1. If the output was different, such as 1.1, then when we fed 1.1 into the transform at the next time step, we'd get out yet another number, maybe 1.23. The filter would run away (diverge).

The fewest number of points that we can use is one per dimension. This is the number that the linear Kalman filter uses. The input to a Kalman filter for the distribution $\mathcal{N}(\mu, \sigma^2)$ is just μ itself. So while this works for the linear case, it is not a good answer for the nonlinear case.

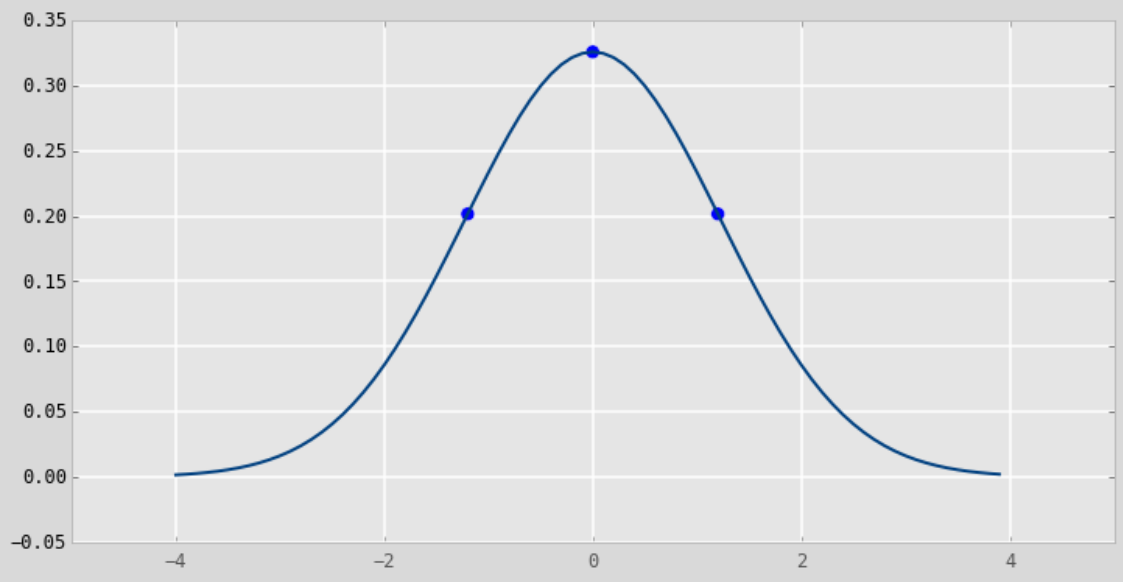
If we were to pass some value $\mu + \Delta$ instead, the identity system would not converge, so

this is not a possible algorithm. Since we cannot set our one point sample to μ, or any value that is not μ, we must conclude that a one point sample will not work.

So, what is the next lowest number we can choose? Consider the fact that Gaussians are symmetric, and that we probably want to always have one of our sample points be the mean of the input. Two points would require us to select the mean, and then one other point. That one other point would introduce an asymmetry in our input that we probably don't want. I recognize that this is rather vague, but I don't want to spend a lot of time on a scheme that doesn't work.

The next lowest number is 3 points. 3 points allows us to select the mean, and then one point on each side of the mean, as depicted on the chart below.

```
In [4]: ukf_internal.show_3_sigma_points()
```



For this to work for identity we will want the sums of the weights to equal one. We can always come up with counterexamples, but in general if the sum is greater or less than one the sampling will not yield the correct output. Given that, we then have to select *sigma points* $\mathcal{X}$ and their corresponding weights so that they compute to the mean and variance of the input Gaussian. So we can write

$$1 = \sum_i w_i \tag{1}$$

$$\mu = \sum_i w_i \mathcal{X}_i \tag{2}$$

$$\Sigma = \sum_i w_i (\mathcal{X}_i - \mu)(\mathcal{X}_i - \mu)^T \tag{3}$$

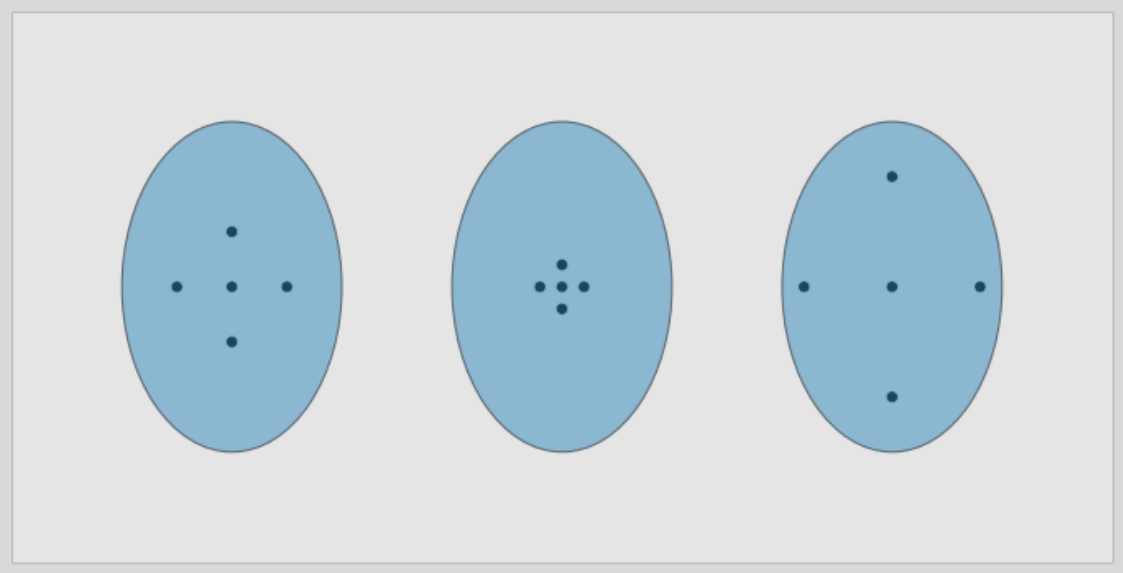
If we look at this is should be clear that there is no one unique answer - the problem is unconstrained. For example, if you choose a smaller weight for the point at the mean for

the input, you could compensate by choosing larger weights for the rest of the $\mathcal{X}$, and vice versa if you chose a larger weight for it. Indeed, these equations do not require that any of the points be the mean of the input at all, though it seems 'nice' to do so, so to speak.

