Bayesian Additive Regression Trees

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Added up Trees works great !!!!

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Basic BART Ideas

The original BART model is:

$$Y_i = f(x_i) + \epsilon_i, \ \epsilon_i \sim N(0, \sigma^2), \ iid.$$

where

the function f is represented as the sum of many regression trees.

How can we find a complex nonlinear function f with little (human) work ???!!!

BART was inspired by the Boosting literature, in particular the work of Jerry Friedman.

The connection to boosting is obvious in that the model is based on a sum of trees

However, BART is a fundamentally different algorithm with some

consequent pros and cons.

BART is a Bayesian MCMC procedure.

We:

- **P** put a prior on the model parameters (f, σ) .
- run a Markov chain with state (f, σ) such that the stationary distribution is the posterior

$$(f,\sigma) \mid D = \{x_i, y_i\}_{i=1}^n.$$

Examine the draws as a representation of the full posterior.

The respresentation of f is complex with changing dimension so it is difficult to look directly of draws of f.

However, we can look at marginals of σ and f(x) at any given x.

Pick of set of $\{x_j\}$, $j=1,2,\ldots,n_p$ and evaluate f at these x values.

So, if f_d is the d^{th} kept MCMC draw, then at every draw we have the fixed dimensional results

$$(f_d(x_1), f_d(x_2), \ldots, f_d(x_{n_p}))$$

Simple Examples

A Simple One Dimensional Simulated Example

Let's simulate some simple data to try BART on.

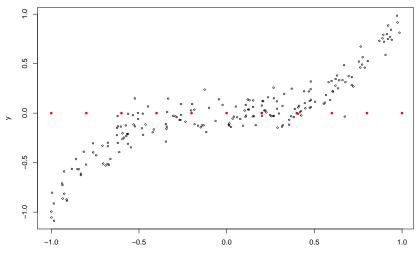
```
##simulate training data
sigma = .1
f = function(x) {x^3}
set.seed(17)
n = 200
x = sort(2*runif(n)-1)
y = f(x) + sigma*rnorm(n)

#xtest: values we want to estimate f(x) at
# this is also our prediction for y.
xtest = seq(-1,1,by=.2)
```

We have just one *x* so we can see the results with simple plots.

Let's have a look at our data:

```
##plot simulated data
plot(x,y,cex=.5)
points(xtest,rep(0,length(xtest)),col="red",pch=16,cex=.8)
```



Now we run BART on the simulated data using the function BART::wbart. $\#\#run \ wbart$ library (BART)

set.seed(14) #it is MCMC, set the seed!!
rb = wbart(x,y,xtest,nskip=500,ndpost=2000)

- nskip: the number of draws (MCMC iterations) that will be treated as burn-in, default is 500.
- ▶ ndpost: results will be kept after burn-in. Default is 1,000.

As usual, rb is a list containing results from the BART run.

wbart is for weighted BART, you can supply weights for each observation, but we won't be using this.

So, rb is the list containing the results of the call to wbart.

What is in rb ?????!!!!!

```
names(rb)

## [1] "sigma" "yhat.train.mean" "yhat.train" "yhat.test.mean"

## [5] "yhat.test" "varrount" "varprob" "treedraws"

## [9] "proc.time" "mu" "varcount.mean" "varprob.mean"

## [13] "rm.const"

dim(rb$yhat.test)

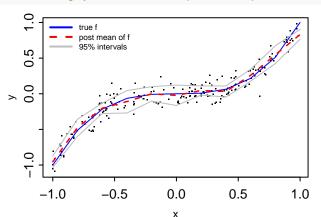
## [1] 2000 11
```

\$yhat.test:

The (d,j) element of yhat.test is the d^{th} draw of f evaluated at the j^{th} value of xtest.

2,000 draws of f, each of which is evaluated at 11 xtest values.

Let's have a look at the fit and uncertainty.



```
names(rb)
## [1] "sigma"
                        "yhat.train.mean" "yhat.train"
                                                          "yhat.test.mean"
                                         "varprob"
## [5] "vhat.test"
                        "varcount"
                                                          "treedraws"
## [9] "proc.time"
                        "m11"
                                         "varcount.mean"
                                                          "varprob.mean"
## [13] "rm.const"
dim(rb$yhat.train)
## [1] 2000 200
summary(rb$yhat.train.mean-apply(rb$yhat.train,2,mean))
        Min. 1st Qu. Median
                                       Mean
                                               3rd Qu.
                                                            Max.
## -1.166e-15 -8.327e-17 -3.469e-18 3.388e-17 5.551e-17 1.665e-15
summary(rb$yhat.test.mean-apply(rb$yhat.test,2,mean))
        Min. 1st Qu. Median
                                       Mean
##
                                               3rd Qu.
                                                            Max.
## -4.441e-16 -9.368e-17 1.041e-17 1.501e-16 1.353e-16 1.665e-15
```

\$yhat.train:

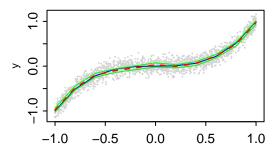
The (d,j) element of yhat.train is the d^{th} draw of f evaluated at the j^{th} value of x.

