

Web Usage Mining

Association Mining Familiarisation Workshop

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Workshop Goal

- Use SPSS Modeler and or R/Rattle to detect pairs or triplets of MSNBC webpages that are commonly visited by the same user in one day
- Contrast results with those obtained using the SPSS Modeler sequence mining node and/or the R “Spade” algorithm implementation

Sequences:

```
6
1 1
6
6 7 7 7 6 6 8 8 8 8
6 9 4 4 4 10 3 10 5 10 4 4 4
1 1 1 11 1 1 1
12 12
```

The data shows the categories of all MSNBC webpages viewed by users on one specific day

Codes for the msnbc.com page categories

category	code	category	code	category	code
frontpage	1	misc	7	summary	13
news	2	weather	8	bbs	14
tech	3	health	9	travel	15
local	4	living	10	msn-news	16
opinion	5	business	11	msn-sport	17
On-air	6	sports	12		

Tools we can use

- Association Mining
 - SPSS Modeler ~ classroom 2-1 & 3-12, breakout rooms
 - R (or Rattle)
 - Weka
 - RapidMiner
- Sequence Mining
 - SPSS Modeler
 - Spade (or other) library in R

Data Formats for Association Finding

In the raw data (as downloaded from the web) each record contains the MSNBC web page categories visited by one user on one day. (Approx. 1 million records).

This must be converted to one of the two common formats that association rule tools accept. (For this workshop I have already converted to transaction format)

Sequences:

```
6
1 1
6
6 7 7 7 6 6 8 8 8 8
6 9 4 4 4 10 3 10 5 10 4 4 4
1 1 1 11 1 1 1
12 12
```

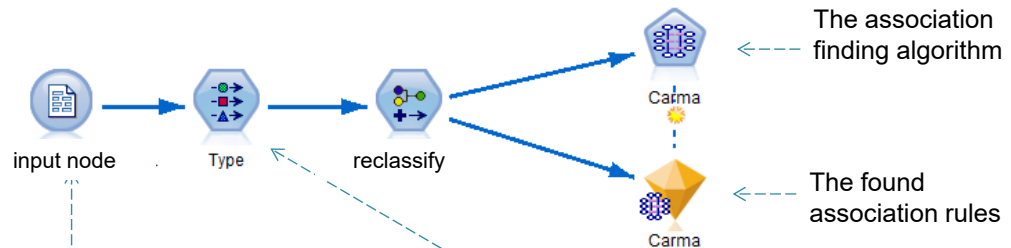
Tabular format: rows represents item-sets. Each item is a separate column

Customer	Jam	Bread	Milk
1	T	F	F
2	F	F	T
3	T	T	F

Transaction format: each row is a single item. An item-set id is required for each row.

Customer	Purchase
1	jam
2	milk
3	jam
3	bread

Association finding using SPSS Modeler



Preview from msnbc990928-PVevents.csv No...

	user	PVcategory
1	1	1
2	1	1
3	2	2
4	3	3
5	3	2
6	3	2
7	3	4
8	3	2
9	3	2
10	3	2

Transaction format data (but can also use tabular)

Type

Preview

Types Format Annotations

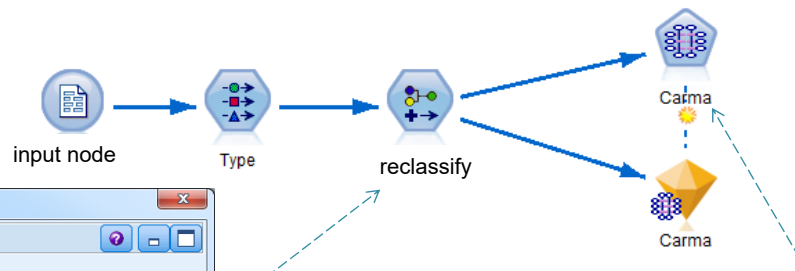
Read Values Clear Values Clear All Values

Field	Measurement	Values	Missing	Check	Role
user	Typeless		None		None
PVcateg...	Nominal	1,2,3,4,...	None		Both

View current fields View unused field settings

OK Cancel Apply Reset

Association finding using SPSS Modeler



PVcatname

Settings Annotations

Mode: ☒ Single ☐ Multiple

Reclassify into: ☒ New field ☐ Existing field

Reclassify field: PVcategory

New field name: PVcatname

Reclassify values:

Get Copy Clear new Auto...

