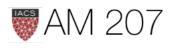
#### Lecture 10

# Sampling and its use in Gradient Descent



#### **Last Time**

- Exchangeability and the exponential model
- Bayesian Regression
- Inverse Transform Sampling
- Rejection Sampling



#### Today:

- Rejection Sampling
- Rejection Sampling (Steroids) or with majorization
- Logistic Regression and Gradient Descent
- Stochastic Gradient Descent (simple)
- Importance Sampling and expectations

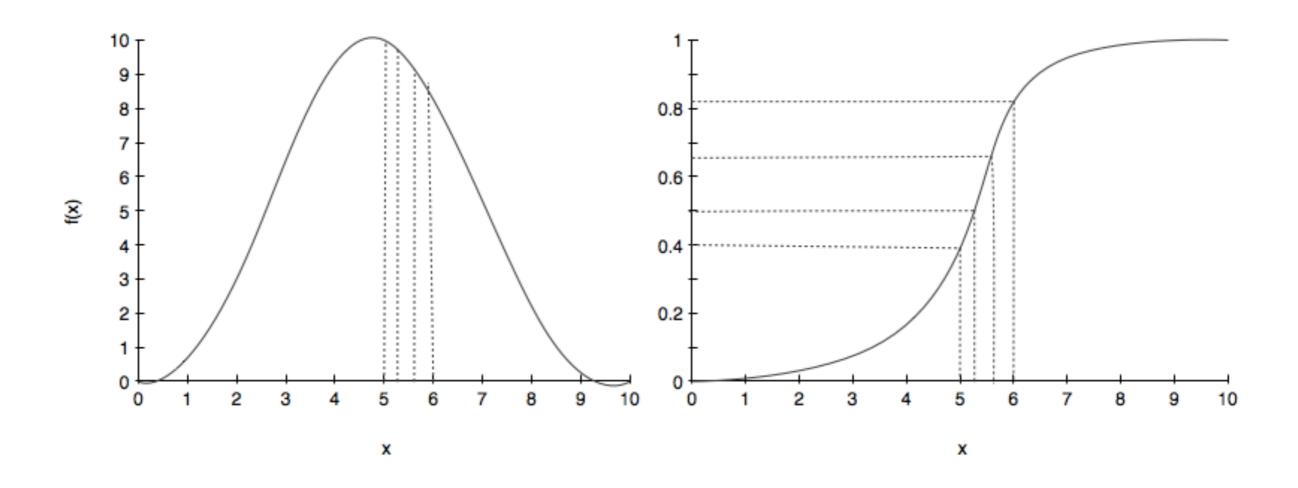


#### Ok. We need Samples

- to compute expectations, integrals and do statistics, we need samples
- we start that journey today
- inverse transform
- rejection sampling
- importance sampling: a direct, low-variance way to do integrals and expectations



#### Inverse transform





#### algorithm

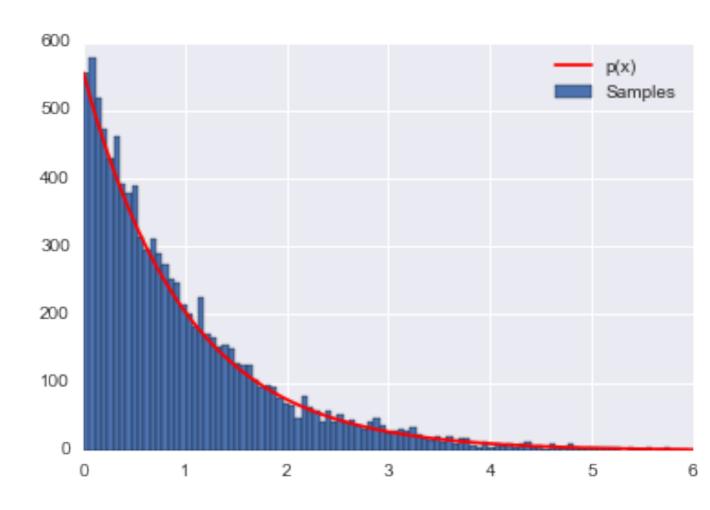
The CDF F must be invertible!

- 1. get a uniform sample u from Unif(0,1)
- 2. solve for x yielding a new equation  $x = F^{-1}(u)$  where F is the CDF of the distribution we desire.
- 3. repeat.

For exponential,  $x = -\lambda \ln(1-u)$ 

#### code

```
p = lambda x: np.exp(-x)
CDF = lambda x: 1-np.exp(-x)
invCDF = lambda r: -np.log(1-r) # invert the CDF
xmin = 0 # the lower limit of our domain
xmax = 6 # the upper limit of our domain
rmin = CDF(xmin)
rmax = CDF(xmax)
N = 10000
# generate uniform samples in our range then invert the CDF
# to get samples of our target distribution
R = np.random.uniform(rmin, rmax, N)
X = invCDF(R)
hinfo = np.histogram(X, 100)
plt.hist(X,bins=100, label=u'Samples');
# plot our (normalized) function
xvals=np.linspace(xmin, xmax, 1000)
plt.plot(xvals, hinfo[0][0]*p(xvals), 'r', label=u'p(x)')
plt.legend()
```





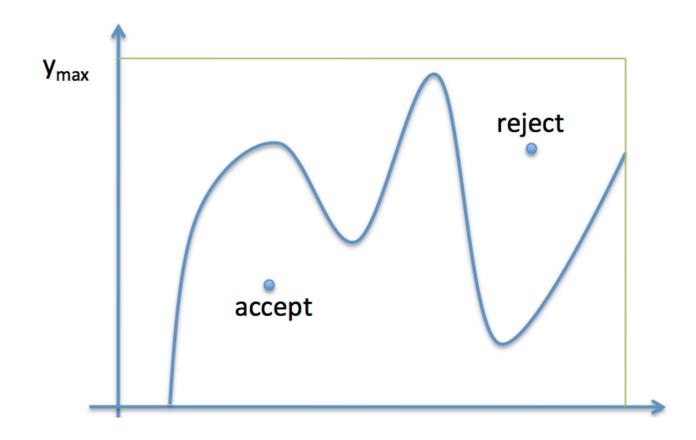
#### Rejection Sampling

- Generate samples from a uniform distribution with support on the rectangle
- See how many fall below y(x) at a specific x.