\$yhat.train(test).mean:

Average the draws to get the estimate of the posterior mean of f(x) (remember, f is the random variable !!).

What should happen when we bump up n (the sample size)?

```
n = 2000 #was 200 before !!
set.seed(17)
x = sort(2*runif(n)-1)
y = f(x) + sigma*rnorm(n)
rb2 = wbart(x,y,xtest) #run at defaults !!
plot(x,y,cex=.1,cex.axis=.8,cex.lab=.7, mgp=c(1.3,.3,0),tcl=-.2,pch=1,col="lightgrey")
lines(xtest,f(xtest),col="blue",lty=1)
lines(xtest,rb2$yhat.test.mean,col="red",lwd=1.5,lty=2)
qm = apply(rb2$yhat.test,2,quantile,probs=c(.025,.975))
lines(xtest,qm[1,],col="green",lty=1,lwd=1.0)
lines(xtest,qm[2,],col="green",lty=1,lwd=1.0)
```



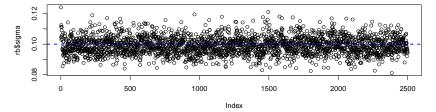
We nail f and the uncertainty goes down.

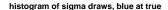
Our only simple parameter is σ . Let's look at the draws. The BART list component is sigma.

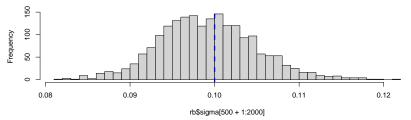
```
length(rb$sigma)
## [1] 2500
```

For σ we keep draws from all MCMC iterations, that is, we include the 500 burn-in draws and the 2,000 post burn-in draws.

```
par(mfrow=c(2,1))
#plot all draws to see burn-in, burns in fast!!
plot(rb\$sigma); abline(h=sigma,lty=2,col='blue',lwd=2)
# just plot draws after (hopefuly) burn-in
hist(rb\$sigma[500+1:2000],nclass=50,main="histogram of sigma draws, blue at true")
abline(v=sigma,lty=2,col="blue",lwd=3)
```





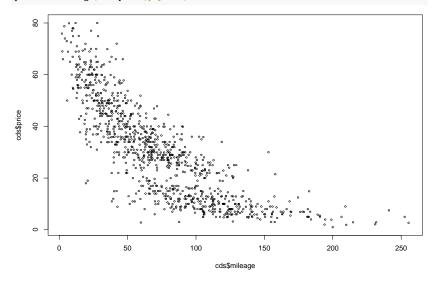


Cars with Mileage and Price

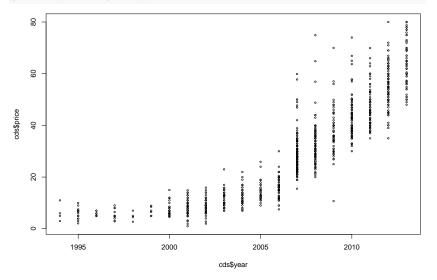
Each observation corresponds to a used car which has been sold.

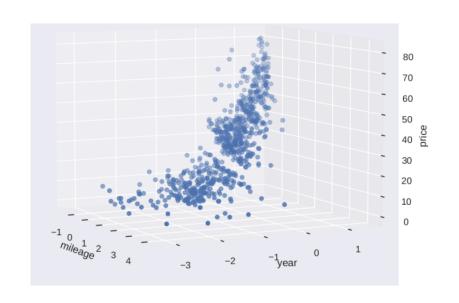
How does the price relate to mileage and year ?





plot(cds\$year, cds\$price,pty='s',cex=.5)



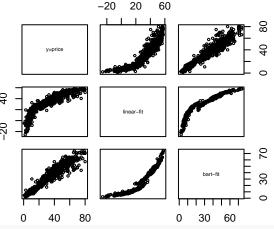


```
cbf = wbart(cds[,2:3],cds[[1]]) #nskip=100, ndpost=1000
plot(cbf$sigma,cex=.3,col='blue',pch=16,cex.lab=.5,cex.axis=.5)
                       6.5
                       6.0
              cbf$sigma
                       5.5
                       5.0
                                      200
                                              400
                                                       600
                                                               800
                                                                       1000
```

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We see the burn in as the Markov chain initially searches for fit.

```
clf = lm(price-.,cds)
fmat = cbind(cds$price,clf$fitted.values,cbf$yhat.train.mean)
colnames(fmat)=c('y=price','linear-fit','bart-fit')
pairs(fmat,cex.labels=.5,cex=.5)
```



```
cor(fmat)
## y=price linear-fit bart-fit
## y=price 1.0000000 0.9123897 0.9634202
## linear-fit 0.9123897 1.0000000 0.9494321
## bart-fit 0.9634202 0.9494321 1.0000000
```