Methods for selecting these sigma points is it own topic. In the next section I will develop the most typically used method in practice. It has the virtue of requiring only 3 sigma points per dimension, which is far lower than we might expect to provide good results. Despite the low number of points, the computations for the weight selections are very easy and efficient, and the numerical performance of the filter is as good as, and usually better than the EKF.

But before we go on I want to make sure the idea is clear. We are choosing 3 points for each dimension in our covariances. That choice is *entirely deterministic*. Below are three different examples for the same covariance ellipse.

```
In [5]: ukf_internal.show_sigma_selections()
```



Note that while I chose the points to lie along the major and minor axis of the ellipse, nothing in the constraints above require me to do that; however, it is fairly typical to do this. Furthermore, in each case I show the points evenly spaced; again, the constraints above do not require that. However, the technique that we develop in the next section *does* do this. It is a reasonable choice, after all; if we want to accurately sample our input it makes sense to sample in a symmetric manner.

There are many published ways for selecting the sigma points. For now I will stick with the original implementation by Julier and Uhlmann. This method defines a constant kappa (κ) which controls how spread out the sigma points are. Their equations for the sigma points are

11.2 The Unscented Transform

So our desire is to have an algorithm for selecting sigma points based on some criteria. Maybe we know something about our nonlinear problem, and we know we want our sigma points to be very close together, or very far apart. Or through experimentation we decide that a certain choice of basis vectors from our hyperellipse are the best axis to choose our sigma points from. But we want this to be an algorithm - we don't want to have to hard code in a specific selection algorithm for each different problem. So we are going to want to be able to set some parameters to tell the algorithm how to automatically select the points and weights for us. That may seem a bit abstract, so let's just launch into it, and try to develop an intuitive understanding as we go.

Assume a n-dimensional state variable $\mathbf{x}$ with mean μ and covariance Σ. We want to choose $2n + 1$ sigma points to approximate the Gaussian distribution of $\mathbf{x}$.

Our first sigma point is always going to be the mean of our input. We will call this $\mathcal{X}_0$. So,

$$\mathcal{X}_0 = \mu$$

Tne corresponding weight for this sigma point is

$$W_0 = \frac{\kappa}{n+\kappa}$$

where n is the dimension of the problem, and κ is a scaling factor that will be discussed in a moment.

So for each dimension we need to select 2 more points. We want them to be symmetric around the mean so that for the linear case they cancel out and we are just left with the mean as the result. Here is how we are going to do that:

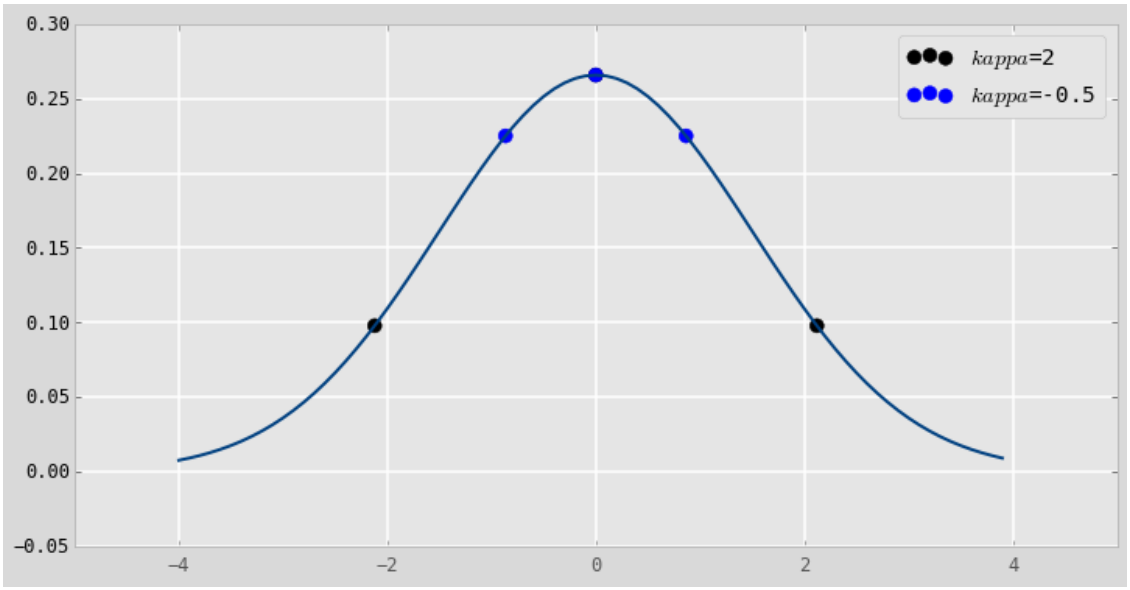
$$\begin{aligned}
\mathcal{X}_i &= \mu + (\sqrt{(n+\kappa)\Sigma})_i && \text{for i=1 .. n} \\
\mathcal{X}_i &= \mu - (\sqrt{(n+\kappa)\Sigma})_{i-n} && \text{for i=(n+1) .. 2n}
\end{aligned}$$

and the corresponding weights are

$$W_i = \frac{1}{2(n+\kappa)} \text{ for i=1,2..2n}$$

κ (kappa) is a scaling factor that controls how far away from the mean we want the points to be. A larger kappa will choose points further away from the mean, and a smaller kappa will choose points nearer the mean. Julier and Uhlmann suggest using $\kappa + n = 3$ if the distribution is Gaussian, and perhaps choosing a different value if it is not Gaussian. So in one dimension we get something like the following. Here I have plotted two different choices for kappa to show how kappa affects the distribution of the points.

```
In [6]: ukf_internal.show_sigmas_for_2_kappas()
```



The remainder of the algorithm follows from our equations above:

$$\mu = \sum_i w_i \mathcal{X}_i \tag{2}$$

$$\Sigma = \sum_i w_i (\mathcal{X}_i - \mu)(\mathcal{X}_i - \mu)^T \tag{3}$$

In other words, we generate sigma points from an existing state variable from its mean and covariance matrix. We pass those sigma points through the nonlinear function that we are trying to filter. Then we use equations (2) and (3) to regenerate an approximation for the mean and covariance of the output.