Original value	New value
1	frontpage
2	news
3	tech
4	local

For unspecified values use: ☒ Original ... ☐ Default ... undef

OK Cancel Apply Reset

Use a reclassify node to turn the category codes (integers) into more meaningful strings

Carma

Fields Model Expert Annotations

☐ Use type node settings ☒ Use custom settings

☒ Use transactional format

ID: user

☒ IDs are contiguous

Content: PVcatname

OK Run Cancel Apply Reset

Edit the association node (Carma or Apriori) to accept transaction format data

Association algorithms in SPSS



Apriori

- Generally faster than Carma
- Input and target fields must be symbolic.
- Set fields as “both” if not sure which should be target or input

If coke then ice

If temp=cold then ice

If temp=cold then buy=coat



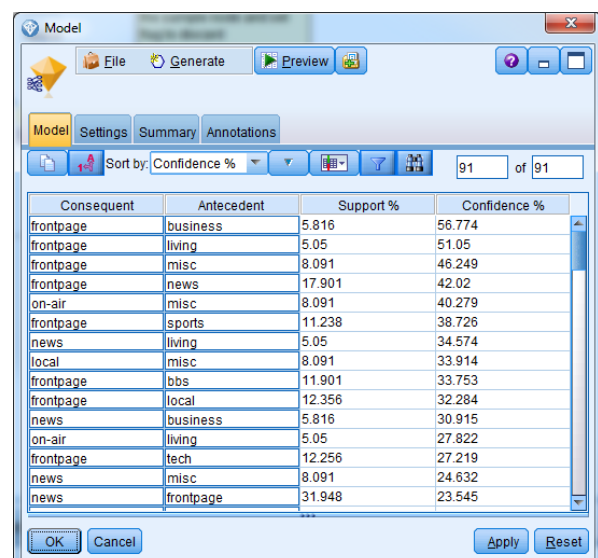
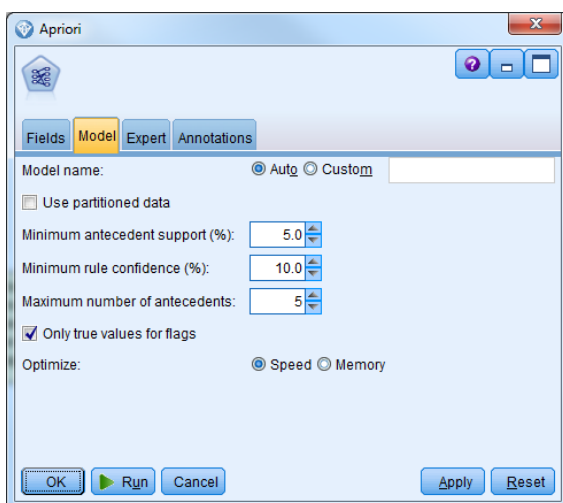
Carma

- Does not require you to define input and output fields.
- All fields should be boolean
- Can generate rules with multiple consequents

If whiskey then ice and coke

Both accept tabular or transaction data. The rules generated using each format are identical

Building Assoc. Rules in SPSS



Apriori

Edit the model node before executing, you may have to reduce the expected rule support and confidence

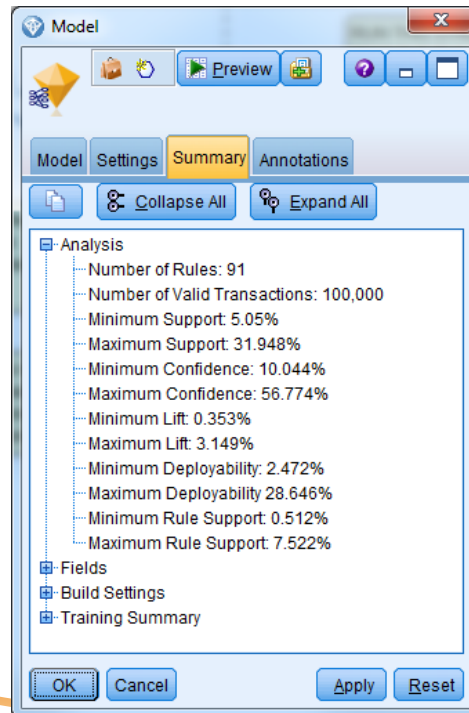


Model

Edit the nugget node to view the built rule set and to set the execution settings (see next slides)