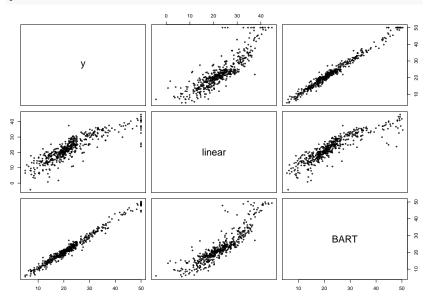
Boston Housing

```
library(MASS)
attach(Boston)
y = Boston$medv
x = Boston[,1:13]
set.seed(99) # Wayne Gretzky
burn=10000; nd=10000
bf = wbart(x,y,nskip=burn,ndpost=nd,printevery=5000) #print progress every 5000th MCMC item
plot(bf$sigma,cex=.3,col='blue',pch=16,cex.lab=.5,cex.axis=.5)
                     3.5
             of$sigma
                     2.5
                     5.
                                      5000
                                                 10000
                                                            15000
                                                                      20000
```

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Longer burn-in.

```
lmf = lm(y~.,data.frame(x,y))
fmat=cbind(y,lmf$fitted.values,bf$yhat.train.mean)
colnames(fmat) = c('y','linear','BART')
pairs(fmat,cex=.5,cex.lab=.5)
```



The Friedman Simulated Example

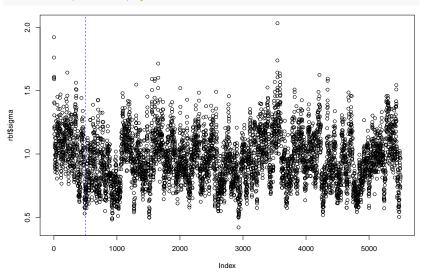
Let's try a tougher simulated problem.

```
## f and sigma
f = function(x) {
   10*\sin(pi*x[,1]*x[,2]) + 20*(x[,3]-.5)^2+10*x[,4]+5*x[,5]
sigma = 1.0 	 #y = f(x) + sigma*z , z~N(0,1)
## simulate
n = 100
             #number of observations
set.seed(99)
x=matrix(runif(n*10),n,10) #10 variables, only first 5 matter
Ev = f(x)
y=Ey+sigma*rnorm(n)
## run BART
burn=500:nd=5000
rbf = wbart(x,y,nskip=burn,ndpost=nd)
dim(rbf$yhat.train); dim(rbf$yhat.test); length(rbf$sigma)
## [1] 5000 100
## [1] 5000 0
## [1] 5500
$sigma:
```

MCMC draws of σ including burn-in. So, the length is nskip + ndpost.

Let's look at the draws of σ including burn-in:

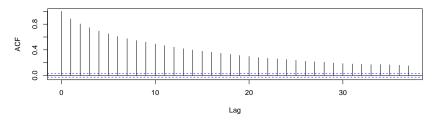
```
plot(rbf$sigma)
abline(v=burn,col="blue",lty=2)
```



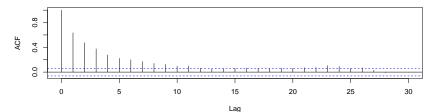
You can see the initial burn-in. Burns in pretty fast, but after that there is substantial autocorrelation!

```
par(mfrow=c(2,1))
acf(rbf$sigma)
ii = burn + (1:1000)*(nd/1000)
acf(rbf$sigm[ii])
```

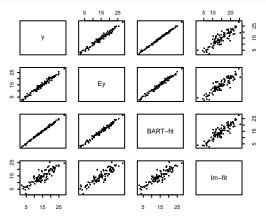
Series rbf\$sigma



Series rbf\$sigm[ii]



Did it work??!!



```
cor(fmat)

## y Ey BART-fit lm-fit

## y 1.000000 0.9847984 0.9973980 0.8841787

## Ey 0.9847984 1.000000 0.9892571 0.9009389

## BART-fit 0.9973980 0.9892571 1.000000 0.9008033

## lm-fit 0.8841787 0.9009389 0.9008033 1.0000000
```

- ▶ BART was able to fit the data very well.
- looks like it overfit a bit.
- burned in fast.
- draws may be autocorrelated, but not so much that you can't thin them out and get something nice.

Our course, whether it and converged and how autocorrelated the draws are can depend on what you look at.

For example, you might really care about f(x) at particular set of x and the draws $f_d(x)$ might exhibit more autocorrelation than σ .

Nevertheless, looking at draws of σ gives you a quick feel for how BART is finding fit.

More on BART: Model and Prior

So far we have been using wbart with only an understanding of the abstract model

$$Y_i = f(x_i) + \epsilon_i, \ \epsilon_i \sim N(0, \sigma^2).$$

To use more of the wbart options we need to have deeper understanding of how the BART model works.

In particular, we need to understand something about the BART prior on the function f.

Regression Trees

First, we review regression trees to set the notation for BART.

Note however that even in the simple regression tree case, our Bayesian approach is very different from the usual CART type approach.

The model will have *parameters* and corresponding *priors*.

