

# Case Studies in Bayesian Data Science

## 5: Big-Data Bayesian Data Science

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SHORT COURSE (DAY 5)  
UNIVERSITY OF READING (UK)

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[users.soe.ucsc.edu/~draper/Reading-2015-Day-5.html](http://users.soe.ucsc.edu/~draper/Reading-2015-Day-5.html)

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- (2001) The defining dimensions of Big Data are identified as the 3Vs: **volume**, **velocity** and **variety**.

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- (2007) Now the estimate is that in **2006** the world created **161 exabytes** of data; between **2006** and **2010** this increased six-fold, to 988 exabytes/year, doubling every 18 months; as of **2012** we were up to **2.8 zettabytes** (1 trillion GB) of data generated/year worldwide.
- (2008) It was estimated that internet protocol (IP) traffic will reach **0.5 zettabytes/year** in **2012** (this prediction was correct), an eightfold increase in 5 years.
- (2009) A study finds that in **2008** Americans consumed information for about 1.3 trillion hours, an average of 12 hours/day/person; consumption totaled **3.6 zettabytes** (11 trillion words), averaging out to 100,000 words and 34 GB per person per day; this means that you were exposed to about **100 words/minute** of your 16 waking hours per day.
- (2011) It's estimated that the world's information storage capacity grew at a compound annual rate of **25%/year** between **1986** and **2007**; moreover, in **1986**, 99% of storage was analog, but in **2007** 94% was digital.

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  - I've seen a trial that would need **420 million** total experimental subjects to find a business-relevant effect with (5%/5%) false positive/negative error rates.

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- The idea is not new — it goes back at least to WR Thompson in 1933 — but it's **not yet been fully exploited** in *eCommerce*, even at cutting-edge companies such as Google and Amazon.

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Of these **four activities**, only **description** involves **no uncertainty**: we're **not sure** about the **answers** to the **inferential**, **predictive** and **decision questions** above, even **after the experiment has been run**.

# Bayesian Analysis of $A/B$ Test Results

**Case Study:** **experiment 5108**, initial outcome variable raw GMB;  
visitors randomized to  $T$  or  $C$  and followed for 2 weeks.

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The **first thing** to **know** about **raw GMB**, even in a **multi-week trial**, is that **most** of the **data values** at the **visitor level** (i.e., **aggregated** across **1 or more visits during the 2 weeks**) are **\$0**:

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```
# experiment id: 5108
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```
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```

**Each group** had **about 12 million observations**, of which **about 90%** were **0**.

# Initial Descriptive Analysis

```
# analysis (1): read in the non-zero treatment data and
# look at it descriptively

setwd( "C:/e-Bay/Lift" )

nonzero.treatment.values <-
  scan( "pgmb-raw-5108-treatment-v1.txt" )

# Read 1133706 items

print( n.nonzero.treatment.values <-
  length( nonzero.treatment.values ) )

# 1133706

nonzero.treatment.values <- sort( nonzero.treatment.values )

print( mean.nonzero.treatment.values <-
  mean( nonzero.treatment.values ) )

# 98.50182
```

# Initial Descriptive Analysis (continued)

```
n.zero.treatment.values <- 11100587
```

```
print( n.treatment.total <- n.nonzero.treatment.values +  
      n.zero.treatment.values )
```

```
# 12234293
```

```
print( overall.treatment.mean <- ( n.zero.treatment.values * 0 +  
      n.nonzero.treatment.values * mean.nonzero.treatment.values ) /  
      n.treatment.total )
```

```
# 9.127794
```

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So the **mean raw GMB value** in the **treatment group** was **\$9.13**.

```
hist( nonzero.treatment.values, breaks = 100000, probability = T,  
      main = '', xlab = 'Nonzero Treatment Values',  
      ylab = 'Density' )
```