Building Assoc. Rules in SPSS

- The summary tab in the nugget node shows information about the built ruleset

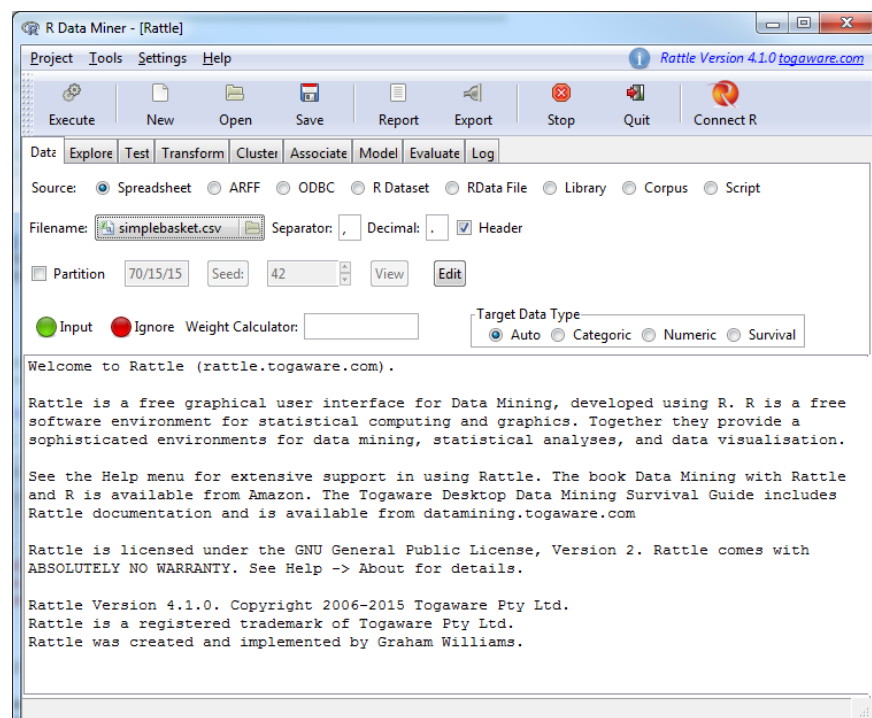


Association Mining Using R/Rattle

In R...

```
library(rattle)
```

```
rattle()
```

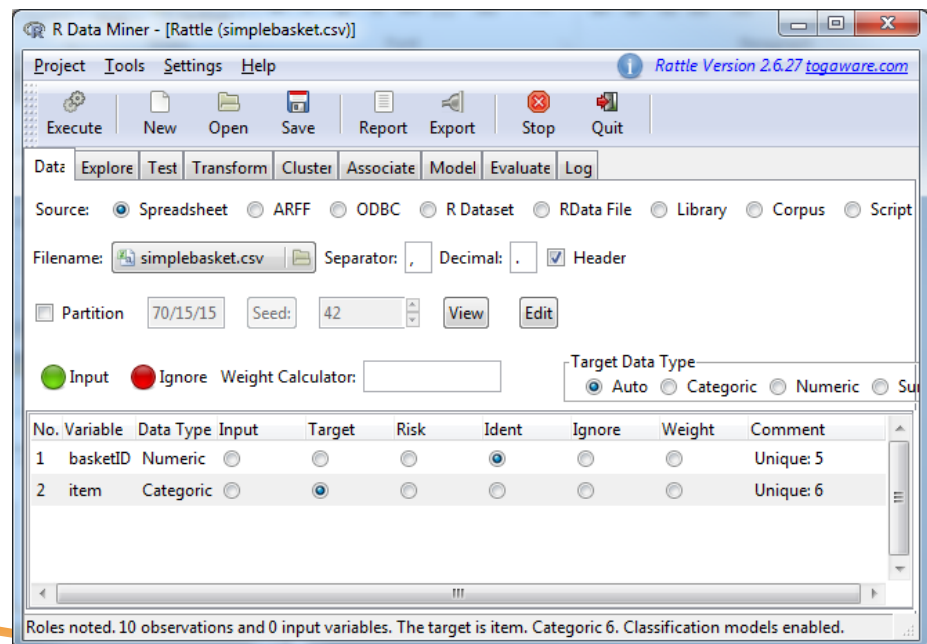


Using R/Rattle

- Click **Execute** to import the training data, then select the basket identifier (Ident) and set the items as target. Ensure **Partition** is deselected.

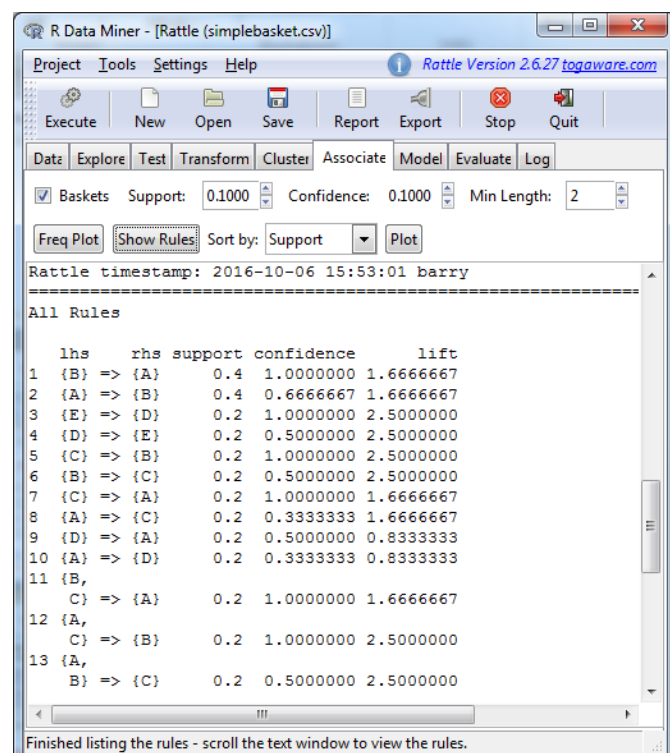
basketID	item
1	A
1	B
1	C
2	A
2	B
3	A
3	D
4	D
4	E
5	F

Simplebasket.csv



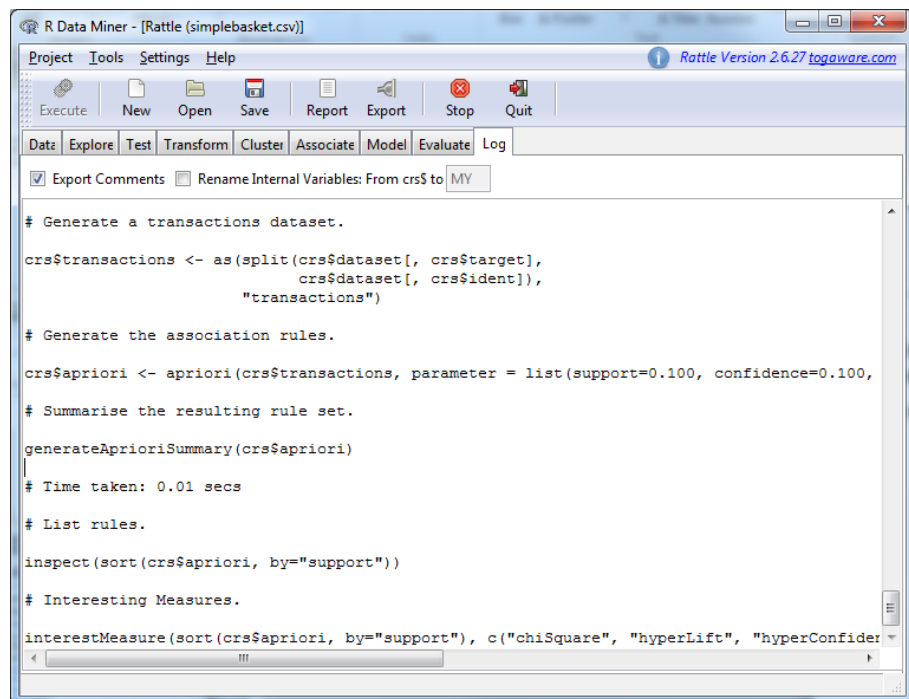
Using R/Rattle

- Go to the Associate tab
- Select **Baskets**, then click **Execute** and then **Show rules**
- Scroll down to see the rules