#### Rejection Sampling Algorithm

- 1. Draw x uniformly from  $[x_{min},\,x_{max}]$
- 2. Draw y uniformly from  $[0, y_{max}]$
- 3. if y < f(x), accept the sample
- 4. otherwise reject it
- 5. repeat

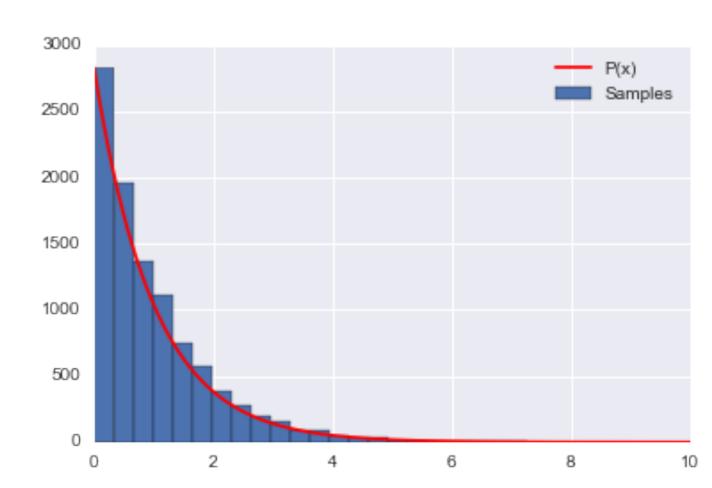


#### example

```
P = lambda x: np.exp(-x)
xmin = ∅ # the lower limit of our domain
xmax = 10 # the upper limit of our domain
ymax = 1
#you might have to do an optimization to find this.
N = 10000 # the total of samples we wish to generate
accepted = 0 # the number of accepted samples
samples = np.zeros(N)
count = ∅ # the total count of proposals
while (accepted < N):
    # pick a uniform number on [xmin, xmax) (e.g. 0...10)
    x = np.random.uniform(xmin, xmax)
    # pick a uniform number on [0, ymax)
    y = np.random.uniform(∅,ymax)
    # Do the accept/reject comparison
    if y < P(x):
        samples[accepted] = x
        accepted += 1
    count +=1
print("Count",count, "Accepted", accepted)
hinfo = np.histogram(samples, 30)
plt.hist(samples,bins=30, label=u'Samples');
xvals=np.linspace(xmin, xmax, 1000)
plt.plot(xvals, hinfo[0][0]*P(xvals), 'r', label=u'P(x)')
plt.legend()
```

#### Count 100294 Accepted 10000





#### problems

- determining the supremum may be costly
- the functional form may be complex for comparison
- even if you find a tight bound for the supremum, basic rejection sampling is very inefficient: low acceptance probability
- infinite support



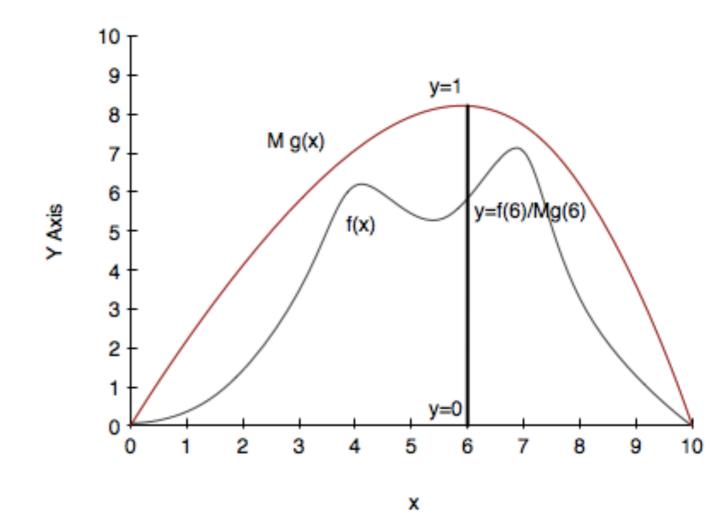
# Variance Reduction



#### Rejection on steroids

Introduce a **proposal density** g(x).

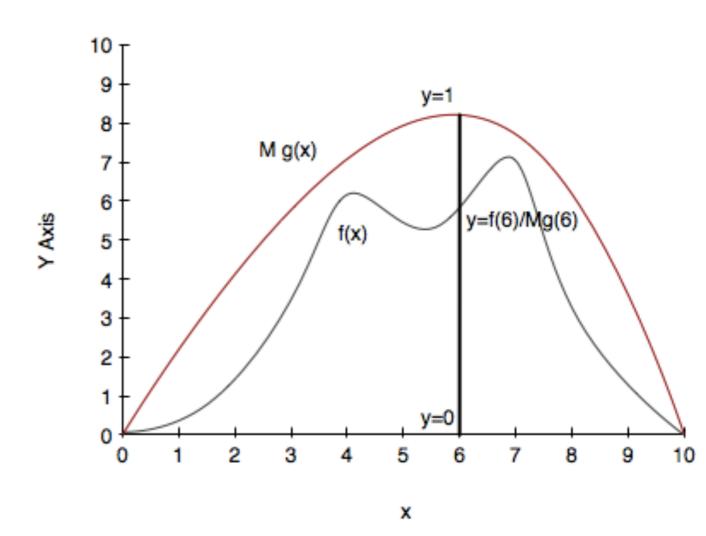
- g(x) is easy to sample from and (calculate the pdf)
- Some M exists so that M g(x) > f(x) in your entire domain of interest
- ideally g(x) will be somewhat close to f
- optimal value for M is the supremum over your domain