# Initial Descriptive Analysis (continued)

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n.zero.treatment.values <- 11100587
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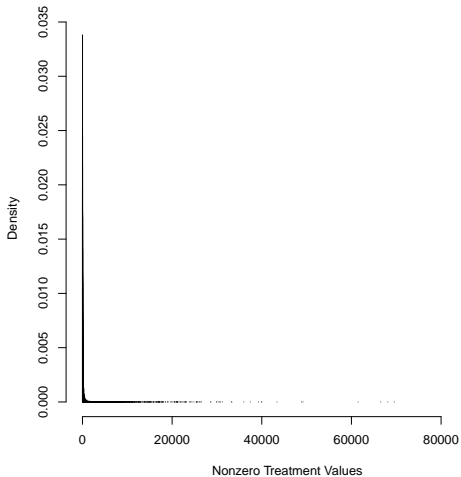
```
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So the **mean raw GMB value** in the **treatment group** was **\$9.13**.

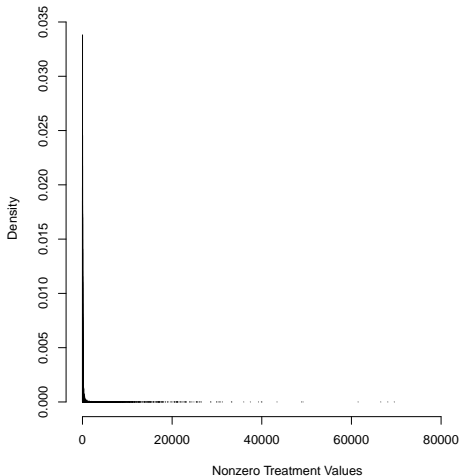
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```

The **histogram** on the **next page** offers a way to get information about the **distributional shape** of the **nonzero raw GMB variable**.

# Initial Descriptive Analysis (continued)

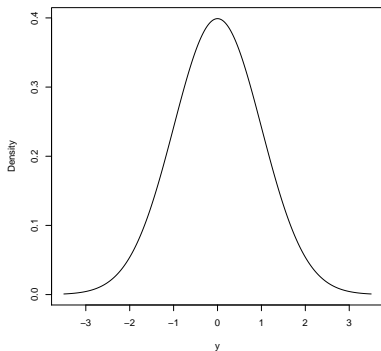


## Initial Descriptive Analysis (continued)

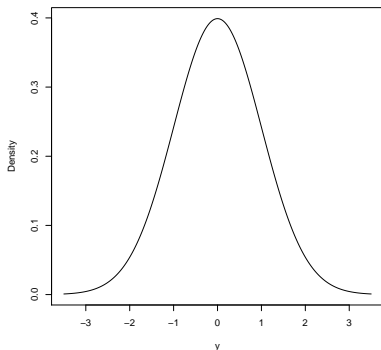


**Nonzero treatment raw GMB** had an **enormously heavy right-hand tail**: most of the **values** were **near \$0**, but the **largest value** was **\$91,417**.

# The Normal, or Gaussian, Distribution

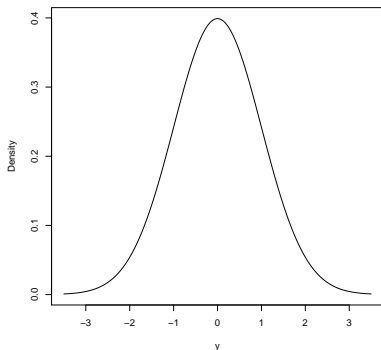


# The Normal, or Gaussian, Distribution



The **most-studied** distributional shape is that of the **normal**, or **Gaussian**, distribution.

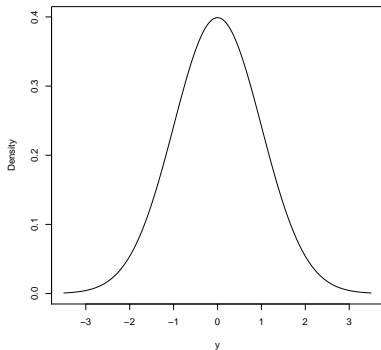
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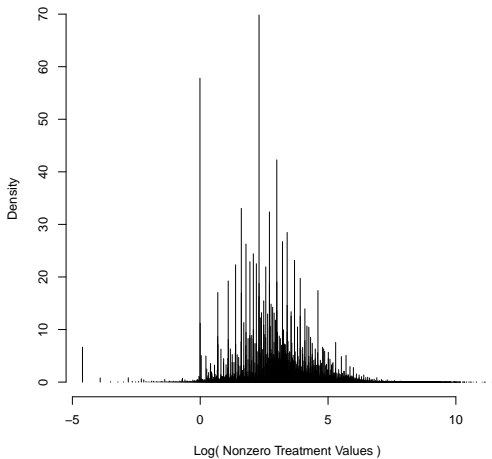


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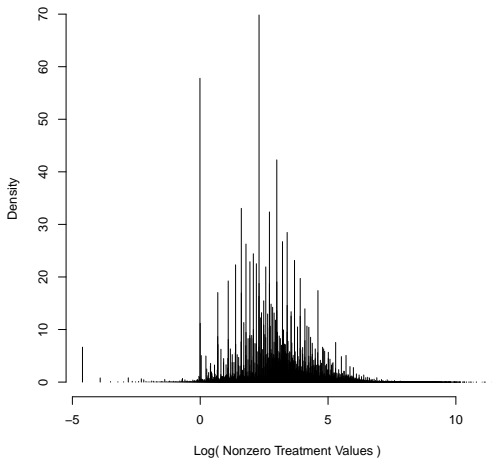
By **contrast**, the **nonzero treatment raw GMB variable** had **skewness** and **kurtosis** values of **+51.0** and **+6,017**, respectively.

# Nonzero Raw GMB on the Log Scale



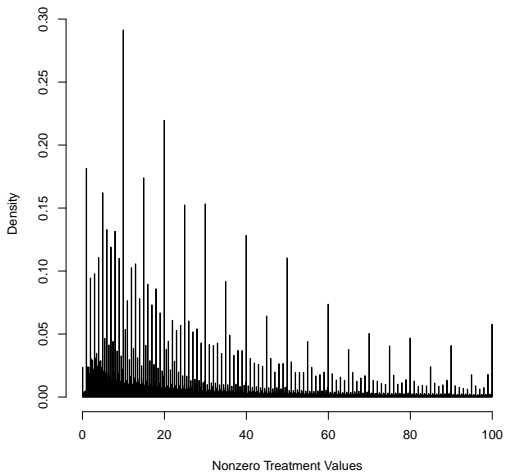


# Nonzero Raw GMB on the Log Scale

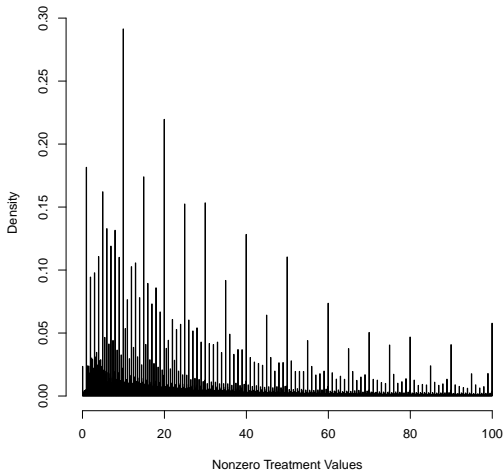


With **heavily positively skewed variables** that **don't take on negative values**, it's **typically helpful** to look at the **histogram** of the **logarithm** of the **variable**.

# Porcupine Quills



# Porcupine Quills



Here we see an interesting behavior that looks like **porcupine quills**: individual values along the number line with much higher frequency than that of their neighbors.

# Psychological Price-Points