11.3 Implementation

So let's just implement this algorithm. First, let's write the code to compute the mean and covariance given the sigma points.

So we will store the sigma points and weights in matrices, like so:

$$weights = \begin{bmatrix} w_1 & w_2 & \dots & w_{2n+1} \end{bmatrix}$$

$$sigmas = \begin{bmatrix} \mathcal{X}_{0,0} & \mathcal{X}_{0,1} & \mathcal{X}_{0,2} \\ \mathcal{X}_{1,0} & \mathcal{X}_{1,1} & \mathcal{X}_{1,2} \\ \vdots & \vdots & \vdots \\ \mathcal{X}_{2n+1,0} & \mathcal{X}_{2n+1,1} & \mathcal{X}_{2n+1,2} \end{bmatrix}$$

In other words, each column contains the $2n + 1$ sigma points for one dimension in our problem. The $0th$ sigma point is always the mean, so first row of sigma's contains the mean

of each of our dimensions. The second through nth row contains the $\mu + \sqrt{(n+\lambda)\Sigma}$ terms, and the $n+1$ to $2n$ rows contains the $\mu - \sqrt{(n+\lambda)\Sigma}$ terms.

Computing the weights in numpy is extremely simple. Recall that

$$W_0 = \frac{\kappa}{n+\kappa}$$
$$W_i = \frac{1}{2(n+\kappa)} \text{ for i=1,2..2n}$$

These two lines of code implenent these equations with the `np.full()` method, which creates and fills an array with the same value. Then the value for the mean(W_0) is computed and overwrites the filled in value. We make W a $(2n+1) \times 1$ dimension array simply because linear algebra with numpy proceeds much more smoothly when all arrays are 2 dimensional, so the one dimensional array `[1,2,3]` is better expressed in numpy as `[[1,2,3]]`.

```
W = np.full((2*n+1,1), .5 / (n+kappa))
W[0] = kappa / (n+kappa)
```

The equations for the sigma points are:

$$\mathcal{X}_0 = \mu$$
$$\mathcal{X}_i = \mu + \left[\sqrt{(n+\kappa)\Sigma}\right]_i \qquad \text{for i=1 .. n}$$
$$\mathcal{X}_i = \mu - \left[\sqrt{(n+\kappa)\Sigma}\right]_{i-n} \qquad \text{for i=(n+1) .. 2n}$$

The Python for this is not much more difficult once we wrap our heads around the $[\sqrt{(n+\kappa)\Sigma}]_i$ term.

The term $[\sqrt{(n+\kappa)\Sigma}]_i$ has to be a matrix because Σ is a matrix. The subscript i is choosing the column vector of the matrix. What is the 'square root of a matrix'? The usual definition is that the square root of a matrix Σ is just the matrix S that, when multiplied by itself, yields Σ.

$$\text{if } \Sigma = SS$$

$$\text{then } S = \sqrt{\Sigma}$$

However there is an alternative definition, and we will chose that because it has numerical properties that makes it much easier for us to compute its value. We can alternatively define the square root as the matrix S, which when multiplied by its transpose, returns Σ:

$$\Sigma = SS^T$$

This latter method is typically chosen in computational linear algebra because this expression is easy to compute using something called the *Cholesky decomposition*. Numpy provides this with the `numpy.linalg.cholesky()` method. If your language of choice is

Fortran, C, C++, or the like standard libraries such as LAPACK also provide this routine. And, of course, matlab provides `chol()`, which does the same thing.

This method returns a lower triangular matrix, so we will take the transpose of it so that in our for loop we can access it row-wise as `U[i]`, rather than the more cumbersome column-wise notation `U[i,:]`.

```
Xi = np.zeros((2*n+1, n))
Xi[0] = X
U = linalg.cholesky((n+kappa)*P).T

for k in range (n):
    Xi[k+1]   = X + U[k]
    Xi[n+k+1] = X - U[k]
```

The full listing from the `filterpy.kalman` library follows.

```
In [7]: def sigma_points (X, P, kappa):
            """ Computes the sigma points and weights for an unscented Kalman filter
            given the mean and covariance of the filter.
            kappa is an arbitrary constant
            constant. Returns tuple of the sigma points and weights.

            Works with both scalar and array inputs:
            sigma_points (5, 9, 2) # mean 5, covariance 9
            sigma_points ([5, 2], 9*eye(2), 2) # means 5 and 2, covariance 9I

            Parameters
            ----------
            X An array of the means for each dimension in the problem space.
                Can be a scalar if 1D.
                examples: 1, [1,2], np.array([1,2])

            P : scalar, or

            Returns
            -------
            sigmas : np.array, of size (n, 2n+1)
                Two dimensional array of sigma points. Each column contains all of
                the sigmas for one dimension in the problem space.

                Ordered by Xi_0, Xi_{1..n}, Xi_{n+1..2n}

            weights : 1D np.array, of size (2n+1)
            """
```

```
    if np.isscalar(X):
        X = np.array([X])

    if  np.isscalar(P):
        P = np.array([[P]])

    """ Xi - sigma points
        W  - weights
    """

    n = np.size(X)  # dimension of problem

    W = np.full((2*n+1,1), .5 / (n+kappa))
    Xi = np.zeros((2*n+1, n))

    # handle values for the mean separately as special case
    Xi[0] = X
    W[0] = kappa / (n+kappa)

    # implements U'*U = (n+kappa)*P. Returns lower triangular matrix.
    # Take transpose so we can access with U[i]
    U = linalg.cholesky((n+kappa)*P).T

    for k in range (n):
        Xi[k+1]   = X + U[k]
        Xi[n+k+1] = X - U[k]

    return (Xi, W)
```