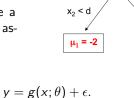
Model with a Single Tree

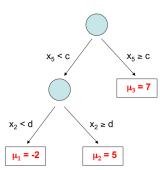
Let T denote the tree structure including the decision rules.

Let $M = \{\mu_1, \mu_2, \dots, \mu_b\}$, denote the set of bottom node μ 's.

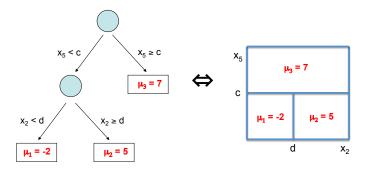
Let $g(x; \theta)$, $\theta = (T, M)$ be a regression tree function that assigns a μ value to x.

A single tree model:





A coordinate view of $g(x; \theta)$



Easy to see that $g(x; \theta)$ is just a step function.

The BART Model

In BART, the function f is expresses as a sum of regression trees:

Y = g(x;T₁,M₁) + g(x;T₂,M₂) + ... + g(x;T_m,M_m) +
$$\sigma$$
z, z ~ N(0,1)

$$m = 200, 1000, \dots, \text{big}, \dots$$

 $f(x \mid \cdot)$ is the sum of all the corresponding μ 's at each bottom node.

Such a model combines additive and interaction effects.

All parameters but σ are unidentified !!!!

... the connection to Boosting is obvious...

But,

Rather than simply adding in fit in an iterative scheme, we will explicitly specify a prior on the model which directly impacts the performance.

In wbart we have the parameter:

ntree: the parameter m, the number of trees in the sum.

Complete the Model with a Regularization Prior

$$\pi(\theta) = \pi((T_1, M_1), (T_2, M_2), \dots, (T_m, M_m), \sigma)$$

$$= \pi(\sigma) \prod_{i=1}^m \pi(T_i, M_i)$$

$$= \pi(\sigma) \prod_{i=1}^m \pi(T_i) \pi(M_i \mid T_i)$$

π wants:

- each T small.
- ightharpoonup each μ small.
- \blacktriangleright "nice" σ (e.g. smaller than the least squares estimate).

We refer to π as a regularization prior because it restrains the overall fit.

In addition, it keeps the contribution of each $g(x; T_i, M_i)$ model component small.

$$\pi(T)$$
, prior on T

Since the T_i are iid, we must choose a single $\pi(T)$.

We specify a process we can use to draw a tree from the prior. The probability a current bottom node, at depth d, gives birth to a left and right child is

$$\frac{\alpha}{(1+d)^{\beta}}$$

In wbart we have the parameters:

base: the parameter α with default value .95.

power: the parameter β with default value 2.0.

This makes non-null but small trees likely.

Prior distribution on the number of bottom nodes:

obability
 5
5
8
9
3
).

But note, if the data demands it, you can build deeper trees than this prior would suggest.

This would be needed to model complex interactions.

$$\pi(M \mid T)$$
, prior on bottom node μ

Let b be the number of bottom nodes in the tree T.

Then
$$M = \{\mu_1, \mu_2, \dots, \mu_b\}.$$

We let,

$$\pi(M \mid T) = \prod_{i=1}^{b} \pi(\mu_i)$$

That is

$$\mu_i \sim \pi(\mu)$$
, iid

Now we only have to choose $\pi(\mu)$.

First of all we *center the data* so that we can assume we want to think f, and hence each μ towards 0.

So, essentially, we fit the model:

$$Y_i = \mu + f(x_i) + \epsilon_i$$

but pick a value $\hat{\mu}$ for μ .

The code just subtracts $\hat{\mu}$ from each y_i and then adds it back to the draws of f(x).

In wbart:

fmean: the value $\hat{\mu}$, with default value \bar{y} .

mu: the $\hat{\mu}$ that was used (so default will just be \bar{y}).

We let

$$\mu_i \sim N(0, \tau^2)$$

where the zero mean is justified by the centering.

How do we choose the key parameter τ ??

The key observation is that:

$$f(x \mid T, M) = \mu_1 + \mu_2 + \cdots + \mu_m.$$

$$Y = g(x; T_1, M_1) + g(x; T_2, M_2) + \dots + g(x; T_m, M_m) + \sigma z, \quad z \sim N(0, 1)$$

$$\mu_i \sim N(0, \tau^2)$$

$$f(x \mid T, M) = \mu_1 + \mu_2 + \cdots + \mu_m.$$

Which gives us,

$$f(x) \mid T \sim N(0, m\tau^2)$$

which does not depend on T or x !!!!!

$$f(x) \mid T \sim N(0, m\tau^2)$$

In wbart we use the parameter k to specify the μ prior via

$$\tau = \frac{\max(y) - \min(y)}{2 \, k \, \sqrt{m}}$$

that way

$$k\sqrt{m}\,\tau = \frac{\max(y) - \min(y)}{2}$$

so that from the "middle" of f to the extreme is k standard deviations.

In wbart, k is called k:

k:

number of standard deviations of f(x) that equal half the range of y, the default value is 2.