Using R/Rattle

- Select the log tab to see the underlying R code that was executed



The screenshot shows the Rattle software interface with the 'Log' tab selected. The R code displayed is as follows:

```
# Generate a transactions dataset.
crs$transactions <- as(split(crs$dataset[, crs$target],
                           crs$dataset[, crs$id],
                           "transactions")

# Generate the association rules.
crs$apriori <- apriori(crs$transactions, parameter = list(support=0.100, confidence=0.100,
# Summarise the resulting rule set.
generateAprioriSummary(crs$apriori)
# Time taken: 0.01 secs
# List rules.
inspect(sort(crs$apriori, by="support"))
# Interesting Measures.
interestMeasure(sort(crs$apriori, by="support"), c("chiSquare", "hyperLift", "hyperConfidence"))
```

Using R Directly

```
library("arules");
```

```
# for transaction format data
```

```
egs = read.transactions(file=filename,rm.duplicates=TRUE,format="single",sep=",",cols=c(1,2));
```

```
rules = apriori(egs, parameter = list(supp=0.1, conf=0.1, minlen=2))
```

```
summary(rules)
```

```
inspect(rules)
```

```
as(rules,"data.frame")
```

	rules	support	confidence	lift
	{E} => {D}	0.1666667	1.0000000	3
	{D} => {E}	0.1666667	0.5000000	3
	{C} => {B}	0.1666667	1.0000000	3
	{B} => {C}	0.1666667	0.5000000	3
	{C} => {A}	0.1666667	1.0000000	2
	{A} => {C}	0.1666667	0.3333333	2
	{D} => {A}	0.1666667	0.5000000	1
	{A} => {D}	0.1666667	0.3333333	1
	{B} => {A}	0.3333333	1.0000000	2
	{A} => {B}	0.3333333	0.6666667	2
	{B,C} => {A}	0.1666667	1.0000000	2
	{A,C} => {B}	0.1666667	1.0000000	3
	{A,B} => {C}	0.1666667	0.5000000	3

Also try...

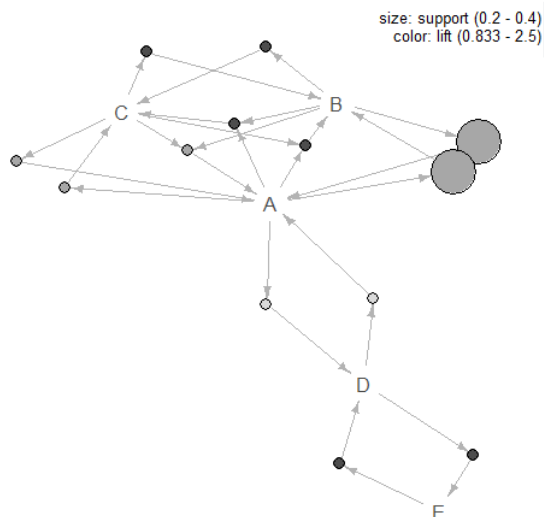
```
itemsets <- eclat(egs, parameter = list(supp = 0.01, maxlen = 5))
```

```
rules2 <- ruleInduction(itemsets, egs, confidence = .1)
```