```
table( nonzero.treatment.values[
  nonzero.treatment.values <= 10 ] )
```

#	0.01	0.02	0.03	0.04	0.05	0.06	0.07	0.08	0.09	...
#	1506	179	20	13	12	186	35	12	28	...
#	0.92	0.93	0.94	0.95	0.96	0.97	0.98	0.99	1	...
#	23	34	58	251	76	127	221	13106	2534	...
#	1.96	1.97	1.98	1.99	2	2.01	2.02	2.03	2.04	...
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The **porcupine quills** are evidently **psychological price-points: people** would **vastly rather transact** at **\$0.99** and **\$1.99** than at **\$1** and **\$2**.

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---

**How about the control raw GMB variable?**

```
print( mean.nonzero.control.values <-
  mean( nonzero.control.values ) )
```

```
# 99.14066
```

# Treatment Versus Control, in Raw GMB Terms

```
print( overall.control.mean <- ( n.zero.control.values * 0 +  
  n.nonzero.control.values * mean.nonzero.control.values ) /  
  n.control.total )
```

```
# 9.203105
```



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```
print( sample.mean.based.lift.estimate <-  
  ( overall.treatment.mean - overall.control.mean ) /  
  overall.control.mean )
```

```
# -0.00818323
```

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**control** using the **raw GMB outcome**, by about  
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The **control histograms** were **similar** to those in **treatment**, but the  
**largest value** in the **control group** was **\$161,572**, leading to **skewness**  
and **kurtosis values** of **+106** and **+26,661**, respectively.

## Treatment Versus Control (continued)

It's **helpful** to **report lift** in **two parts**: the **change** in the **percentage of 0 values** and the **change** in the **nonzero mean**.

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```
print( treatment.percent.zero <- n.zero.treatment.values /  
      n.treatment.total )
```

```
# 0.9073338
```

```
print( control.percent.zero <- n.zero.control.values /  
      n.control.total )
```