Now let's implement the unscented transform. Recall the equations

$$\mu = \sum_i w_i \mathcal{X}_i \tag{2}$$

$$\Sigma = \sum_i w_i (\mathcal{X}_i - \mu)(\mathcal{X}_i - \mu)^T \tag{3}$$

We implement the sum of the means with

```
X = np.sum (Xi*W, axis=0)
```

If you are not a heavy user of numpy this may look foreign to you. Numpy is not just a library that make linear algebra possible; under the hood it is written in C to achieve much faster speeds than Python can reach. A typical speedup is 100x. To get that speedup we must avoid using for loops, and instead use numpy's built in functions to perform calculations. So, instead of writing a for loop to compute the sum, we call the built in `numpy.sum()` method

which takes an entire array and computes the sum in C. The `axis` parameter tells sum over which axis to sum the array. For example, if

$$Xi = \begin{bmatrix} 1 & 2 & 3 \\ 1 & 2 & 3 \\ 1 & 2 & 3 \end{bmatrix}$$

then

```
sum(Xi) == 18
sum(Xi,axis=0) == [3,6,9]
sum(Xi,axis=1) == [6,6,6]
```

All that is left is to compute $\Sigma = \sum_i w_i(\mathcal{X}_i - \mu)(\mathcal{X}_i - \mu)^T$

```
P = np.zeros((n,n))
for k in range (2*n+1):
    s = (Xi[k]-X)[np.newaxis] # needs to be 2D to perform transform
    P += W[k]*s*s.T
```

This introduces another new feature of numpy. The state variable X is one dimensional, as is $Xi[k]$, so the difference $Xi[k] - X$ is also one dimensional. numpy will not compute the transpose of a 1-D array; it considers the transpose of `[1,2,3]` to be `[1,2,3]`. I consider that a deficiency of numpy, but you have to live with it. So we need to make the array two dimensional, with the second dimension of size 1. You do this in numpy by appending `[np.newaxis]` to the array. For example, `np.array([1,2])[np.newaxis]` returns `array([[1, 2]])`.

The following code is the implementation from the `filterpy.kalman` library. The function includes the ability to sum a noise covariance into the covariance matrix; this feature will be used to implement the full blown unscented Kalman filter.

```
In [8]: def unscented_transform (Xi, W, NoiseCov=None):
            """ computes the unscented transform of a set of signma points and weights
            returns the mean and covariance in a tuple
            """
            kmax,n = Xi.shape

            X = np.sum (Xi*W, axis=0)
            P = np.zeros((n,n))

            for k in range (kmax):
                s = (Xi[k]-X)[np.newaxis] # needs to be 2D to perform transform
                P += W[k]*s*s.T

            if NoiseCov is not None:
                P += NoiseCov

            return (X, P)
```

11.4 Unscented Kalman Filter

We are now ready to consider implementing a Kalman filter using the approximations for the mean and covariances afforded by the unscented transform.

Chapter 12

Designing Nonlinear Kalman Filters

12.1 Introduction

blah blah

We see that the Kalman filter reasonably tracks the ball. However, as already explained, this is a silly example; we can predict trajectories in a vacuum with arbitrary precision; using a Kalman filter in this example is a needless complication.

12.1.1 Kalman Filter with Air Drag

I will dispense with the step 1, step 2, type approach and proceed in a more natural style that you would use in a non-toy engineering problem. We have already developed a Kalman filter that does excellently at tracking a ball in a vacuum, but that does not incorporate the effects of air drag into the model. We know that the process model is implemented with **F**, so we will turn our attention to that immediately.

Notionally, the computation that **F** computes is

$$x' = Fx$$

With no air drag, we had

$$\mathbf{F} = \begin{bmatrix} 1 & \Delta t & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & \Delta t & \frac{1}{2}\Delta t^2 \\ 0 & 0 & 0 & 1 & \Delta t \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

which corresponds to the equations

$$
\begin{aligned}
x &= x + v_x \Delta t \\
v_x &= v_x
\end{aligned}
$$

$$
\begin{aligned}
y &= y + v_y \Delta t + \frac{a_y}{2} \Delta t^2 \\
v_y &= v_y + a_y \Delta t \\
a_y &= a_y
\end{aligned}
$$

From the section above we know that our new Euler equations must be

$$
\begin{aligned}
x &= x + v_x \Delta t \\
v_x &= v_x
\end{aligned}
$$

$$
\begin{aligned}
y &= y + v_y \Delta t + \frac{a_y}{2} \Delta t^2 \\
v_y &= v_y + a_y \Delta t \\
a_y &= a_y
\end{aligned}
$$

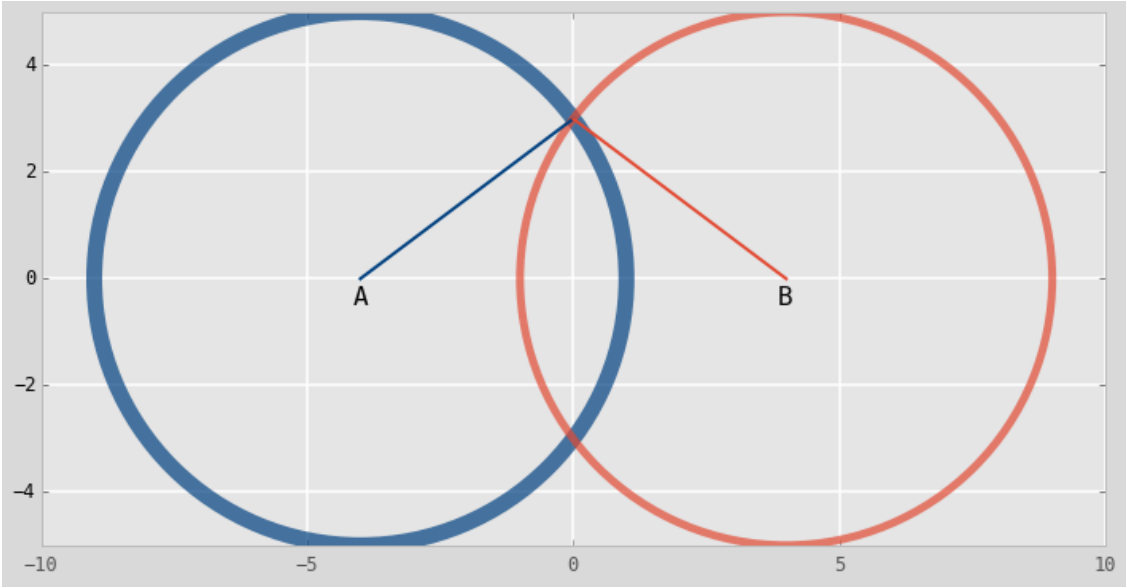
12.2 Realistic 2D Position Sensors

The position sensor in the last example are not very realistic. In general there is no 'raw' sensor that provides (x,y) coordinates. We have GPS, but GPS already uses a Kalman filter to create a filtered output; we should not be able to improve the signal by passing it through another Kalman filter unless we incorporate additional sensors to provide additional information. We will tackle that problem later.