You can also just directly set the standard deviation of f(x).

$$f(x) \sim N(0, \sigma_f^2)$$

which is the same as just setting

$$\tau^2 = \frac{\sigma_f^2}{m}$$

In wbart:

sigmaf: prior standard deviation of f(x).

 $\pi(\sigma)$, prior on σ .

$$\sigma^2 \sim \frac{\nu \lambda}{\chi^2}$$

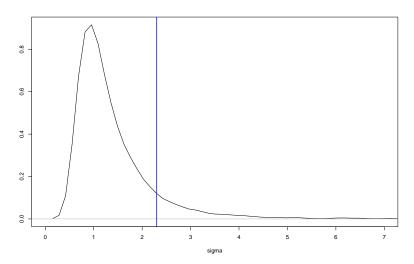
The wbart strategy is to choose ν and a rough estimate of σ , $\hat{\sigma}$.

If p < n, $\hat{\sigma}$ is the usual least squares estimate, else sd(y).

We then choose λ so that $\hat{\sigma}$ is at a chosen quantile q of the prior.

Solid blue line at $\hat{\sigma}$.

$$p(\sigma < \hat{\sigma}) = q.$$



In wbart:

 $sigdf: \nu$, default is 3.

sigquant: q, default is .9.

sigest: $\hat{\sigma}$, default is least squares estimate if p < n and sd(y) otherwise.

You can also just set λ directly:

lambda: λ .

wbart Prior Options

In summary:

wbart has the following BART prior related parameters:

T: power, base.

M: k, sigmaf.

 σ : sigest, sigdf, sigquant, lambda

In addition, you must choose ntree and numcut.

numcut is the number of cutpoints c used for the decision rules $x_i < c$.

Let's just look at a few examples to get some intuition for the effect of these prior choices on the BART inference.

```
Back to our 1-D example so we can see what happens.
sigma = .1
f = function(x) \{x^3\}
set.seed(17)
n = 100
x = sort(2*runif(n)-1)
v = f(x) + sigma*rnorm(n)
lmf = lm(y~x,data.frame(x,y))
sigest = summary(lmf)$sigma
cat("least squares estimate of sigma is: ", sigest ,"\n")
## least squares estimate of sigma is: 0.1742962
#density of sigma for sigma^2 ~ nu*lam/chisq nu
sden=function(sv,nu,lam) {
   dchisq(nu*lam/sv^2,df=nu)*(2*nu*lam)/sv^3
#lam val which puts sigest and sigguant quantile
lamval = function(sigest, sigquant, nu) {
   qchi = qchisq(1.0-sigquant,nu)
```

lambda = (sigest*sigest*qchi)/nu #lambda parameter for sigma prior

lambda

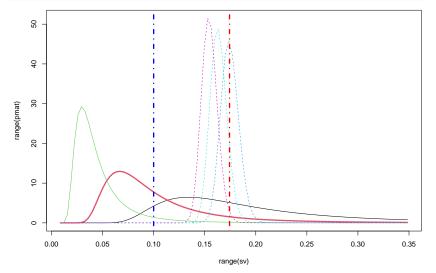
sv = seq(from=.05*sigest,to=2*sigest,length.out=100)

pmat[,i] = sden(sv,pg[i,2],lamval(sigest,pg[i,1],pg[i,2]))

pmat = matrix(0.0,length(sv),nrow(pg))

for(i in 1:nrow(pg)) {

```
plot(range(sv),range(pmat),type="n")
lwv = rep(1,nrow(pg)); lwv[2]=3; ltyv = 1+floor(0:5/3)
for(i in 1:nrow(pg)) lines(sv,pmat[,i],col=i,lwd=lwv[i],lty=ltyv[i])
abline(v=sigest,col="red",lty=4,lwd=3)
abline(v=sigma,col="blue",lty=4,lwd=3)
```

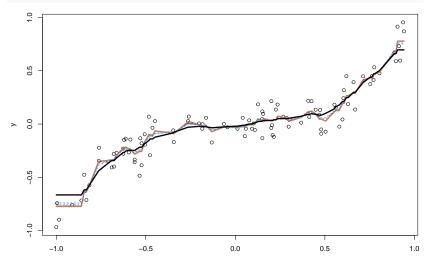


Run BART at our 6 prior settings and a seventh where we use ntree=5000 and k=5, this will give us a smoother function.

bf2 = wbart(x,y,ntree=5000,k=5)

```
fmat = matrix(0.0,n,nrow(pg))
for(i in 1:nrow(pg)) {
   bf = wbart(x,y,sigquant=pg[i,1],sigdf=pg[i,2])
   fmat[,i] = bf$yhat.train.mean
}
#more trees and more shrinkage => smoother f
```

```
plot(x,y)
for(i in 1:nrow(pg)) lines(x,fmat[,i],col=i,lwd=lwv[i],lty=ltyv[i])
lines(x,bf2$yhat.train.mean,lty=1,lwd=3)
```



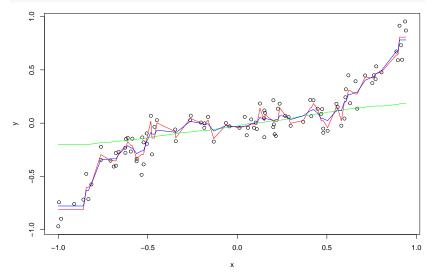
The fit with a lot of trees is indeed smoother, but the other fits are remarkably similar.

