

Almost Famous: Analyse Newsletter Signup Rate Per Experiment

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Load variable names and types:

```
nameTypeDataFile <- "../data/raw_variables.csv"
variableNames <- read.csv(nameTypeDataFile, header=TRUE, stringsAsFactors=FALSE)
variableNames

##      name      type
## 1  visit_id  factor
## 2      uid   factor
## 3  campaign  factor
## 4     tstamp character
## 5 experiments factor
## 6     action  factor
## 7      query  factor

factorIdx <- which(variableNames$type=="factor")
factorNames <- variableNames$name[factorIdx]
```

Read the per visit aggregated web log data:

```
visitFile <- "../data/web_visits.csv"
# visitFile <- "../data/head2000.csv"
visitData <- read.csv(visitFile, stringsAsFactors=FALSE, col.names=variableNames$name,
                      colClasses=variableNames$type, na.strings=c("NA",""))
visitData$tstamp <- as.POSIXct(visitData$tstamp)
str(visitData)

## 'data.frame': 1482602 obs. of 7 variables:
## $ visit_id : Factor w/ 1482602 levels "10000024498",...: 1252062 128641 583195 349394 830165 690964 ...
## $ uid      : Factor w/ 1064214 levels "100000493","100000682",...: 858988 92339 95584 929716 656934 ...
## $ campaign : Factor w/ 10 levels "103","127","14",...: 7 1 7 1 4 8 1 1 1 2 ...
## $ tstamp   : POSIXct, format: "2014-09-18 05:43:18" "2014-09-16 21:24:08" ...
## $ experiments: Factor w/ 4 levels "[1 3]","[1 4]",...: 2 1 4 1 3 2 1 3 2 1 ...
## $ action    : Factor w/ 8 levels "[landed adclick adclick adclick]",...: 8 8 8 8 8 8 8 8 8 8 ...
## $ query     : Factor w/ 5 levels "advanced analytics",...: 1 5 1 5 3 5 5 5 4 ...
```

```
summary(visitData)

##          visit_id          uid          campaign          tstamp
## 10000024498:      1 102486699:      7 558 :324872 Min. :2014-09-15 00:00:01
## 10000032484:      1 123618732:      7 103 :324027 1st Qu.:2014-09-18 16:32:04
## 10000079220:      1 143588980:      7 59 :232002 Median :2014-09-22 16:55:36
## 10000092303:      1 159226004:      7 31 :231685 Mean :2014-09-22 20:33:11
## 10000132469:      1 168873739:      7 127 : 92681 3rd Qu.:2014-09-26 19:41:15
## 10000206890:      1 171898393:      7 94 : 92436 Max. :2014-09-30 23:53:20
## (Other) :1482596 (Other) :1482560 (Other):184899
## experiments          action
## [1 3]:370018 landed :1291256
## [1 4]:371852 [landed signup] : 84889
## [2 3]:370082 [landed order] : 43930
## [2 4]:370650 [landed adclick] : 28233
## [landed adclick adclick adclick]: 14956
## [landed adclick adclick] : 14875
## (Other) : 4463
##          query
## advanced analytics :463687
## building predictive models: 92454
## data science : 92445
## data science training :185117
## predictive modeling :648899
##
##
```

1 Newsletter Signup Rate Per Experiment

Compute the overall newsletter signup rate (defined as the number of users who signed up to the newsletter divided by the total number of users) for each of the experiments.

What are the actions per visit?

```
table(visitData$action)

##
## [landed adclick adclick adclick] [landed adclick adclick]
## 14956 14875
## [landed adclick] [landed order]
## 28233 43930
## [landed signup adclick] [landed signup order]
## 1045 3418
## [landed signup] landed
## 84889 1291256
```

Look at visits with signups:

```
signupIdx <- getPatternIndex(visitData$action, "signup")

## Concerned pattern levels are [landed signup adclick], [landed signup order], [landed signup]
```

```
totalSignups <- length(signupIdx)
```

I conclude from the factor levels for action that there is at most 1 signup per visit and overall 89352 signups. I cross check with a simple grep on the command line on the unaggregated web data which gives us the same result:

```
$ grep -o signup web.log | wc -l
$ 89352
```