#### Algorithm

- 1. Draw x from your proposal distribution g(x)
- 2. Draw y uniformly from [0,1]
- 3. if y < f(x)/M g(x), accept the sample
- 4. otherwise reject it
- 5. repeat





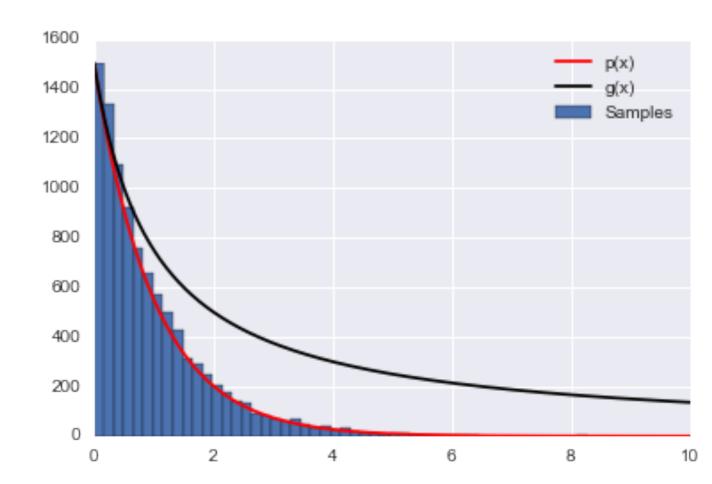
#### Example

```
p = lambda x: np.exp(-x) # our distribution
q = lambda x: 1/(x+1) # our proposal pdf (we're thus choosing M to be 1)
invCDFg = lambda x: np.log(x + 1) # generates our proposal using inverse sampling
xmin = 0 # the lower limit of our domain
xmax = 10 # the upper limit of our domain
# range limits for inverse sampling
umin = invCDFg(xmin)
umax = invCDFg(xmax)
N = 10000 # the total of samples we wish to generate
accepted = 0 # the number of accepted samples
samples = np.zeros(N)
count = 0 # the total count of proposals
while (accepted < N):</pre>
    # Sample from g using inverse sampling
    u = np.random.uniform(umin, umax)
    xproposal = np.exp(u) - 1
    # pick a uniform number on [0, 1)
    y = np.random.uniform(0,1)
    # Do the accept/reject comparison
    if y < p(xproposal)/g(xproposal):</pre>
        samples[accepted] = xproposal
        accepted += 1
    count +=1
print("Count", count, "Accepted", accepted)
# get the histogram info
hinfo = np.histogram(samples,50)
plt.hist(samples,bins=50, label=u'Samples');
xvals=np.linspace(xmin, xmax, 1000)
plt.plot(xvals, hinfo[0][0]*p(xvals), 'r', label=u'p(x)')
plt.plot(xvals, hinfo[0][0]*g(xvals), 'k', label=u'g(x)')
```

#### Count 23809 Accepted 10000



plt.legend()



#### Importance sampling

The basic idea behind importance sampling is that we want to draw more samples where h(x), a function whose integral or expectation we desire, is large. In the case we are doing an expectation, it would indeed be even better to draw more samples where h(x)f(x) is large, where f(x) is the pdf we are calculating the integral with respect to.

Unlike rejection sampling we use all samples!!



$$E_f[h] = \int_V f(x)h(x)dx.$$

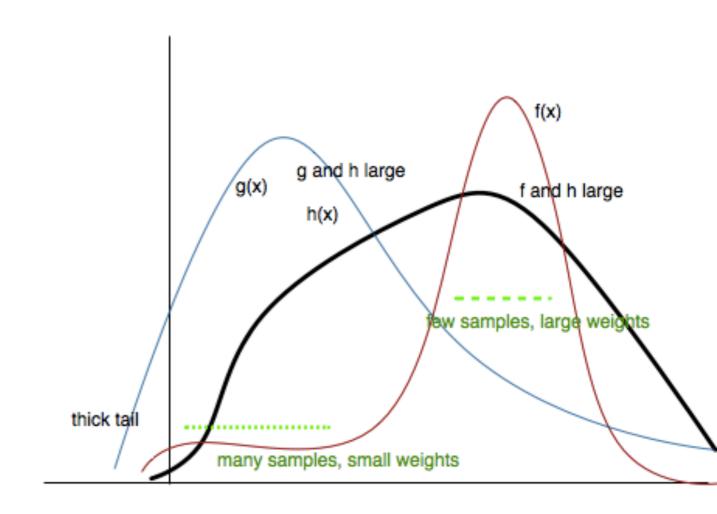
Choosing a proposal distribution g(x):

$$E_f[h] = \int h(x)g(x)rac{f(x)}{g(x)}dV$$

$$E_f[h] = \lim_{N o \infty} rac{1}{N} \sum_{x_i \sim g(.)} h(x_i) rac{f(x_i)}{g(x_i)}$$

If 
$$w(x_i) = f(x_i)/g(x_i)$$
:

$$E_f[h] = \lim_{N o \infty} rac{1}{N} \sum_{x_i \sim g(.)} w(x_i) h(x_i)$$





#### Variance reduction

Usually: 
$$\hat{V} = rac{V_f[h(x)]}{N}$$

Importance Sampling: 
$$\hat{V} = \frac{V_g[w(x)h(x)]}{N}$$

Minimize  $V_g[w(x)h(x)]$  (make 0), if:

$$w(x)h(x) = C \implies f(x)h(x) = Cg(x),...$$

Gives us 
$$g(x)=rac{f(x)h(x)}{E_f[h(x)]}$$

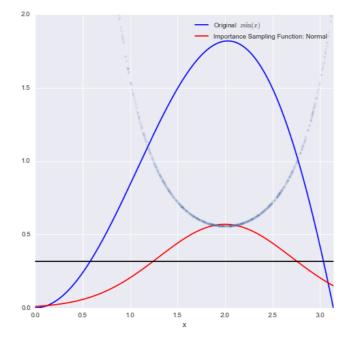
To get low variance, we must have g(x) large where the product f(x)h(x) is large.