Ok, let's mess it up!!

We'll put in σ too small prior, a σ too big prior, and a σ just right prior.

```
bfb1 = wbart(x,y,sigest=.01,sigdf=500) #sigma small => overfit
bfb2 = wbart(x,y,sigest=3,sigdf=500) #sigma big => underfit
bfg = wbart(x,y,sigest=sigma,sigdf=5000) #got sigma right!
```

```
plot(x,y)
lines(x,bfb1$yhat.train.mean,col="red")
lines(x,bfb2$yhat.train.mean,col="green")
lines(x,bfg$yhat.train.mean,col="blue")
```



That worked.



$$\begin{split} Y &= g(x; T_1, M_1) + ... + g(x; T_m, M_m) + \sigma z \\ & \text{plus} \\ & \pi((T_1, M_1), (T_m, M_m), \sigma) \end{split}$$

First, it is a "simple' Gibbs sampler:

$$(T_i, M_i) \mid (T_1, M_1, \dots, T_{i-1}, M_{i-1}, T_{i+1}, M_{i+1}, \dots, T_m, M_m, \sigma)$$

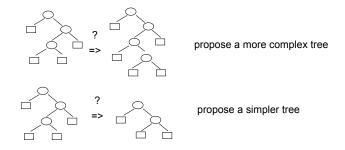
 $\sigma \mid (T_1, M_1, \dots, T_m, M_m)$

To draw $(T_i, M_i) \mid \cdot$ we subtract the contributions of the other trees from both sides to get a simple one-tree model.

We integrate out M to draw T and then draw $M \mid T$.

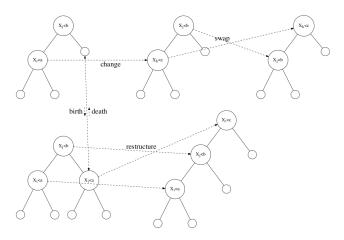
To draw T we use a Metropolis-Hastings with Gibbs step.

We use various moves, but the key is a "birth-death' step.

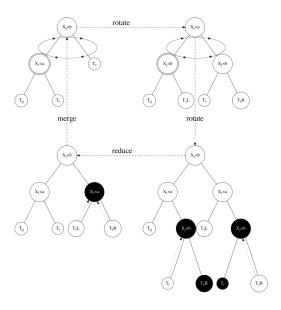


Getting the MCMC to work well with a single tree model is quite difficult.

Original Bayesian CART moves:

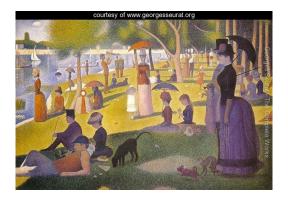


Matt Pratola has developed as set a sophisticated moves that help.



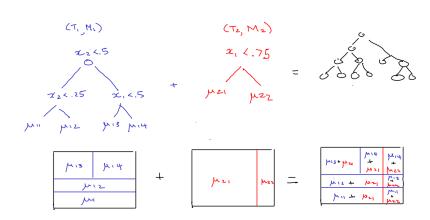
Added up Trees works great !!!!

But, the BART MCMC works amazingly well !!!!



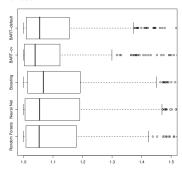
Adding in little bits of fit at a time make for a great model and a great MCMC !!!!!.

But, the BART MCMC works amazingly well !!!!



Did out of sample predictive comparisons on 42 data sets. (thanks to Wei-Yin Loh!!)

- p=3-65, n=100-7,000.
- ▶ for each data set 20 random splits into 5/6 train and 1/6 test
- use 5-fold cross-validation on train to pick hyperparameters (except BART-default!)
- gives 20*42 = 840 out-of-sample predictions, for each prediction, divide rmse of different methods by the smallest
- + each boxplots represents 840 predictions for a method
- + 1.2 means you are 20% worse than the best
- + BART-cv best
- + BART-default (use default prior) does amazingly well!!



Using Predict and Controlling What Is Saved

Up to now we have given wbart (X, y, X_p) .

At every iteration of the MCMC, (f, σ) is updated.

Updating f means all the $(T_i, M_i), j = 1, 2, \dots, m$ are updated.

In addition, we evaluate f at each x in X and each x in X_p .

We can simplify things and speed things up by thinning these evaluations for both $x \in X$ and $x \in X_p$.