Add the number of signups per visit as variable to the data frame:

```
nbSignup <- rep(0, nrow(visitData))
nbSignup[signupIdx] <- 1
visitData$nb_signups <- nbSignup
```

There are 93.97% of visits that don't have a signup and only 6.03% that do.
Checkout experiment information:

```
prop.table(table(visitData$experiments))

##
##      [1 3]      [1 4]      [2 3]      [2 4]
## 0.2495734 0.2508104 0.2496166 0.2499997
```

Split up the experiment information into separate variables

```
expIdx1 <- getPatternIndex(visitData$experiments, 1)
## Concerned pattern levels are [1 3], [1 4]

totalExp1 <- length(expIdx1)
expIdx2 <- getPatternIndex(visitData$experiments, 2)
## Concerned pattern levels are [2 3], [2 4]

totalExp2 <- length(expIdx2)
expIdx3 <- getPatternIndex(visitData$experiments, 3)
## Concerned pattern levels are [1 3], [2 3]

totalExp3 <- length(expIdx3)
expIdx4 <- getPatternIndex(visitData$experiments, 4)
## Concerned pattern levels are [1 4], [2 4]

totalExp4 <- length(expIdx4)
```

and add them pairwise to the data frame:

```
stopifnot(!any(intersect(expIdx1, expIdx2)),
          totalExp1 + totalExp2 == nrow(visitData),
          !any(intersect(expIdx3, expIdx4)),
          totalExp3 + totalExp4 == nrow(visitData))
```

```

experiment12 <- rep(1, nrow(visitData))
experiment12[expIdx2] <- 2
visitData$experiment_12 <- factor(experiment12, levels=1:2)

experiment34 <- rep(3, nrow(visitData))
experiment34[expIdx4] <- 4
visitData$experiment_34 <- factor(experiment34, levels=3:4)

```

Checkout experiment distribution:

```

prop.table(table(visitData$experiment_12))

##
##      1      2
## 0.5003838 0.4996162

prop.table(table(visitData$experiment_34))

##
##      3      4
## 0.4991899 0.5008101

```

How many signups are there per experiment?

```

visitAggExp12 <- aggregatePerExperiment12(visitData)
visitAggExp12

##   experiment_12 nb_visits nb_uids total_signups total_non_signups signup_rate
## 1              1   741870   532225         45145         487080  0.08482315
## 2              2   740732   531989         44207         487782  0.08309758

visitAggExp34 <- aggregatePerExperiment34(visitData)
visitAggExp34

##   experiment_34 nb_visits nb_uids total_signups total_non_signups signup_rate
## 1              3   740100   531345         46819         484526  0.08811413
## 2              4   742502   532869         42533         490336  0.07981887

```

Write the result into file overall_signup_rate.json:

```

library(jsonlite)
overallSignupRates <- c(visitAggExp12$signup_rate, visitAggExp34$signup_rate)
names(overallSignupRates) <- paste("experiment", 1:4, sep="")
jsonString <- toJSON(as.data.frame(t(overallSignupRates)), dataframe="rows", pretty=TRUE)
jsonString

## [
##   {
##     "experiment1": 0.0848,
##     "experiment2": 0.0831,
##     "experiment3": 0.0881,
##     "experiment4": 0.0798
##   }

```

```
## ]
##
write(jsonString, file="../q4_newsletter_signup/out/overall_signup_rate.json")
```

2 Performance of Experiments

Use a G-test to compare the performance of experiment one vs. experiment two and experiment three vs. experiment four overall.

I assume that the performance of an experiment is measured by the number of signups for the newsletter.

```
gTestTable12 <- cbind(visitAggExp12$total_signups, visitAggExp12$total_non_signups)
rownames(gTestTable12) <- paste("Experiment",1:2,sep="")
colnames(gTestTable12) <- c("signups","ignorations")
gTestTable12

##           signups ignorations
## Experiment1   45145      487080
## Experiment2   44207      487782

gTestTable34 <- cbind(visitAggExp34$total_signups, visitAggExp34$total_non_signups)
rownames(gTestTable34) <- paste("Experiment",3:4,sep="")
colnames(gTestTable34) <- c("signups","ignorations")
gTestTable34

##           signups ignorations
## Experiment3   46819      484526
## Experiment4   42533      490336
```

Run G-Test, which is a test of independence (just like the Chi-Square test). The null hypothesis is that the two variables are independent, which is rejected if the p-value is smaller than a chosen significance level α . Usually one uses $\alpha = 5\%$ but with such a large sample size I would opt for $\alpha = 0.1\%$, which means that if we decide to reject the null hypothesis and assume the variables are dependent (i.e. in this case this means one experiment is better than the other), we might be wrong for $\alpha \times n = 1064$ observations.