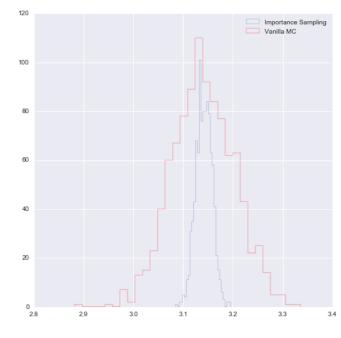
Or,  $\frac{g(x)}{f(x)}$  ought to be large where h(x) is large. This

means that, as we said earlier, choose more samples near the peak.

## Example: integral of x sin(x)

```
mu = 2;
siq = .7;
f = lambda x: np.sin(x)*x
infun = lambda x: np.sin(x)-x*np.cos(x)
p = lambda x: (1/np.sqrt(2*np.pi*sig**2))*np.exp(-(x-mu)**2/(2.0*sig**2))
normfun = lambda x: norm.cdf(x-mu, scale=sig)
# range of integraion
xmax =np.pi
xmin =0
N =1000 # Number of draws
# Just want to plot the function
x=np.linspace(xmin, xmax, 1000)
plt.plot(x, f(x), 'b', label=u'Original $x \sin(x)$')
plt.plot( x, p(x), 'r', label=u'Importance Sampling Function: Normal')
plt.plot(x, np.ones(1000)/np.pi,'k')
xis = mu + sig*np.random.randn(N,1);
plt.plot(xis, 1/(np.pi*p(xis)),'.', alpha=0.1)
# IMPORTANCE SAMPLING
Iis = np.zeros(1000)
for k in np.arange(0,1000):
   # DRAW FROM THE GAUSSIAN mean =2 std = sqrt(0.4)
   xis = mu + sig*np.random.randn(N,1);
   xis = xis[ (xis<xmax) & (xis>xmin)] ;
   # normalization for gaussian from 0..pi
   normal = normfun(np.pi)-normfun(∅);
   Iis[k] =np.mean(f(xis)/p(xis))*normal;
Exact solution is: 3.14159265359
Mean basic MC estimate: 3.14068341144
Standard deviation of our estimates: 0.0617743877206
Mean importance sampling MC estimate: 3.14197268362
Standard deviation of our estimates: 0.0161935244302
```







Remember Convex (bowl) like functions have 1 global minimum



# 25 20 1.5 1.0 0.0 0.2 0.4 0.8 0.8 1.0

# Statement of the Learning Problem

The sample must be representative of the population!

 $egin{aligned} A:R_{\mathcal{D}}(g) \; smallest \, on \, \mathcal{H} \ B:R_{out}(g) pprox R_{\mathcal{D}}(g) \end{aligned}$ 

A: Empirical risk estimates insample risk.

B: Thus the out of sample risk is also small.



#### What we'd really like: population

i.e. out of sample RISK

$$\langle R_{out}
angle = E_{p(x,y)}[R(h(x),y)] = \int dy dx \, p(x,y) R(h(x),y)$$

- But we only have the in-sample risk, furthermore its an empirical risk
- And its not even a full on empirical distribution, as
   N is usually quite finite

#### LLN, again

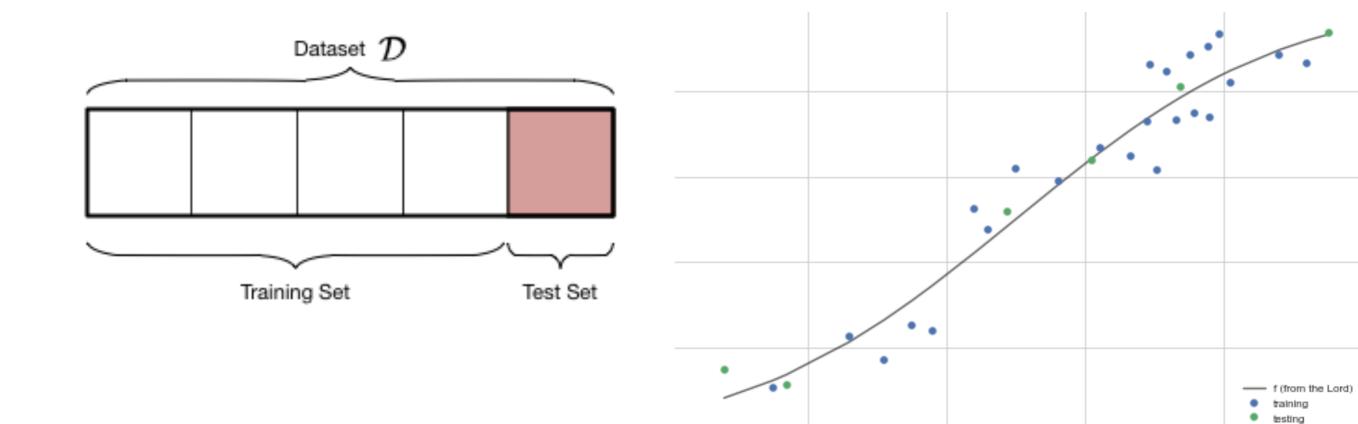
# The sample empirical distribution converges to the true population distribution as $N \to \infty$

Then we'll want an average over possible samples generated from the population.