Consider the following set up. In an open field we put two transmitters at a known location, each transmitting a signal that we can detect. We process the signal and determine how far we are from that signal, with some noise. First, let's look at a visual depiction of that.

```
In [2]: circle1=plt.Circle((-4,0),5,color='#004080',fill=False,linewidth=10, alpha=.7)
        circle2=plt.Circle((4,0),5,color='#E24A33', fill=False, linewidth=5, alpha=.7)

        fig = plt.gcf()
        ax = fig.gca()

        plt.axis('equal')
        plt.xlim((-10,10))
        plt.ylim((-10,10))

        plt.plot ([-4,0], [0,3], c='#004080')
        plt.plot ([4,0], [0,3], c='#E24A33')
        plt.text(-4, -.5, "A", fontsize=16, horizontalalignment='center')
```

```
plt.text(4, -.5, "B", fontsize=16, horizontalalignment='center')
#plt.scatter ([-4],[0], 'r')

ax.add_artist(circle1)
ax.add_artist(circle2)
plt.show()
```



Here I have attempted to show transmitter A, drawn in red, at (-4,0) and a second one B, drawn in blue, at (4,0). The red and blue circles show the range from the transmitters to the robot, with the width illustrating the effect of the 1σ angular error for each transmitter. Here I have given the red transmitter more error than the blue one. The most probable position for the robot is where the two circles intersect, which I have depicted with the red and blue lines. You will object that we have two intersections, not one, but we will see how we deal with that when we design the measurement function.

This is a very common sensor set up. Aircraft still use this system to navigate, where it is called DME (Distance Measuring Equipment). Today GPS is a much more common navigation sytem, but I have worked on an aircraft where we integrated sensors like this into our filter along with the GPS, INS, altimeters, etc. We will tackle what is called *multi-sensor fusion* later; for now we will just address this simple configuration.

The first step is to design our state variables. We will assume that the robot is travelling in a straight direction with constant velocity. This is unlikely to be true for a long period of time, but is acceptable for short periods of time. This does not differ from the previous problem - we will want to track the values for the robot's position and velocity. Hence,

$$\mathbf{x} = \begin{bmatrix} x \\ v_x \\ y \\ v_y \end{bmatrix}$$

The next step is to design the state transistion function. This also will be the same as the previous problem, so without further ado,

$$\mathbf{x}' = \begin{bmatrix} 1 & \Delta t & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & \Delta t \\ 0 & 0 & 0 & 1 \end{bmatrix} \mathbf{x}$$

The next step is to design the control inputs. We have none, so we set $\mathbf{B} = 0$.

The next step is to design the measurement function $\mathbf{z} = \mathbf{Hx}$. We can model the measurement using the Pythagorean theorem.

$$z_a = \sqrt{(x - x_A)^2 + (y - y_A)^2} + v_a z_b = \sqrt{(x - x_B])^2 + (y - y_B)^2} + v_b$$

where v_a and v_b are white noise.

We see an immediate problem. The Kalman filter is designed for linear equations, and this is obviously nonlinear. In the next chapters we will look at several ways to handle nonlinear problems in a robust way, but for now we will do something simpler. If we know the approximate position of the robot than we can linearize these equations around that point. I could develop the generalized mathematics for this technique now, but instead let me just present the worked example to give context to that development.

Instead of computing $\mathbf{H}$ we will compute the partial derivative of $\mathbf{H}$ with respect to the robot's position $\mathbf{x}$. You are probably familiar with the concept of partial derivative, but if not, it just means how $\mathbf{H}$ changes with respect to the robot's position. It is computed as the partial derivative of $\mathbf{H}$ as follows:

$$\frac{\partial \mathbf{h}}{\partial \mathbf{x}} = \begin{bmatrix} \frac{\partial h_1}{\partial x_1} & \frac{\partial h_1}{\partial x_2} & \cdots \\ \frac{\partial h_2}{\partial x_1} & \frac{\partial h_2}{\partial x_2} & \cdots \\ \vdots & \vdots & \end{bmatrix}$$

Let's work the first partial derivative. We want to find

$$\frac{\partial}{\partial x} \sqrt{(x - x_A)^2 + (y - y_A)^2}$$

Which we compute as

$$\begin{aligned} \frac{\partial h_1}{\partial x} &= ((x - x_A)^2 + (y - y_A)^2))^{\frac{1}{2}} \\ &= \frac{1}{2} \times 2(x - x_a) \times ((x - x_A)^2 + (y - y_A)^2))^{-\frac{1}{2}} \\ &= \frac{x_r - x_A}{\sqrt{(x_r - x_A)^2 + (y_r - y_A)^2}} \end{aligned}$$

We continue this computation for the partial derivatives of the two distance equations with respect to x, y, dx and dy, yielding

$$\frac{\partial \mathbf{h}}{\partial \mathbf{x}} = \begin{bmatrix} \frac{x_r - x_A}{\sqrt{(x_r-x_A)^2+(y_r-y_A)^2}} & 0 & \frac{y_r - y_A}{\sqrt{(x_r-x_A)^2+(y_r-y_A)^2}} & 0 \\ \frac{x_r - x_B}{\sqrt{(x_r-x_B)^2+(y_r-y_B)^2}} & 0 & \frac{y_r - y_B}{\sqrt{(x_r-x_B)^2+(y_r-y_B)^2}} & 0 \end{bmatrix}$$

That is pretty painful, and these are very simple equations. Computing the Jacobian can be extremely difficult or even impossible for more complicated systems. However, there is an easy way to get Python to do the work for you by using the `sympy` module [1]. `sympy` is a Python library for symbolic mathematics. The full scope of its abilities are beyond this book, but it can perform algebra, integrate and differentiate equations, find solutions to differential equations, and much more. We will use it to compute our Jabobian!