In addition, we can save draws of f and evaluate them at x after we have run the MCMC as you would with a "predict" function.

wbart has the parameters:

nkeeptrain:

number of draws of f to evaluate the training data at. The draws are evenly spaced so that if ndpost=1,000 and nkeeptran=100, then we would evaluate every 10th draw of f at the $x \in X$.

nkeeptest: same thing for the test data.

nkeeptestmean: number of draws of f to evaluate the test data in order to compute pat.test.mean.

nkeeptreedraws: number of draws of f (the set of (T_j, M_j)) to return.

The tree draws are not terribly interpretable, but by saving them we can evaluate f draws at a new set of x vectors without rerunning the MCMC.

Let's try it.

np=100000

Xp = matrix(rnorm(np*p),ncol=p)

```
##simulate data
set.seed(99)
n=5000
p=10
beta = 3*(1:p)/p
sigma=1.0
X = matrix(rnorm(n*p),ncol=p)
y = 10+X %*% matrix(beta,ncol=1) + sigma*rnorm(n)
y=as.double(y)
```

[1] 100 100000
names(bfk\$treedraws)
[1] "cutpoints" "trees"
str(bfk\$treedraws\$trees)

The trees are stored in one long character string which is not too useful to look at but we can see that there are 100 draws each consisting of 200 trees.

chr "100 200 10\n3\n1 5 85 0.03572449378\n2 0 0 0.1218427186\n3 0 0 0.4938837128\n3\n1

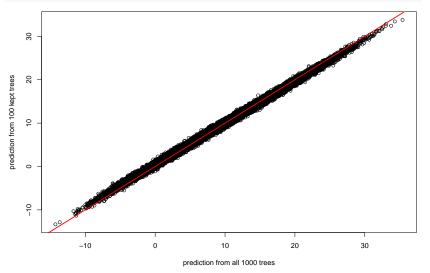
For example, it might be fast to just keep 100 trees:

```
t1 = system.time({bfk1 = wbart(X.v.Xp)})
t2 = system.time({bfk2 = wbart(X,y,Xp,
                      nkeeptrain=0,nkeeptest=0,nkeeptestmean=0,nkeeptreedraws=100)})
t3 = system.time({pred2 = predict(bfk2, Xp, mc.cores=8)})
dim(pred2)
## [1] 100 100000
t.1
     user system elapsed
##
## 115.793 0.400 116.630
t.2
##
     user system elapsed
## 23.347 0.000 23.344
t.3
##
      user system elapsed
   72.003 0.033 9.077
```

pred2 has row dimension equal to the number of kept tree draws (100) and column dimension equal to the number of row in X_p (100,000).

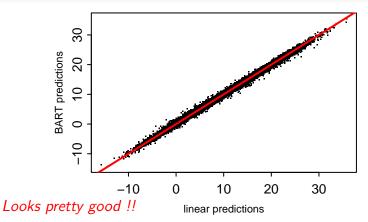
33+18 seconds to get predictions on 100,000 observations using 100 stored trees. while it took 188 seconds to do it the old way.

Let's compare the predictions:



Could be perfectly good as a practical matter.

Let's compare the BART fit to a linear fit (we simulated from the linear model).



The Diabetes Example

Let's look at an example with real data.

We'll try the diabetes data which is available at Hastie, Tibshirani, Wainright website.

Diabetes data

These data consists of observations on 442 patients, with the response of interest being a quantitative measure of disease progression one year after baseline. There are ten baseline variables—age, sex, body-mass index, average blood pressure, and six blood serum measurements—plus quadratic terms, giving a total of 64 features.

First used in LARS paper

Tab-delimited diabetes data (text file)

Note that these data are first standardized to have zero mean and unit L2 norm before they are used in the examples.

Let's read in the data.

```
db = read.csv("http://www.rob-mcculloch.org/data/diabetes.csv")
#first col is y, 2-11 are x, 12-65 are xi^2, x_i * x_j (except sex dummy)
xB = as.matrix(dbl,2:11]) #x for BART
xL = as.matrix(dbl,2:ncol(db)]) #x for lasso, includes transformations
yBL = db$y #y for BART and lasso

dim(db)
## [1] 442 65
names(db[,1:15])
## [1] "y" "age" "sex" "bmi" "map" "tc" "ldl" "hdl" "tch"
## [10] "ltg" "glu" "age.2" "bmi.2" "map.2" "tc.2"
```

So there are 442 observations. The first column is our response and the next 10 columns are the x's.

The rest of the columns are the squares and products of the original 10 x's giving 64 "variables'.

For BART we just want a matrix of the 10 x's.

We will compare BART with just the 10 original vars to glmnet with all 64 predictors.

Note that all the predictors have been standardized. This is crucial for glmnet and does not matter for BART.

We'll just do some random train/test splits and to compare the out of sample performance of BART to that of the lasso.

```
rmsef = function(y,yhat) {return(sqrt(mean((y-yhat)^2)))}
nd=30 #number of train/test splits

n = length(yBL)
ntrain=floor(.75*n) #75% in train each time

rmseB = rep(0,nd) #BART rmse
rmseL = rep(0,nd) #lasso rmse
fmatL=matrix(0.0,n-ntrain,nd) #out-of-sample lasso predictions
fmatB=matrix(0.0,n-ntrain,nd) #out-of-sample BART predictions
```

So, 30 times we will randomly pick 75% of the data to be train and predict on the remaining 25%.