We dont have that, so we:

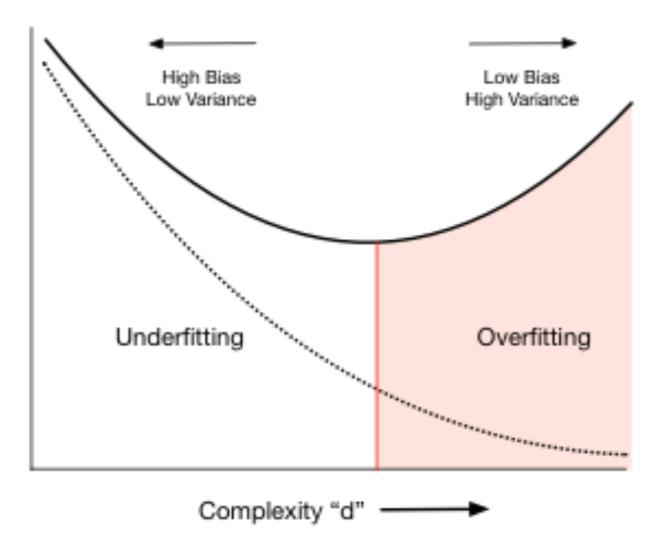
- stick to empirical risk in one sample, but then
- engage in train-test, validation, and cross-validation in our sample

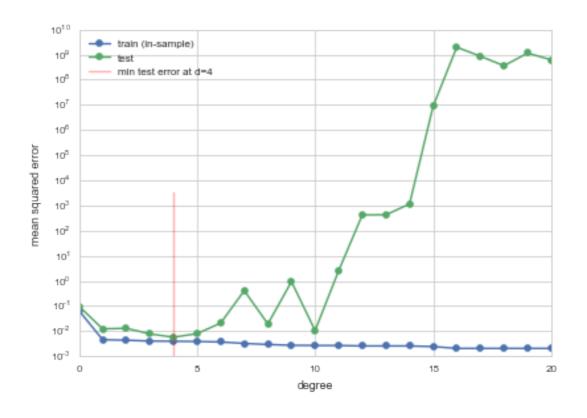




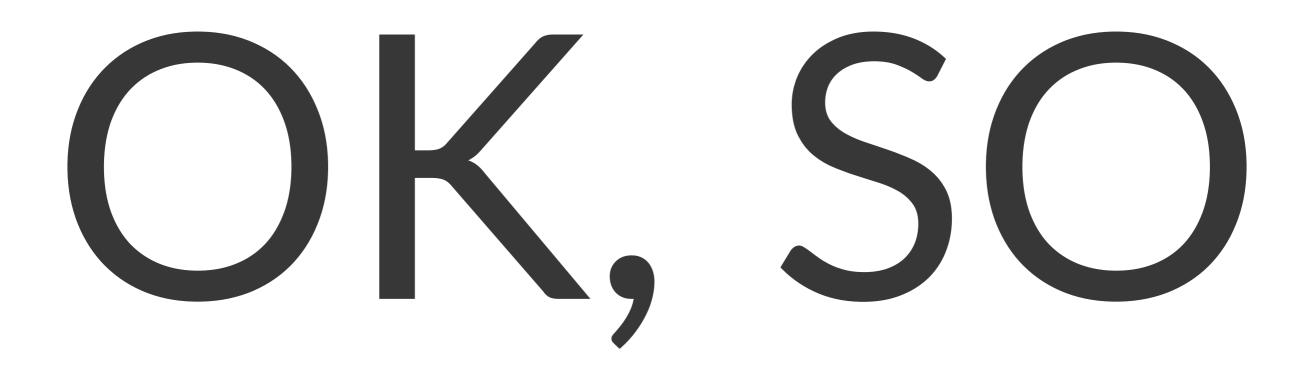


# BALANCE THE COMPLEXITY







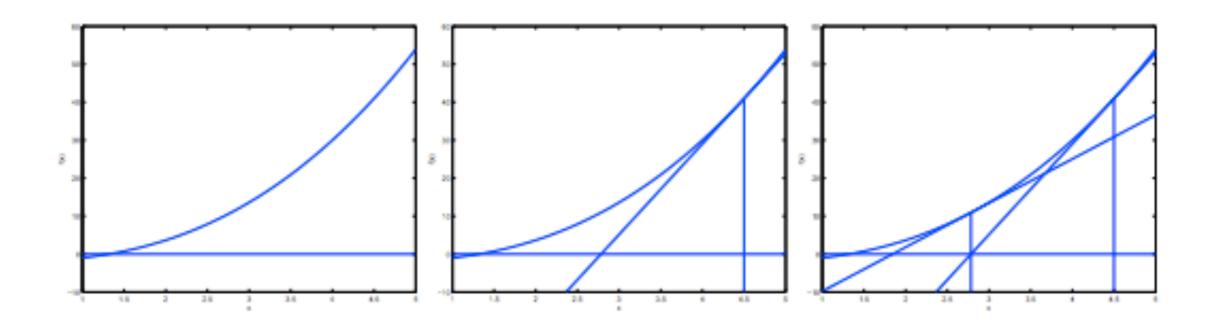


Is the In-Sample error small?

GET DERIVATIVES AND MINIMIZE



#### One way: Newton's Method



Find a zero of the first derivative. Need its slope.

Second Derivative or Hessian Matrix:  $\frac{\partial}{\partial \theta_i} \frac{\partial}{\partial \theta_i} R$ 



#### **Gradients and Hessians**

$$J(ar{ heta})= heta_1^2+ heta_2^2$$

Gradient: 
$$abla_{ar{ heta}}(J)=rac{\partial J}{\partial ar{ heta}}=egin{pmatrix} 2 heta_1 \ 2 heta_2 \end{pmatrix}$$

Hessian H = 
$$\begin{pmatrix} 2 & 0 \\ 0 & 2 \end{pmatrix}$$

Hessian gives curvature. Why not use it?

### MLE for Logistic Regression

- example of a Generalized Linear Model (GLM)
- "Squeeze" linear regression through a Sigmoid function
- this bounds the output to be a probability
- What is the sampling Distribution?