First, a simple example. We will import sympy, initialize its pretty print functionality (which will print equations using LaTeX). We will then declare a symbol for numpy to use.

```
In [3]: import sympy
        from sympy import  init_printing
        #from sympy.interactive import printing
        init_printing(use_latex='mathjax')

        phi, x = sympy.symbols('\phi, x')
        phi
```

Out[3]:

$$\phi$$

Notice how we use a latex expression for the symbol `phi`. This is not necessary, but if you do it will render as LaTeX when output. Now let's do some math. What is the derivative of $\sqrt{\phi}$?

```
In [4]: sympy.diff('sqrt(phi)')
```

Out[4]:

$$\frac{1}{2\sqrt{\phi}}$$

We can factor equations.

```
In [5]: sympy.factor('phi**3 -phi**2 + phi - 1')
```

Out[5]:

$$(\phi - 1)\left(\phi^2 + 1\right)$$

`sympy` has a remarkable list of features, and as much as I enjoy exercising its features we cannot cover them all here. Instead, let's compute our Jacobian.

In [6]:
```
phi = sympy.symbols('\phi')
phi

x, y, xa, xb, ya, yb, dx, dy = sympy.symbols('x, y, x_a, x_b, y_a, y_b, dx, dy')

H = sympy.Matrix([[sympy.sqrt((x-xa)**2 + (y-ya)**2)],
                  [sympy.sqrt((x-xb)**2 + (y-yb)**2)]])

state = sympy.Matrix([x, dx, y, dy])
H.jacobian(state)
```

Out[6]:

$$\begin{bmatrix} \frac{x-x_a}{\sqrt{(x-x_a)^2+(y-y_a)^2}} & 0 & \frac{y-y_a}{\sqrt{(x-x_a)^2+(y-y_a)^2}} & 0 \\ \frac{x-x_b}{\sqrt{(x-x_b)^2+(y-y_b)^2}} & 0 & \frac{y-y_b}{\sqrt{(x-x_b)^2+(y-y_b)^2}} & 0 \end{bmatrix}$$

In a nutshell, the entry (0,0) contains the difference between the x coordinate of the robot and transmitter A's x coordinate divided by the distance between the robot and A. (2,0) contains the same, except for the y coordintates of the robot and transmitters. The bottom row contains the same computations, except for transmitter B. The 0 entries account for the velocity components of the state variables; naturally the range does not provide us with velocity.

The values in this matrix change as the robot's position changes, so this is no longer a constant; we will have to recompute it for every time step of the filter.

If you look at this you may realize that this is just a computation of x/dist and y/dist, so we can switch this to a trigometic form with no loss of generality:

$$\frac{\partial \mathbf{h}}{\partial \mathbf{x}} = \begin{bmatrix} -\cos\theta_A & 0 & -\sin\theta_A & 0 \\ -\cos\theta_B & 0 & -\sin\theta_B & 0 \end{bmatrix}$$

However, this raises a huge problem. We are no longer computing $\mathbf{H}$, but $\Delta\mathbf{H}$, the change of $\mathbf{H}$. If we passed this into our Kalman filter without altering the rest of the design the output would be nonsense. Recall, for example, that we multiply $\mathbf{Hx}$ to generate the measurements that would result from the given estimate of $\mathbf{x}$ But now that $\mathbf{H}$ is linearized around our position it contains the *change* in the measurement function.

We are forced, therefore, to use the *change* in $\mathbf{x}$ for our state variables. So we have to go back and redesign our state variables.

> Please note this is a completely normal occurance in designing Kalman filters. The textbooks present examples like this as *fait accompli*, as if it is trivially obvious that the state variables needed to be velocities, not positions. Perhaps once you do enough of these problems it would be trivially obvious, but at that point why are you reading a textbook? I find myself reading through a presentation multiple times, trying to figure out why they made a choice, finally to realize that it is because of the consequences of something on the next page. My presentation is longer, but it reflects what actually happens when you design a filter.

> You make what seem reasonable design choices, and as you move forward you discover properties that require you to recast your earlier steps. As a result, I am going to somewhat abandon my **step 1**, **step 2**, etc., approach, since so many real problems are not quite that straightforward.

If our state variables contain the velocities of the robot and not the position then how do we track where the robot is? We can't. Kalman filters that are linearized in this fashion use what is called a *nominal trajectory* - i.e. you assume a position and track direction, and then apply the changes in velocity and acceleration to compute the changes in that trajectory. How could it be otherwise? Recall the graphic showing the intersection of the two range circles - there are two areas of intersection. Think of what this would look like if the two transmitters were very close to each other - the intersections would be two very long cresent shapes. This Kalman filter, as designed, has no way of knowing your true position from only distance measurements to the transmitters. Perhaps your mind is already leaping to ways of working around this problem. If so, stay engaged, as later sections and chapters will provide you with these techniques. Presenting the full solution all at once leads to more confusion than insight, in my opinion.

So let's redesign our *state transition function*. We are assuming constant velocity and no acceleration, giving state equations of

$$\dot{x}' = \dot{x}\ddot{x}' = 0\dot{y}' = \dot{y}\dot{y}' = 0$$

This gives us the the *state transition function* of

$$\mathbf{F} = \begin{bmatrix} 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

A final complication comes from the measurements that we pass in. **Hx** is now computing the *change* in the measurement from our nominal position, so the measurement that we pass in needs to be not the range to A and B, but the *change* in range from our measured range to our nomimal position.