```
# 0.9071712
```

	percent	non-zero	overall
# group	zeros	mean	mean
# treatment	90.73	\$98.50	\$9.128
# control	90.72	\$99.14	\$9.203

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The **treatment** had **0.02% more zeros** than **control**; the **treatment nonzero mean** was **0.64% lower** than the **control nonzero mean**; the **net result** was a **lift** of **-0.82%**.

# Building a Full Stochastic Model

So **in this experiment** the **treatment** was **worse both ways** on **raw GMB**: it had a **slightly higher percentage** of **zero transactions**, and it **also had a somewhat lower mean** for the **nonzero transactions**.

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# Building a Full Stochastic Model

So in this experiment the treatment was worse both ways on raw GMB: it had a slightly higher percentage of zero transactions, and it also had a somewhat lower mean for the nonzero transactions.

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One way to build a full stochastic model — for the raw GMB variable, one group at a time — would be to break it up into three parts, or mixture components (this is **Bayesian hierarchical/mixture modeling**):

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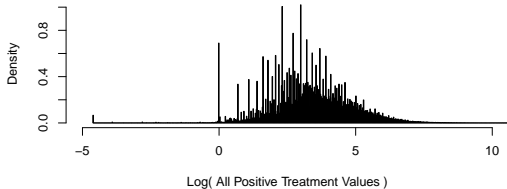
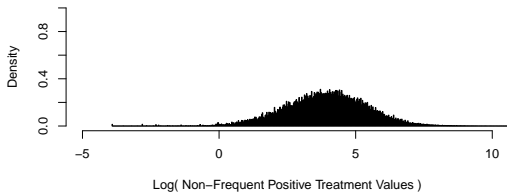
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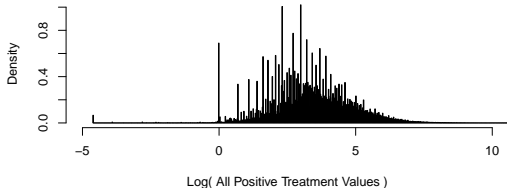
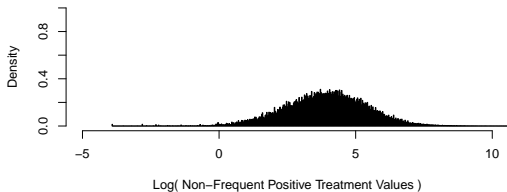
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- an **appropriate continuous distribution** for **what's left over**.

The **histograms** on the **next page** (for the **treatment group**) show that **what's left over** looks **roughly Gaussian** on the **log scale**:

# Bayesian Hierarchical/Mixture Modeling

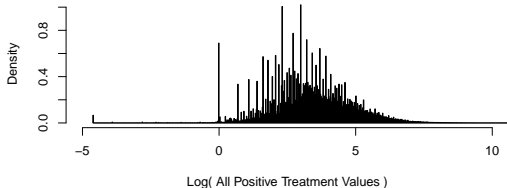
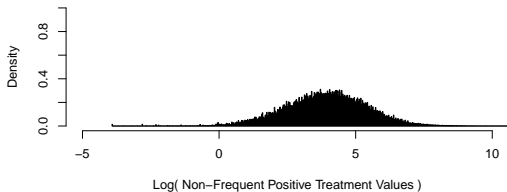


# Bayesian Hierarchical/Mixture Modeling



However, **careful analysis demonstrates** that a **mixture of 2 Gaussian distributions** on the **log scale**

# Bayesian Hierarchical/Mixture Modeling



However, **careful analysis demonstrates** that a **mixture of 2 Gaussian distributions** on the **log scale**

(a) **fits a lot better** than a **single Gaussian** and

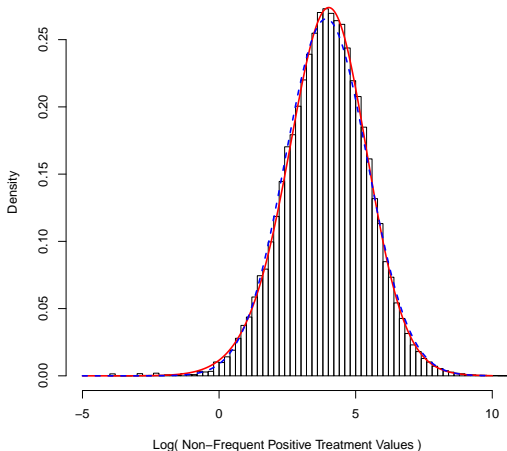


## Bayesian Hierarchical/Mixture Modeling (continued)

(b) fits the **treatment data well** (**blue dotted curve = 1 Gaussian**;  
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# Bayesian Hierarchical/Mixture Modeling (continued)

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## Taking a Step Back

It looks like we have a good Bayesian (parametric) probability model for the raw GMB data: a mixture of Bernoulli for the spike at 0, multinomial for the psychological price-points, and a mixture of 2 Gaussians on the log scale for what's left; however,

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- Exact Bayesian computations with 12 million observations in each of the treatment and control groups in this model are infeasible, and
- raw GMB appears to have a serious defect, which seems to make it unacceptable as the basis for decisions on whether to launch promising-looking treatment interventions.

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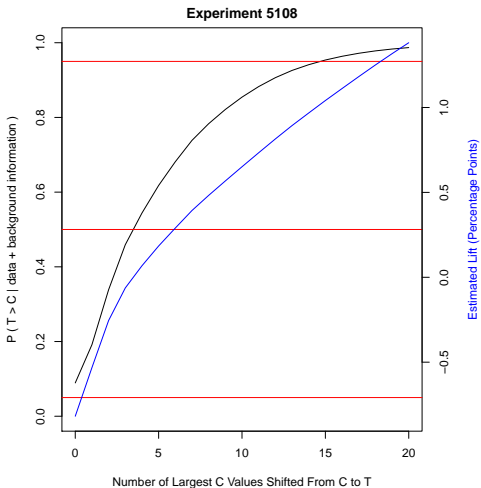
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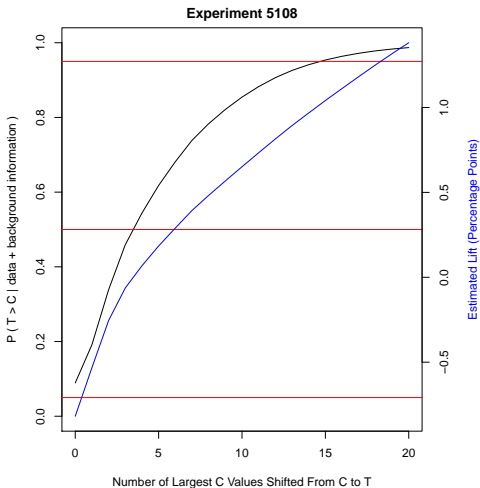
**Raw GMB can be extremely sensitive to a small number of very large observations that, arguably, were not causally influenced by offering or withholding the treatment intervention.**



# Sensitivity of Lift Estimate to a Single Outlier



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Shifting only the **3** largest  $C$  values to  $T$  drives the estimated lift from **-0.8%** to **0%**, and shifting only the largest **14** observations (out of **12,231,500**) from  $C$  to  $T$  is enough to move the posterior probability that  $T$  is better than  $C$  from **0.1** to over **0.95**.

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- **Compute**  $\hat{\theta}_{Winsorized} = \frac{\bar{y}_{T,Winsorized} - \bar{y}_{C,Winsorized}}{\bar{y}_{C,Winsorized}}$ , and **base decisions** on  $\hat{\theta}_{Winsorized}$  **instead of** on  $\hat{\theta} = \frac{\bar{y}_T - \bar{y}_C}{\bar{y}_C}$ .



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$RMSE$  is an acceptable (frequentist) criterion to use when choosing among estimators, but only when the bias of the  $RMSE$ -minimizing estimator is low; otherwise (in  $A/B$  experimentation) You get a distorted view of lift.

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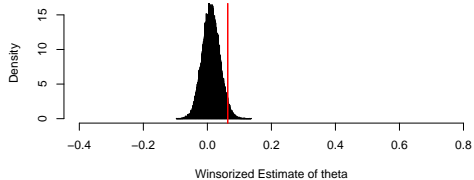
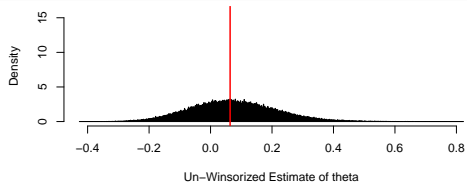
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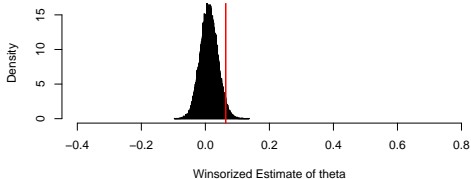
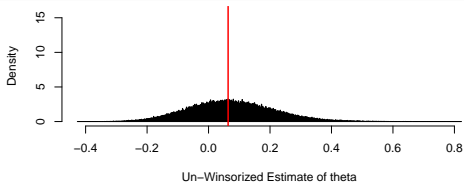
$\theta = \text{lift} \left( \frac{\mu_T - \mu_C}{\mu_C} \right)$  that **would be observed** if **all users** in the **population  $\mathcal{P}$  of interest (future users)** were to **counterfactually either receive the email (resulting population mean =  $\mu_T$ ) or not receive it (population mean =  $\mu_C$ ): here  $k = 1$** .



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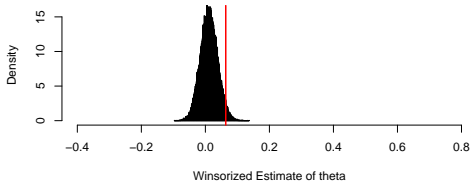
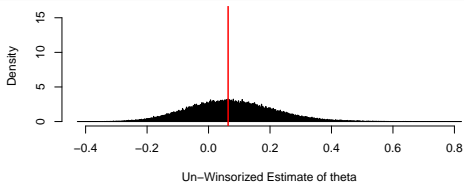


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Bottom panel: Inference with  $\hat{\theta}_{Winsorized}$  appears to be **less noisy**, because extreme observations have been **Winsorized**, but is **enormously biased** on the **low side**.