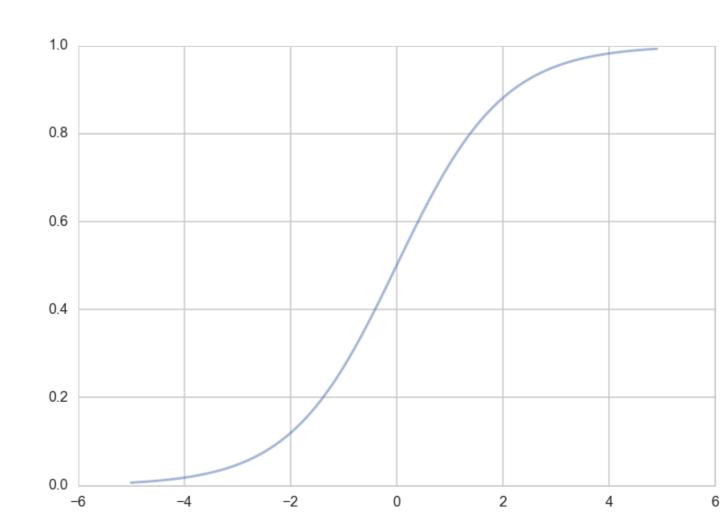


#### Sigmoid function

#### This function is plotted below:

```
h = lambda z: 1./(1+np.exp(-z))
zs=np.arange(-5,5,0.1)
plt.plot(zs, h(zs), alpha=0.5);
```

Identify:  $z = \mathbf{w} \cdot \mathbf{x}$  and  $h(\mathbf{w} \cdot \mathbf{x})$  with the probability that the sample is a '1' (y = 1).





Then, the conditional probabilities of y=1 or y=0 given a particular sample's features  $\mathbf{x}$  are:

$$P(y = 1|\mathbf{x}) = h(\mathbf{w} \cdot \mathbf{x})$$
  
 $P(y = 0|\mathbf{x}) = 1 - h(\mathbf{w} \cdot \mathbf{x}).$ 

These two can be written together as

$$P(y|\mathbf{x}, \mathbf{w}) = h(\mathbf{w} \cdot \mathbf{x})^y (1 - h(\mathbf{w} \cdot \mathbf{x}))^{(1-y)}$$

**BERNOULLI!!** 



#### Multiplying over the samples we get:

$$P(y|\mathbf{x},\mathbf{w}) = P(\{y_i\}|\{\mathbf{x}_i\},\mathbf{w}) = \prod_{y_i \in \mathcal{D}} P(y_i|\mathbf{x}_i,\mathbf{w}) = \prod_{y_i \in \mathcal{D}} h(\mathbf{w} \cdot \mathbf{x}_i)^{y_i} (1 - h(\mathbf{w} \cdot \mathbf{x}_i))^{(1-y_i)}$$

A noisy y is to imagine that our data  $\mathcal{D}$  was generated from a joint probability distribution P(x, y). Thus we need to model y at a given x, written as  $P(y \mid x)$ , and since P(x) is also a probability distribution, we have:

$$P(x,y) = P(y \mid x)P(x),$$

Indeed its important to realize that a particular sample can be thought of as a draw from some "true" probability distribution.

maximum likelihood estimation maximises the likelihood of the sample y,

$$\mathcal{L} = P(y \mid \mathbf{x}, \mathbf{w}).$$

Again, we can equivalently maximize

$$\ell = log(P(y \mid \mathbf{x}, \mathbf{w}))$$

#### Thus

$$egin{aligned} \ell &= log \left( \prod_{y_i \in \mathcal{D}} h(\mathbf{w} \cdot \mathbf{x}_i)^{y_i} (1 - h(\mathbf{w} \cdot \mathbf{x}_i))^{(1 - y_i)} 
ight) \ &= \sum_{y_i \in \mathcal{D}} log \left( h(\mathbf{w} \cdot \mathbf{x}_i)^{y_i} (1 - h(\mathbf{w} \cdot \mathbf{x}_i))^{(1 - y_i)} 
ight) \ &= \sum_{y_i \in \mathcal{D}} log h(\mathbf{w} \cdot \mathbf{x}_i)^{y_i} + log \left( 1 - h(\mathbf{w} \cdot \mathbf{x}_i) 
ight)^{(1 - y_i)} \ &= \sum_{y_i \in \mathcal{D}} \left( y_i log (h(\mathbf{w} \cdot \mathbf{x})) + (1 - y_i) log (1 - h(\mathbf{w} \cdot \mathbf{x})) 
ight) \end{aligned}$$

#### Logistic Regression: NLL

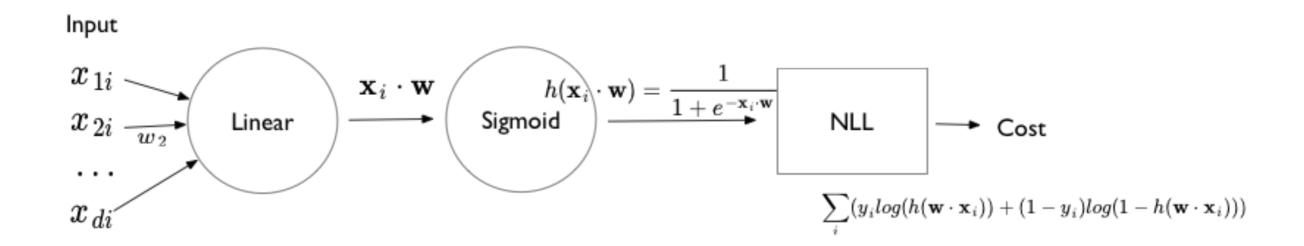
The negative of this log likelihood (NLL), also called *cross-entropy*.

$$NLL = -\sum_{y_i \in \mathcal{D}} \left( y_i log(h(\mathbf{w} \cdot \mathbf{x})) + (1 - y_i) log(1 - h(\mathbf{w} \cdot \mathbf{x})) 
ight)$$

Gradient: 
$$abla_{\mathbf{w}} NLL = \sum_i \mathbf{x}_i^T (p_i - y_i) = \mathbf{X}^T \cdot (\mathbf{p} - \mathbf{w})$$