There is a lot here to take in, so let's work through the code bit by bit. First we will define a function to compute $\frac{\partial \mathbf{h}}{\partial \mathbf{x}}$ for each time step.

```
In [7]: from math import sin, cos, atan2

        def H_of (pos, pos_A, pos_B):
            """ Given the position of our object at 'pos' in 2D, and two transmitters
            A and B at positions 'pos_A' and 'pos_B', return the partial derivative
            of H
            """

            theta_a = atan2(pos_a[1]-pos[1], pos_a[0] - pos[0])
            theta_b = atan2(pos_b[1]-pos[1], pos_b[0] - pos[0])
```

```
        return np.array([[0, -cos(theta_a), 0, -sin(theta_a)],
                         [0, -cos(theta_b), 0, -sin(theta_b)]])
```

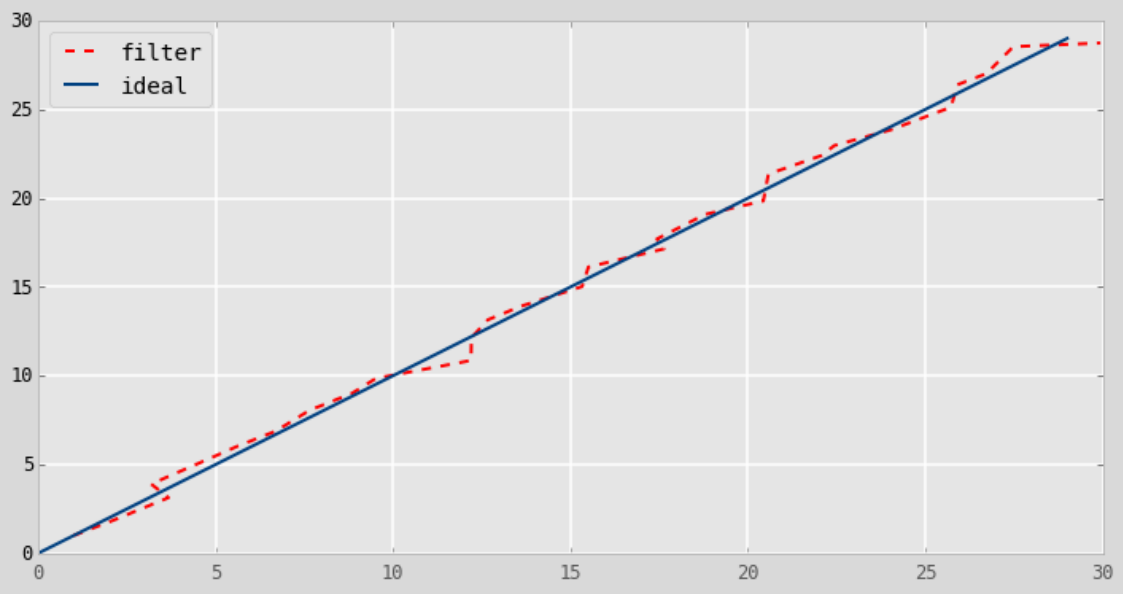
Now we need to create our simulated sensor.

In [8]:
```
from numpy.random import randn

class DMESensor(object):
    def __init__(self, pos_a, pos_b, noise_factor=1.0):
        self.A = pos_a
        self.B = pos_b
        self.noise_factor = noise_factor

    def range_of (self, pos):
        """ returns tuple containing noisy range data to A and B
        given a position 'pos'
        """

        ra = math.sqrt((self.A[0] - pos[0])**2 + (self.A[1] - pos[1])**2)
        rb = math.sqrt((self.B[0] - pos[0])**2 + (self.B[1] - pos[1])**2)

        return (ra + randn()*self.noise_factor,
                rb + randn()*self.noise_factor)
```

Finally, we are ready for the Kalman filter code. I will position the transmitters at x=-100 and 100, both with y=-20. This gives me enough space to get good triangulation from both as the robot moves. I will start the robot at (0,0) and move by (1,1) each time step.

In [9]:
```
import math
from filterpy.kalman import KalmanFilter
import numpy as np

pos_a = (100,-20)
pos_b = (-100, -20)

f1 = KalmanFilter(dim_x=4, dim_z=2)

f1.F = np.array ([[0, 1, 0, 0],
                  [0, 0, 0, 0],
                  [0, 0, 0, 1],
                  [0, 0, 0, 0]], dtype=float)

f1.R *= 1.
f1.Q *= .1
```

```
f1.x = np.array([[1,0,1,0]], dtype=float).T
f1.P = np.eye(4) * 5.

# initialize storage and other variables for the run
count = 30
xs, ys = [],[]
pxs, pys = [],[]

# create the simulated sensor
d = DMESensor (pos_a, pos_b, noise_factor=3.)

# pos will contain our nominal position since the filter does not
# maintain position.
pos = [0,0]

for i in range(count):
    # move (1,1) each step, so just use i
    pos = [i,i]

    # compute the difference in range between the nominal track and measured
    # ranges
    ra,rb = d.range_of(pos)
    rx,ry = d.range_of((pos[0]+f1.x[0,0], pos[1]+f1.x[2,0]))
    z = np.array([[ra-rx],[rb-ry]])

    # compute linearized H for this time step
    f1.H = H_of (pos, pos_a, pos_b)

    # store stuff so we can plot it later
    xs.append (f1.x[0,0]+i)
    ys.append (f1.x[2,0]+i)
    pxs.append (pos[0])
    pys.append(pos[1])

    # perform the Kalman filter steps
    f1.predict ()
    f1.update(z)


p1, = plt.plot (xs, ys, 'r--')
p2, = plt.plot (pxs, pys)
plt.legend([p1,p2], ['filter', 'ideal'], 2)
plt.show()
```



12.3 Linearizing the Kalman Filter

Now that we have seen an example of linearizing the Kalman filter we are in a position to better understand the math.

We start by assuming some function **f**

12.4 References

[1] http://sympy.org

Chapter 13

Appendix: Installation, Python, Numpy, and filterpy

This book is written in IPython Notebook, a browser based interactive Python environment that mixes Python, text, and math. I choose it because of the interactive features - I found Kalman filtering nearly impossible to learn until I started working in an interactive environment. It is difficult to form an intuition of the effect of many of the parameters that you can tune until you can change them rapidly and immediately see the output. An interactive environment also allows you to play 'what if' scenarios out. "What if I set **Q** to zero?" It is trivial to find out with Ipython Notebook.

Another reason I choose it is because I find that a typical textbook leaves many things opaque. For example, there might be a beautiful plot next to some pseudocode. That plot was produced by software, but software that is not available to me as a reader. I want everything that went into producing this book to be available to the reader. How do you plot a covariance ellipse? You won't know if you read most books. With IPython Notebook all you have to do is look at the source code.