# It's Possible to Run Too Many "Small" Experiments

As an **outcome variable**, **GMB** is a **nightmare**: in **typical experiments**, its **noise-to-signal ratio** is on the **order of 15 to 1** (this is **exceptionally noisy**, meaning that **You'll need a lot of data to find small-but-still-business-relevant improvements**).

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false positive rate	false negative rate	true lift	sample size required in each of T and C groups
5%	20%	1.0%	12,365,114
5	50	1.0	12,174,946
15	50	0.5	19,334,495
10	20	1.0	20,285,382
10	50	0.5	29,562,739
10	10	1.0	29,562,739
5	10	1.0	38,537,313
5	50	0.5	48,699,782
5	10	0.5	154,149,252
5	5	0.5	221,307,004

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It's unwise to ignore Fisher's advice on the topic of experimental design.



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It's unwise to ignore Fisher's advice on the topic of experimental design. And yet that's exactly what many eCommerce companies are doing now:

## Another Recommendation

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- factor  $C = \{3 \text{ different ways to re-structure the Amazon server farm to try to deliver web pages faster}\}$ .

# Interactions; Fractional-Factorial Designs

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That's a lot of  $T$  groups, but fractional-factorial experimental design technology (which permits you to experiment with a well-chosen subset of the 180 groups and still get the information You want — has been available since the 1950s to help structure these designs efficiently, and the analysis of variance (which is a good method to analyze fractional-factorial designs) has been around since the 1920s to help analyze the results from these experiments.

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It would be good for eCommerce to at least get up to 1950s-era speed in experimentation.



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Recommendation: eCommerce should do more of this.

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    - This cripples your ability to do sensible longitudinal data analysis:
      - To stratify on important variables at design time, to improve accuracy of  $A/B$  tests; and
      - To move eCommerce into the era of “personalized medicine,” in which users get targeted treatments that are known to work in the recent past on similar users.

# Technical Interlude: Optimal Analysis

Q: From an information-processing point of view, can (static) A/B tests be analyzed optimally, even with sample sizes in the tens of millions?

A: Yes.

To see how, first look at a tiny case study, then go big.

**Case Study (1970s Version):** Captopril, a new type of anti-hypertension drug, was developed in the mid-1970s.

- Nothing was known about captopril's effects prior to the first experiment on it (MacGregor et al., 1979; I've changed a few of the details for ease of exposition): 24 representative hypertensive people, randomized (12 to C [placebo], 12 to T [captopril]; SD = standard deviation; outcome variable = systolic blood pressure [mmHg] at the end of the trial).

group	sample size	sample mean	sample SD
C	12	185.3	17.1
T	12	166.8	14.9

# Captopril Case Study

Summary: sample sizes  $(n_C, n_T) = (12, 12)$ ; sample means  $(\bar{y}_C, \bar{y}_T) = (185.3, 166.8)$ ; sample SDs  $(s_C, s_T) = (17.1, 14.9)$ .

Intuitive estimated lift  $\hat{\theta} = \frac{\bar{y}_T - \bar{y}_C}{\bar{y}_C} = \frac{166.8 - 185.3}{185.3} \doteq -0.0998 = -10.0\%$ .

We estimate that captopril causes a 10% reduction in systolic blood pressure (sounds like a big win), but how much uncertainty is associated with this estimate, in generalizing inferentially from the patients in the experiment to  $\mathcal{P} = \{\text{all hypertensive patients}\}$ ?

We need to finish the model specification to answer this question.

- $p(\theta|\mathcal{B})$  — the “prior” distribution for  $\theta$  (given  $\mathcal{B}$ ):

Since nothing was known about captopril prior to this experiment, the external-information distribution should contain essentially no information.

In other words, from an entropy point of view it should be close to uniform, so take  $p(\theta|\mathcal{B}) \propto 1$  (this is a diffuse or flat prior).

# Captopril Case Study (continued)

- $p(D|\theta \mathcal{B})$  — the “sampling” distribution for  $D$  given  $\theta$  and  $\mathcal{B}$ :

Off-the-shelf specification for this is as follows — let  $\{y_{iC}\}_{i=1}^{n_C}$  and  $\{y_{jT}\}_{j=1}^{n_T}$  be the  $C$  and  $T$  outcome values, respectively; then

$$\begin{aligned}(y_{iC}|\mu_C \sigma_C^2 \mathcal{B} \mathcal{G}) &\stackrel{\text{IID}}{\sim} N(\mu_C, \sigma_C^2) \\ (y_{jT}|\mu_T \sigma_T^2 \mathcal{B} \mathcal{G}) &\stackrel{\text{IID}}{\sim} N(\mu_T, \sigma_T^2),\end{aligned}\quad (2)$$

in which  $\mathcal{G}$  = assumption of Gaussian sampling distributions in  $C$  and  $T$ .

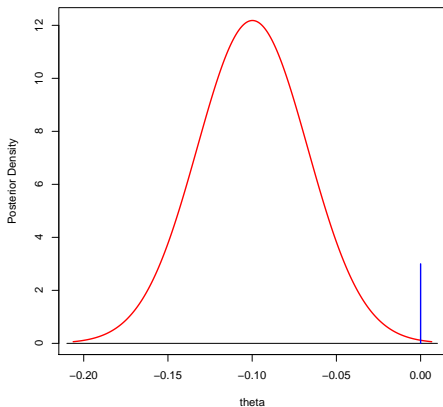
Fact: With this sampling distribution, the induced likelihood distribution for  $\theta$  is

$$\ell(\theta|D \mathcal{B} \mathcal{G}) \doteq \text{Normal with mean } \hat{\theta} \text{ and SD } \sqrt{\frac{\bar{y}_T^2 s_C^2}{\bar{y}_C^4 n_C} + \frac{s_T^2}{\bar{y}_C^2 n_T}}, \quad (3)$$

and, with the prior distribution  $p(\theta|\mathcal{B}) \propto 1$ , the resulting posterior distribution is