Hessian:  $H = \mathbf{X}^T diag(p_i(1-p_i))\mathbf{X}$  positive definite  $\implies$  convex

# Units based diagram

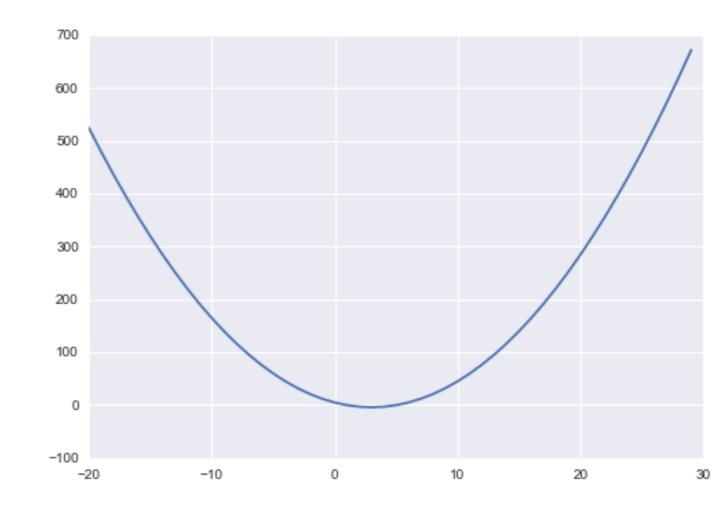


# Gradient ascent (descent)

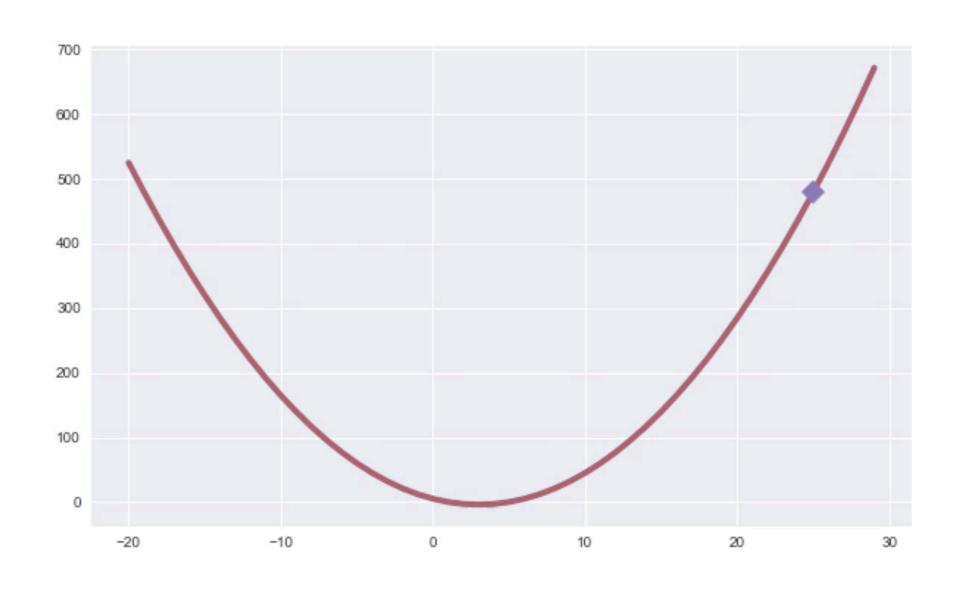
basically go opposite the direction of the derivative.