Run G-Test for experiments 1 and 2:

```
library(Deducer)
test12 <- likelihood.test(gTestTable12)
print(test12)

##
## Log likelihood ratio (G-test) test of independence without correction
##
## data: gTestTable12
## Log likelihood ratio statistic (G) = 10.3003, X-squared df = 1, p-value =
## 0.00133
# sampleSize
sum(visitAggExp12$nb_uids)
## [1] 1064214
```

Run G-Test for experiments 3 and 4:

```
test34 <- likelihood.test(gTestTable34)
print(test34)

##
## Log likelihood ratio (G-test) test of independence without correction
##
## data: gTestTable34
## Log likelihood ratio statistic (G) = 238.1123, X-squared df = 1, p-value <
## 2.2e-16

#sample size
sum(visitAggExp34$nb_uids)

## [1] 1064214
```

I would interpret the results as follows:

- With a p-value of $p_{12} = 0.0013301$ experiments 1 and 2 are indistinguishable - it doesn't matter for the newsletter signup whether the color scheme of the page is blue or green.
- With a p-value of $p_{34} = 0$ there is a statistically significant difference between experiment 3 and 4 - based on the number of newsletter signups the promotional blurb by Josh Willis performs better.

Write the result into file `performance_of_experiment_1_versus_2.json`:

```
write(test12$p.value, file="../q4_newsletter_signup/out/performance_of_experiment_1_versus_2.json")
write(test34$p.value, file="../q4_newsletter_signup/out/performance_of_experiment_3_versus_4.json")
```

3 Required Days for 99% Confidence in G-Test Result

How many full days of data, starting from the first day, are required to determine that the newsletter signup rate for experiment one is better than experiment two at the 99% confidence level?

The number of days is "encoded" within the number of visits and users. Reformulated the question is "Given the current signup rate for each experiment and $\alpha = 1\%$, how long does an experiment need to run in order to generate enough users/visits for the G-Test to be significant?"

I simulate the answer¹.

Define a function to get the p-value from a G-Test:

```
library(Deducer)
getPValue <- function(signupRates, nbUsers) {
  # parameters:
  #   signupRates: vector of signup rate for experiments
  #   nbUsers:     vector of number of users how saw the experiment
  # returns:
  #   p-value
  # description:
```

¹just I like did for proportion test: https://github.com/clamm/R_dev/blob/master/ab_testing.R

```

# H0: experiments perform equally well based on signup rate
# accept H1 if pval < alpha (i.e. the 2 experiments perform differently)
dataExperiments <- c(signupRates * nbUsers, (1-signupRates) * nbUsers)
tableExperiments <- matrix(dataExperiments, nrow=2, byrow=FALSE)
rownames(tableExperiments) <- paste("Experiment", LETTERS[1:2], sep=" ")
colnames(tableExperiments) <- c("signups", "ignorations")
print(tableExperiments)
res <- likelihood.test(tableExperiments)
return(res$p.value)
}

```

Double check that this function gives the same results as manual extraction of the p-value:

```

newPvalue <- getPValue(overallSignupRates[1:2], visitAggExp12$nb_uids)

##           signups ignorations
## Experiment A   45145      487080
## Experiment B   44207      487782

newPvalue == test12$p.value

## p.value
##      TRUE

```

Next steps would be to

- group visit data per day and count daily number of users per experiment
- take care of doing a one sided G-Test (since experiment 1 should perform better than experiment 2)
- run the G-Test for each day starting with the first day in the logs and up to the day at which the p-value is the first time smaller than 0.01

However I didn't have time for that anymore...