$$(\theta|D \mathcal{B} \mathcal{G}) \doteq N\left(\hat{\theta}, \sqrt{\frac{\bar{y}_T^2 s_C^2}{\bar{y}_C^4 n_C} + \frac{s_T^2}{\bar{y}_C^2 n_T}}\right) \doteq N(-0.0998, 0.0334^2). \quad (4)$$

# Captopril Case Study (continued)



The signal-to-noise ratio here is  $\frac{|\text{posterior mean of } \theta|}{\text{posterior SD of } \theta} \doteq \frac{0.0998}{0.0334} \doteq 2.99$ , and the posterior probability  $p(\theta < 0 | D \mathcal{B} \mathcal{G})$  that captopril would be beneficial, on average, if administered to the population of {all hypertensive patients similar to those in this study} — given the data set  $D$ , the background information  $\mathcal{B}$ , and the Gaussian sampling-distribution assumption  $\mathcal{G}$  — is about 0.999.

# Optimal Bayesian Model Specification

Of course we don't want  $p(\theta < 0 | D \mathcal{B} \mathcal{G})$ , because  $\mathcal{G}$  is not part of the known-to-be-true background information  $\mathcal{B}$ ; we want  $p(\theta < 0 | D \mathcal{B})$ .

Definition (Draper, 2015): Given  $(\theta, D, \mathcal{B})$  from

$\mathbb{C} = (\text{problem context, data-gathering protocol})$ ,

a Bayesian model specification  $[p(\theta | \mathcal{B}), p(D | \theta \mathcal{B})]$  is optimal if it includes only assumptions rendered true by the structure of  $\mathbb{C}$ .

Fact: One way to achieve optimal Bayesian model specification is via Bayesian non-parametric (BNP) methods, which place prior distributions on cumulative distribution functions (CDFs).

Fact: With little loss of generality, an optimal Bayesian model specification for  $\{y_{iC}\}_{i=1}^{n_C}$  and  $\{y_{jT}\}_{j=1}^{n_T}$  in the current Case Study involves Dirichlet-process (DP) priors, as follows:

$$\begin{aligned}(F_C | \mathcal{B}) &\sim DP(\alpha, F_{0C}) \\ (y_{iC} | F_C \mathcal{B}) &\stackrel{\text{i.i.d.}}{\sim} F_C\end{aligned}\tag{5}$$

and similarly for  $\{y_{jT}\}_{j=1}^{n_T}$ , where  $F_C$  is the CDF of the outcome values in the population of (patients, users) similar to those in experiment.

# Bayesian Non-Parametric Methods

Fact: With no information about  $F_C$  external to  $D$ , the optimal BNP analysis is based on the DP posterior

$$(F_C|DB) \sim DP(n_C, \hat{F}_{n_C}) , \quad (6)$$

where  $\hat{F}_{n_C}$  is the empirical CDF based on  $\{y_{iC}\}_{i=1}^{n_C}$ .

Definition: Given a real-valued data set  $y = (y_1, \dots, y_n)$ , the (frequentist) bootstrap distribution of the sample mean  $\bar{y} = \frac{1}{n} \sum_{i=1}^n y_i$  may be approximated by

- (a) choosing a sample of values  $y_i^*$  at random with replacement from the  $y$  vector and computing  $\bar{y}^* = \frac{1}{n} \sum_{i=1}^n y_i^*$ , and
- (b) repeating (a)  $M$  times (for large positive integer  $M \geq 100,000$ ) and making a histogram or kernel density trace of the values  $(\bar{y}_1^*, \dots, \bar{y}_M^*)$ .

Fact (Draper 2015): The posterior distribution  $p(\mu_C|DB)$  induced by  $DP(n_C, \hat{F}_{n_C})$  distribution may be sampled from accurately and quickly by (frequentist) bootstrapping the sample mean and interpreting the resulting distribution as a good approximation to  $p(\mu_C|DB)$ .

# Summary of Conclusions

- fact: (a) bootstrap is 30 times faster than standard DP sampling algorithm (stick-breaking), and  
(b) bootstrap is embarrassingly parallelizable
- 

- captopril: bnp analysis coincides with gaussian-assumption analysis, because clt has kicked in even with only 12 obs per group, because skewness and kurtosis values in C and T are both so close to 0
- gold-standard analysis in some eCommerce companies: hope that captopril gaussian-assumption analysis is 'close to optimal'; no proof that this hope is justified

fact: gmb has hideously non-gaussian skewness and kurtosis values

fact: but the gaussian-assumption analysis is still approximately optimal, provided that the C and T sample sizes  $n.C$  and  $n.T$  are large enough for the Central Limit Theorem (CLT) to save us



# Case Study Details

group	number of zero values	number of nonzero values	total number of values	proportion of zero values	nonzero mean	SD	total mean	SD
treatment	90,006	38,343	128,349	0.7013	3,618.0	60,476	1080.9	33,096
control	89,863	38,509	128,372	0.7000	3,387.5	66,554	1016.2	36,485

group	all values skewness	all values kurtosis	non-zero values skewness	non-zero values kurtosis	all values noise-to-signal ratio	non-zero values noise-to-signal ratio
treatment	205.9	52,887.9	112.8	15,861.1	30.62	16.72
control	289.1	92,750.5	158.7	27,902.6	35.90	19.65

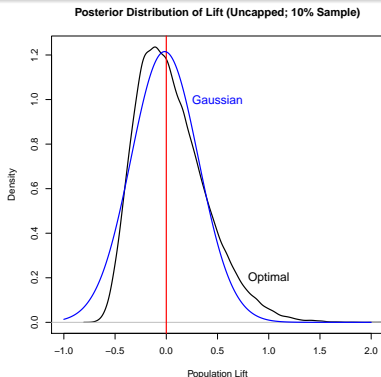
	nonzero values	
	min	max
treatment	0.09	9,381,532
control	0.09	12,018,199

lift estimate +0.0636 = + 6.36%

sd of lift estimate 0.1400 = +14.00%

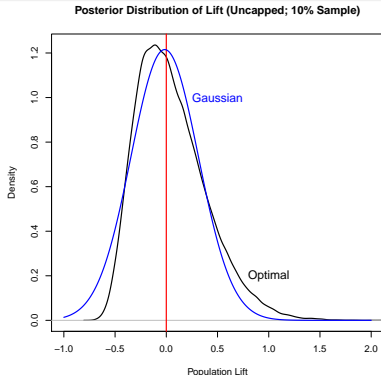
p( theta > 0 | data, background information ): gaussian 0.675 optimal 0.696

# Example of Setting Where CLT is Not Good Enough



Let  $\eta = P(\theta > 0 | \text{data, background information})$  in a **segment** (subset, stratum) of users that comprises 10% of traffic in the **Case Study** (12,837 observations in each of  $T$  and  $C$ ).

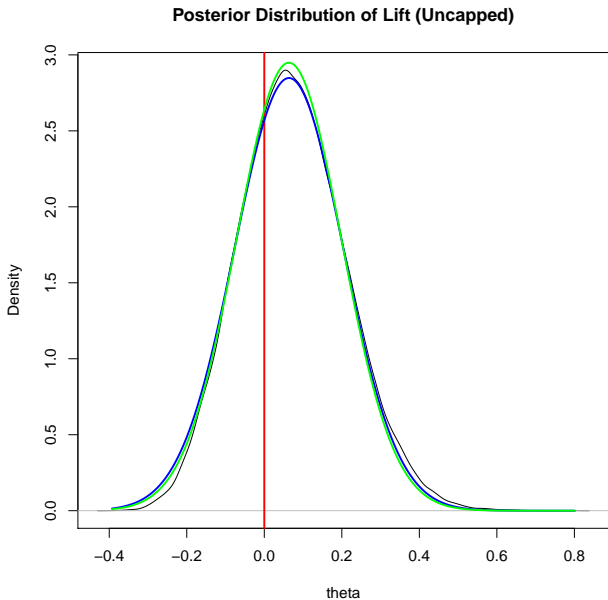
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Here **Gaussian analysis** (current best practice in some of eCommerce) produces an estimate of  $\eta$  that's **too low** by **about 5%**, in relation to an **optimal analysis**; this **underestimation gets worse** with **decreasing segment sample size**.

# eCommerce Case Study Details (continued)



# R Code For Parallel Bootstrapping