Consider the objective function:  $J(x) = x^2 - 6x + 5$ 

gradient = fprime(old\_x)
move = gradient \* step
current\_x = old\_x - move

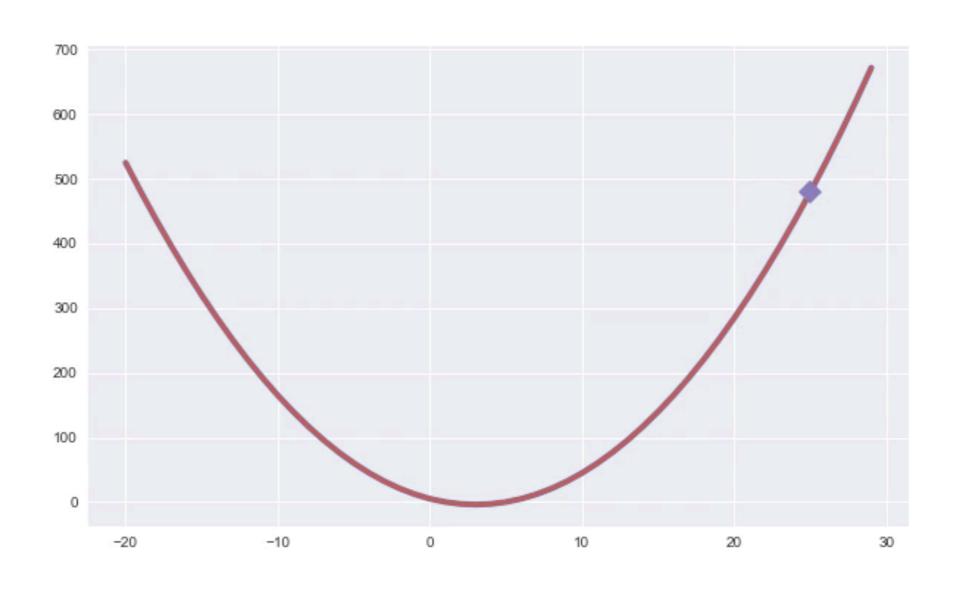


# good step size



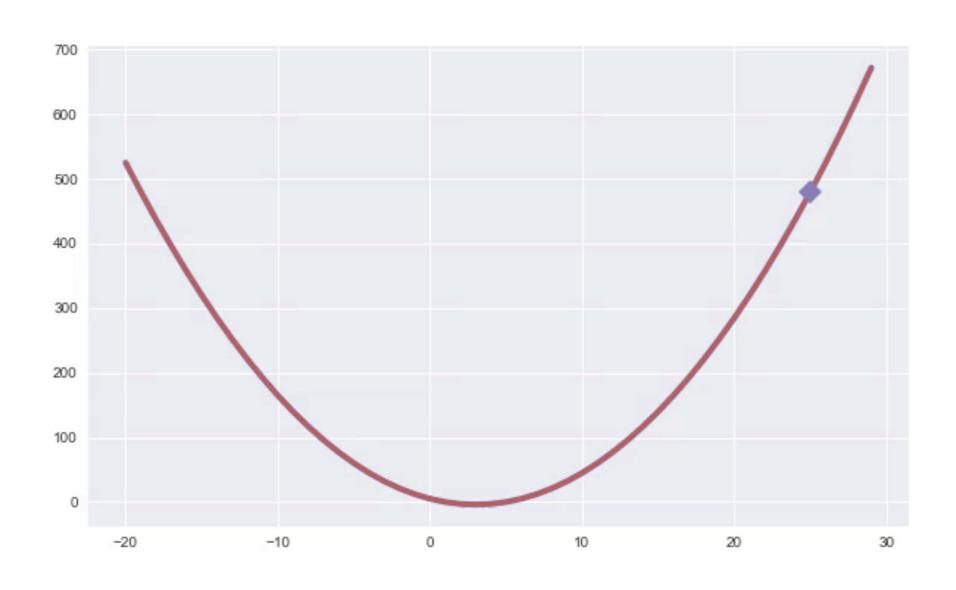


# too big step size





# too small step size





### **Example: Linear Regression**

$$\hat{y} = f_{ heta}(x) = heta^T x$$

**Cost Function:** 

$$R( heta) = rac{1}{2} \sum_{i=1}^m (f_ heta(x^{(i)} - y^{(i)})^2$$

Units Diagram: TODO. Minibarch SGD formula

### **Gradient Descent**

$$heta := heta - \eta 
abla_{ heta} R( heta) = heta - \eta \sum_{i=1}^m 
abla R_i( heta)$$

where  $\eta$  is the learning rate.

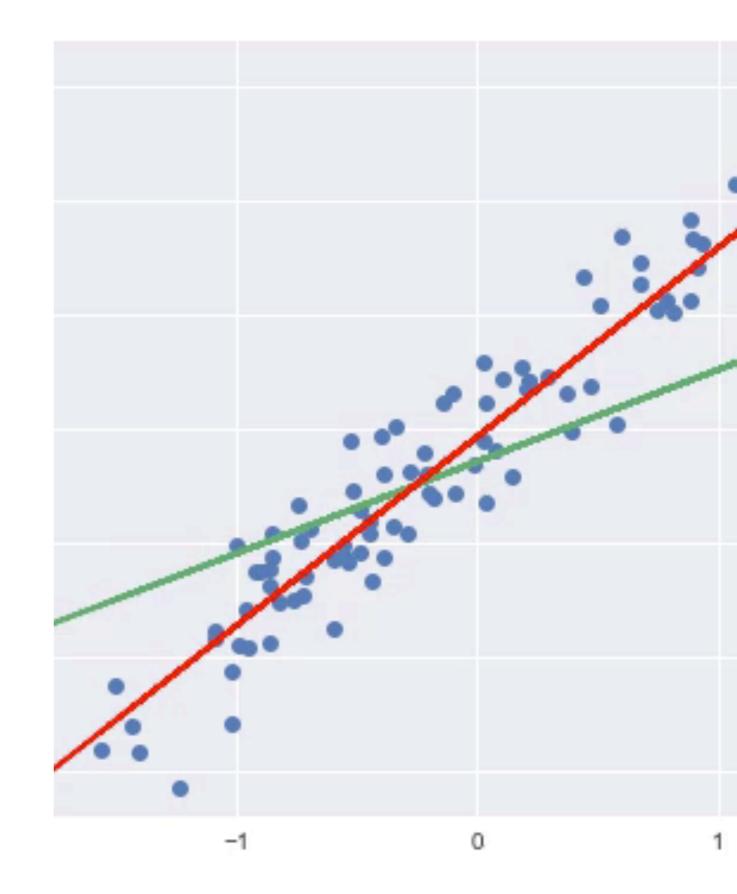
#### ENTIRE DATASET NEEDED

```
for i in range(n_epochs):
   params_grad = evaluate_gradient(loss_function, data, params)
   params = params - learning_rate * params_grad`
```



### Linear Regression: Gradient Descent

$$heta_j := heta_j + lpha \sum_{i=1}^m (y^{(i)} - f_ heta(x^{(i)})) x_j^{(i)}$$





# Gradient Descent.

We want:

$$abla_h R_{out}(h) = 
abla_h \int dx p(x,y) R_{out}(h(x),y)$$

For a particular sample, use the LLN

$$abla_h R_{out}(h) \sim 
abla_h rac{1}{N} \sum_{i \in \mathcal{D}} R_{in}(h(x_i), y_i)$$

SGD takes gradient inside sum

### Stochastic Gradient Descent

$$heta:= heta-lpha
abla_{ heta}R_i( heta)$$

#### ONE POINT AT A TIME

### For Linear Regression:

$$heta_j := heta_j + lpha(y^{(i)} - f_ heta(x^{(i)})) x_j^{(i)}$$

```
for i in range(nb_epochs):
    np.random.shuffle(data)
    for example in data:
        params_grad = evaluate_gradient(loss_function, example, params)
        params = params - learning rate * params grad
```



### Mini-Batch: do some at a time

- the risk surface changes at each gradient calculation
- thus things are noisy
- cumulated risk is smoother, can be used to compare to SGD
- epochs are now the number of times you revisit the full dataset
- shuffle in-between to provide even more stochasticity