A downside to this format is that you have to install IPython onto your machine if you want the book's interactive features. This is normally not an onerous burden as if you are interested in programming in Python you should already have Python installed on your system.

Still, I know I have not downloaded some IPython Notebooks that are of interest to me. There is the free nbviewer.org site which will statically render a notebook that is hosted elsewhere. My book is hosted on github, so you can always read my book for free by going to

Chapter 14

Appendix I : Symbology

This is just notes at this point.

State

x (Brookner, Zarchan, Brown)
$\underline{x}$ Gelb)

State at step n

x_n (Brookner)
x_k (Brown, Zarchan)
$\underline{x}_k$ (Gelb)

Prediction

x^-
$x_{n,n-1}$ (Brookner)
$x_{k+1,k}$

14.0.1 measurement

x^*
Y_n (Brookner)

14.0.2 control transition Matrix

G (Zarchan)
Not used (Brookner)

14.1 Nomenclature

14.1.1 Equations

Brookner

$$
\begin{aligned}
X^*_{n+1,n} &= \Phi X^*_{n,n} \\
X^*_{n,n} &= X^*_{n,n-1} + H_n(Y_n - MX^*_{n,n-1}) \\
H_n &= S^*_{n,n-1}M^T[R_n + MS^*_{n,n-1}M^T]^{-1} \\
S^*_{n,n-1} &= \Phi S^*_{n-1,n-1}\Phi^T + Q_n \\
S^*_{n-1,n-1} &= (I - H_{n-1}M)S^*_{n-1,n-2}
\end{aligned}
$$

Gelb

$$
\begin{aligned}
\underline{\hat{x}}_k(-) &= \Phi_{k-1}\underline{\hat{x}}_{k-1}(+) \\
\underline{\hat{x}}_k(+) &= \underline{\hat{x}}_k(-) + K_k[Z_k - H_k\underline{\hat{x}}_k(-)] \\
K_k &= P_k(-)H_k^T[H_kP_k(-)H_k^T + R_k]^{-1} \\
P_k(+) &= \Phi_{k-1}P_{k-1}(+)\Phi_{k-1}^T + Q_{k-1} \\
P_k(-) &= (I - K_kH_k)P_k(-)
\end{aligned}
$$

Brown

$$
\begin{aligned}
\hat{\mathbf{x}}^-_{k+1} &= \phi_k\hat{\mathbf{x}}_k \\
\hat{\mathbf{x}}_k &= \hat{\mathbf{x}}^-_k + \mathbf{K}_k[\mathbf{z}_k - \mathbf{H}_k\hat{x}^-_k] \\
\mathbf{K}_k &= \mathbf{P}^-_k\mathbf{H}^T_k[\mathbf{H}_k\mathbf{P}^-_k\mathbf{H}^T_k + \mathbf{R}_k]^{-1} \\
\mathbf{P}^-_{k+1} &= \phi_k\mathbf{P}_k\phi^T_k + \mathbf{Q}_k \\
\mathbf{P}_k &= (\mathbf{I} - \mathbf{K}_k\mathbf{H}_k)\mathbf{P}^-_k
\end{aligned}
$$

##

Zarchan

$$
\begin{aligned}
\hat{x}_k &= \Phi_k\hat{x}_{k-1} + G_ku_{k-1} + K_k[z_k - H\Phi_k\hat{x}_{k-1} - HG_ku_{k-1}] \\
M_k &= \Phi_kP_{k-1}\phi^T_k + Q_k \\
K_k &= M_kH^T[HM_kH^T + R_k]^{-1} \\
P_k &= (I - K_kH)M_k
\end{aligned}
$$

Wikipedia

$$
\begin{aligned}
\hat{\mathbf{x}}_{k|k-1} &= \mathbf{F}_k\hat{\mathbf{x}}_{k-1|k-1} + \mathbf{B}_k\mathbf{u}_k \\
\mathbf{P}_{k|k-1} &= \mathbf{F}_k\mathbf{P}_{k-1|k-1}\mathbf{F}_k^{\mathrm{T}} + \mathbf{Q}_k \\
\tilde{\mathbf{y}}_k &= \mathbf{z}_k - \mathbf{H}_k\hat{\mathbf{x}}_{k|k-1} \\
\mathbf{S}_k &= \mathbf{H}_k\mathbf{P}_{k|k-1}\mathbf{H}_k^{\mathrm{T}} + \mathbf{R}_k \\
\mathbf{K}_k &= \mathbf{P}_{k|k-1}\mathbf{H}_k^{\mathrm{T}}\mathbf{S}_k^{-1} \\
\hat{\mathbf{x}}_{k|k} &= \hat{\mathbf{x}}_{k|k-1} + \mathbf{K}_k\tilde{\mathbf{y}}_k \\
\mathbf{P}_{k|k} &= (I - \mathbf{K}_k\mathbf{H}_k)\mathbf{P}_{k|k-1}
\end{aligned}
$$

Labbe

$$
\begin{aligned}
\hat{\mathbf{x}}_{k+1}^{-} &= \mathbf{F}_k\hat{\mathbf{x}}_k + \mathbf{B}_k\mathbf{u}_k \\
\mathbf{P}_{k+1}^{-} &= \mathbf{F}_k\mathbf{P}_k\mathbf{F}_k^{T} + \mathbf{Q}_k \\
\mathbf{y}_k &= \mathbf{z}_k - \mathbf{H}_k\hat{x}_k^{-} \\
\mathbf{S}_k &= \mathbf{H}_k\mathbf{P}_k^{-}\mathbf{H}_k^{T} + \mathbf{R}_k \\
\mathbf{K}_k &= \mathbf{P}_k^{-}\mathbf{H}_k^{T}\mathbf{S}_k^{-1} \\
\hat{\mathbf{x}}_k &= \hat{\mathbf{x}}_k^{-} + \mathbf{K}_k\mathbf{y} \\
\mathbf{P}_k &= (\mathbf{I} - \mathbf{K}_k\mathbf{H}_k)\mathbf{P}_k^{-}
\end{aligned}
$$

##