```
library( doParallel )
n.processors <- makeCluster( 1024 )
registerDoParallel( n.processors )

parallel.mean.bootstrap <- function( y, M, n, p.hat.0 ) {
  foreach( i = 1:M, .inorder = F, .multicombine = T,
           .combine = 'c' ) %dopar% {
    sum( sample( y, n - rbinom( 1, n, p.hat.0 ),
                replace = T ) ) / n
  }
}

seed <- 1
set.seed( seed )
M.b <- 100000

system.time(
  mu.T.star.uncapped.1 <-
    parallel.mean.bootstrap( nonzero.T.values.uncapped, M.b, n.T,
                             p.hat.0.T )
)
```

## Summary of Conclusions (continued)

(eCommerce, not captopril) case study:  $n.C$  and  $n.T$  are just barely big enough for gaussian-assumption analysis to be decent

fact: when clt has not yet kicked in, gaussian-assumption analysis will be conservative in the right tail (positive lift) and liberal in the left tail

conservative in the right tail means that the gaussian-assumption analysis might say  $p(\theta > 0 | D\mathcal{B}\mathcal{G}) = 0.88$  when really the optimal analysis concludes that  $p(\theta > 0 | D\mathcal{B}) = 0.97$

this conservatism can be noticeable if  $n.C$  and  $n.T$  are quite small and the outcome variable is quite skewed and kurtotic

# Summary of A/B Testing Analysis Algorithms

**Design:** Identify  $n = (n_C + n_T)$  users representative of

$\mathcal{P} = \{\text{all future users relevant to this experiment}\}$

(You have to specify relevant).

Randomize  $n_C$  of these users to  $C$  (current best environment without the  $T$  intervention) and  $n_T$  to  $T$  (identical to  $C$  but with the  $T$  intervention).

(This is a completely-randomized experiment; better designs exist, but that's another talk.)

**Data summaries:** sample means  $(\bar{y}_C, \bar{y}_T)$ , sample SDs  $(s_C, s_T)$  for an outcome  $y$  such as GMB.

Inferential target: population lift  $\theta = \frac{\mu_T - \mu_C}{\mu_C}$ , in which  $\mu_C$  ( $\mu_T$ ) is the population mean of  $y$  under the  $C$  ( $T$ ) condition.

**Algorithm (Gaussian approximation):** (extremely fast, but may underestimate the posterior probability that the  $T$  intervention is beneficial, especially in segments with small sample sizes)

# Gaussian Approximation Algorithm

$$\hat{\theta} = \frac{\bar{y}_T - \bar{y}_C}{\bar{y}_C}, \quad \widehat{SD}(\hat{\theta}) = \sqrt{\frac{\bar{y}_T^2 s_C^2}{\bar{y}_C^4 n_C} + \frac{s_T^2}{\bar{y}_C^2 n_T}}$$
$$p(\theta > 0 | D\mathcal{B}\mathcal{G}) \doteq 1 - \Phi \left[ \frac{-\hat{\theta}}{\widehat{SD}(\hat{\theta})} \right], \quad (7)$$

in which  $\Phi(\cdot)$  is the standard normal CDF.

inferential suggestion (not yet a proper decision algorithm): consider launching the  $T$  if  $p(\theta > 0 | D\mathcal{B}\mathcal{G}) > c$ , where conventional (not necessarily in any sense optimal) values of  $c$  include 0.9, 0.95, and 0.99

this logic may be applied not only to the entire data set but also to smaller segments defined by covariates (features) (e.g., separately for male and female users)

arriving at many such inferential suggestions —

{entire data set, segment 1, segment 2, ..., segment  $S$ }

— (for large  $S$ ) creates a multiplicity problem that's best solved with Bayesian decision theory (another talk)



# Gaussian Approximation Algorithm (continued)

R code to implement this approximate algorithm:

```
lift.estimate <- ( y.bar.T - y.bar.C ) / y.bar.C

SD.lift.estimate <- sqrt( ( y.bar.T^2 * s.C^2 ) /
  ( y.bar.C^4 * n.C ) + s.T^2 / ( y.bar.C^2 * n.T ) )

gaussian.posterior.probability.of.improvement <-
  1 - pnorm( ( 0 - lift.estimate ) / SE.lift.estimate )
```

even with  $(n_C, n_T)$  each on the order of 10–100 million, this code takes less than 1 second to run on a laptop with one decent core and decent RAM

approximate validity of Gaussian algorithm depends on  $(n_C, n_T)$  and the sample skewness and kurtosis values in each of  $C$  and  $T$

(\*) unfavorable conditions for this algorithm: {small sample size, large skewness, large kurtosis} in either or both groups

in a future white paper (published to the experimentation wiki) i'll quantify (\*)

# Optimal Analysis Algorithm

Algorithm (optimal analysis): (accurate assessment of the posterior probability that the  $T$  intervention is beneficial, but may be slow; however, the bootstrap is embarrassingly parallelizable)

to make a valid draw  $\mu_T^*$  from the posterior distribution  $p(\mu_T | y^T \mathcal{B})$  induced by the  $DP(n, \hat{F}_T)$  posterior on  $F_T$ ,

(a) choose a random sample  $(y_1^{T*}, \dots, y_{n_T}^{T*})$  of size  $n_T$  with replacement from the data vector  $y^T$ , and

(b) compute  $\mu_T^* = \frac{1}{n_T} \sum_{\ell=1}^{n_T} y_\ell^{T*}$ ;

now repeat this  $M_b$  times (for large  $M_b$ ) and use a histogram or kernel density trace of the resulting  $\mu_T^*$  draws to approximate  $p(\mu_T | y^T \mathcal{B})$ .

this reasoning obviously applies in parallel to obtain the corresponding posterior  $p(\mu_C | y^C \mathcal{B})$  for the control-group population mean, and then to simulate from  $p(\theta | y \mathcal{B})$ , where  $y = (y^C, y^T)$ . You just

(a) bind the columns  $(\mu_{C1}^*, \dots, \mu_{CM_b}^*)$  and  $(\mu_{T1}^*, \dots, \mu_{TM_b}^*)$  together to make a matrix with  $M_b$  rows and 2 columns,

# Optimal Analysis Algorithm

- (b) calculate  $\theta_m^* = \frac{\mu_{Tm}^* - \mu_{Cm}^*}{\mu_{Cm}^*}$  in row  $m = 1, \dots, M_b$  of this matrix, and
- (c) use a histogram or kernel density trace of the resulting  $M_b$   $\theta^*$  draws to approximate  $p(\theta|DB)$ .

Mb	Elapsed Time (Sec) With		Bootstrap Distribution of mu.T.star			
	8 Threads	24 Threads	Mean	SD	Skewness	Kurtosis
10,000	104.82	65.67	9.1279	0.036707	0.070319	-0.095457
			9.1276	0.037139	0.053797	0.017913
100,000	1049.81	694.97	9.1278	0.037074	0.041394	0.00094482
			9.1276	0.037086	0.048562	0.0087070

Mb	Elapsed Time (Sec) With		Bootstrap Distribution of mu.C.star			
	8 Threads	24 Threads	Mean	SD	Skewness	Kurtosis
10,000	114.64	---	9.2031	0.042402	0.046275	0.019909
100,000	1076.14	---	9.2031	0.042352	0.086158	0.058135

# Analysis of Large-Scale Observational Studies

Sometimes you can't run randomized controlled trials in eCommerce.

Example: you release a new version of your mobile app every 4–6 months, but you allow users to choose when to pull it (rather than pushing it to everyone at the same time)

Q: Is the new app a disaster? (Want answer to this as fast as possible after release)

Users in the “treatment” group (early adopters of the new release) and the “control” group (people who initially continue to use the old release) are not assigned to T and C at random: the early adopters choose when to early-adopt, and they're systematically different from the later-adopters (this is called selection bias)

typically the early-adopters are enthusiastic buyers

if you just look at monetary outcomes among T and C users (say) 4 weeks after release, the new release will look (much) better than it really is, because of selection bias

# Large-Scale Observational Studies (continued)

there will be millions of users in each of T and C,  
but this does not save you:

taking more measurements with a systematically biased data-gathering process just perpetuates the bias (unlike non-systematic noise, which you can damp down by averaging over many users)

there are many ways to attempt to estimate the size of the selection bias and adjust for it: standardization, regression, propensity scores, ...

with a Ph.D. student who's interning in eCommerce, i'm currently working on large-scale time-series methods (based on dynamic linear models) for solving this problem

the idea is to let each user's past buying behavior help you estimate what her/his buying would have been if she/he did/didn't early adopt (plus adjusting for lots of other things too)

this method works well (paper coming soon)

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- Do all of this better than the machine-learning guys.

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- (*eCommerce Q:*)

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 $\theta = \frac{\mu_A - \mu_B}{\mu_B}.$

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false positive rate	false negative rate	true lift	sample size required in each of A and B groups
5%	20%	1.0%	12,365,114
5	50	1.0	12,174,946
15	50	0.5	19,334,495
10	20	1.0	20,285,382
10	50	0.5	29,562,739
10	10	1.0	29,562,739
5	10	1.0	38,537,313
5	50	0.5	48,699,782
5	10	0.5	154,149,252
5	5	0.5	221,307,004

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