We'll just do some random train/test splits and to compare the out of sample performance of BART to that of the lasso.

```
library(glmnet)
for(i in 1:nd) {
   set.seed(i)
  # train/test split
   ii=sample(1:n,ntrain)
   #u
   yTrain = yBL[ii]; yTest = yBL[-ii]
   #x for BART
  xBTrain = xB[ii.]: xBTest = xB[-ii.]
   #x for lasso
  xLTrain = xL[ii.]: xLTest = xL[-ii.]
   #lasso
   cvL = cv.glmnet(xLTrain.vTrain.familv="gaussian".standardize=FALSE)
   bestlam = cvL$lambda.min
   fLTrain = glmnet(xLTrain,yTrain,family="gaussian",lambda=c(bestlam),
                           standardize=FALSE)
   #RART
   bfTrain = mc.wbart(xBTrain.vTrain.xBTest.mc.cores=8.keeptrainfits=FALSE)
   #get predictions on test
   yBhat = bfTrain$yhat.test.mean
   vLhat = predict(fLTrain,xLTest,s=bestlam,type="response")[,1]
   #store results
   rmseB[i] = rmsef(yTest,yBhat); rmseL[i] = rmsef(yTest,yLhat)
  fmatL[,i]=yLhat; fmatB[,i]=yBhat
```

Just using default BART!!		

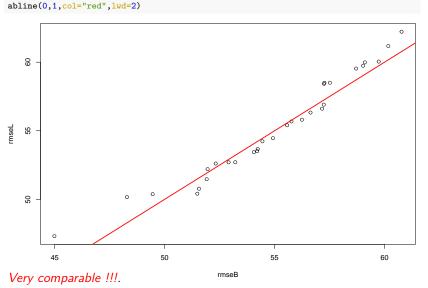
Data is already standardized so don't have standardize=FALSE in glmnet.

The basic arguments for mc.wbart are the same as in wbart.

Using parallel version of wbart.

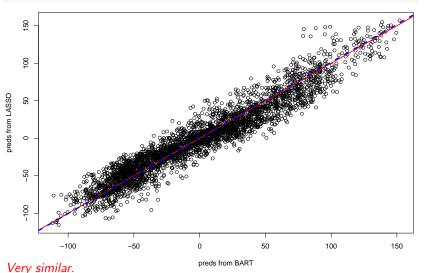
Let's compare the out of sample RMSEs.

```
qqplot(rmseB,rmseL)
```



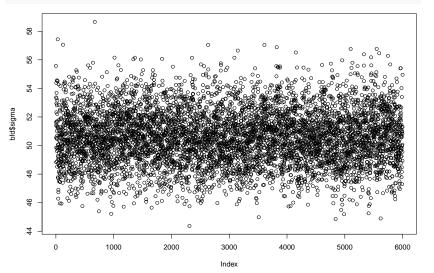
Let's compare the out of sample predictions.

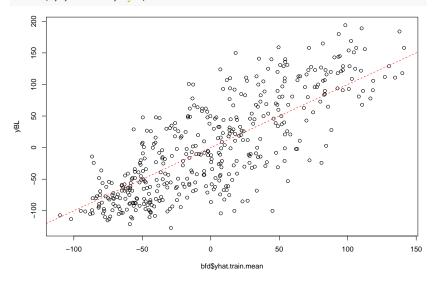
```
plot(as.double(fmatB),as.double(fmatL),xlab="preds from BART",ylab="preds from LASSO")
abline(0,1,col="red",lwd=2)
lmtemp = lm(B-L,data.frame(B=as.double(fmatB),L=as.double(fmatL)))
abline(lmtemp$coef,col="blue",lty=2,lwd=3)
```



Now that we know the default prior *may* be giving reasonable results let's look at a longer run.

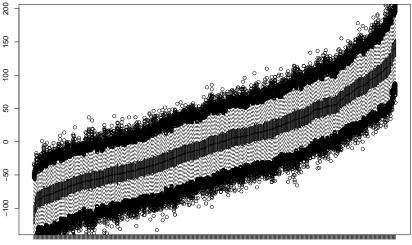
```
bfd = wbart(xB,yBL,nskip=1000,ndpost=5000) #keep it simple
plot(bfd$sigma)
```





 σ is about 50 !!

```
ii = order(bfd$yhat.train.mean)
boxplot(bfd$yhat.train[,ii],ylim=range(yBL))
```



17 35 53 71 89 110 133 156 179 202 225 248 271 294 317 340 363 386 409 432

A lot of uncertainty !!!!

Very automatically,	BART gaves	s us good o	out of sample results, did	

not have to choose transformations to include !!

▶ BART gave us the uncertainty!!!