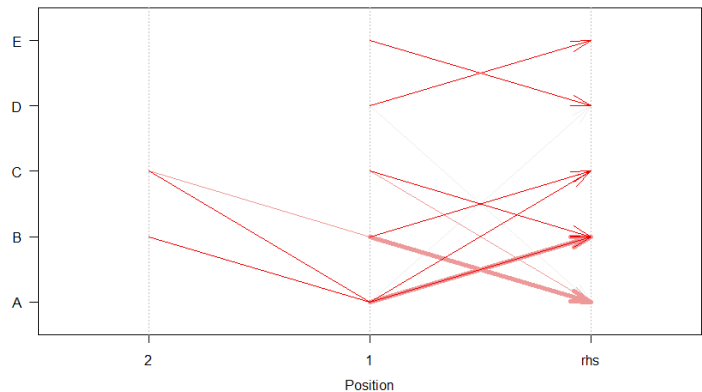

Visualising Rules

```
library(arulesViz)
plot(rules)
plot(rules, method="graph", nodeCol=grey.colors(10), edgeCol=grey(.7), alpha=1)
plot(rules, method="paracoord", control=list(reorder=TRUE))
```

Graph for 13 rules



Parallel coordinates plot for 13 rules



<https://cran.r-project.org/web/packages/arulesViz/vignettes/arulesViz.pdf>
<https://cran.r-project.org/web/packages/arulesViz/arulesViz.pdf>

Sequence finding using SPSS Modeler

- Use the Sequence modelling node (based on Carma algorithm)
- Finds sequences of item-sets.
 - e.g. {coffee, milk, sugar} => {bread, butter}
- The item-set can be a row in tabular format data or a single transaction in transaction format data.
- Requires an item-set ID field PLUS a timestamp field for each item-set.
 - If no timestamp field is given then it uses the row number to indicate the sequence (assumes rows are in temporal order in the database)
 - e.g. (userID, date-time, news)
(userID, date-time, sports)
(userID, date-time, finance) for transaction format
 - e.g. (userID, date-time, news, sports, finance) ...for tabular format
- Variable types must be specified in the Sequence node (not Type node)



Sequence

Examining SPSS Modeler Sequence Rules

- Sequence rules in modeler look like:

Antecedent	Consequent
beer and cannedveg and frozenmeal	frozenmeal
beer and cannedveg	beer
fish	fish
fish	
softdrink	softdrink

fish->fish->fish (not very useful)

For example:

Antecedent	Consequent	Support %	Confidence %
onair misc	misc	2.664	88.124
onair misc	misc	3.035	87.766
weather weather weather	weather	4.432	85.089

Sequence finding using R

- The Spade algorithm is a popular sequence mining algorithm

```
library(arules)
library(arulesSequences)
x <- read_baskets(con=system.file("misc", "zaki.txt",
  package = "arulesSequences"),info=c("sequenceID","eventID","SIZE"))
s1 <- cspade(x, parameter = list(support = 0.4), control = list(verbose = TRUE))
as(s1, "data.frame")
```

sequences found
#total sequences (i.e. 4)

```
> as(x, "data.frame")
```

	items	sequenceID	eventID	SIZE
1	{C,D}	1	10	2
2	{A,B,C}	1	15	3
3	{A,B,F}	1	20	3
4	{A,C,D,F}	1	25	4
5	{A,B,F}	2	15	3
6	{E}	2	20	1
7	{A,B,F}	3	10	3
8	{D,G,H}	4	10	3
9	{B,F}	4	20	2
10	{A,G,H}	4	25	3



```
as(s1, "data.frame")
```

	sequence	support
1	<{A}>	1.00
2	<{B}>	1.00
3	<{D}>	0.50
4	<{F}>	1.00
5	<{A,F}>	0.75
6	<{B,F}>	1.00
7	<{D},{F}>	0.50
8	<{D},{B,F}>	0.50
9	<{A,B,F}>	0.75
10	<{A,B}>	0.75
11	<{D},{B}>	0.50
12	<{B},{A}>	0.50
13	<{D},{A}>	0.50
14	<{F},{A}>	0.50
15	<{D},{F},{A}>	0.50
16	<{B,F},{A}>	0.50
17	<{D},{B,F},{A}>	0.50
18	<{D},{B},{A}>	0.50

Note: the read_baskets() above is not necessary since this dataset is preloaded with the arulesSequences library and called zaki. Use data("zaki") then inspect(zaki) to view it.






Location of data files

Sample code to explore

Files / Lecture Notes / barry / demo-code-and-data

demo-code-and-data

Please select the file(s) or folder which you want to manage.





<input type="checkbox"/>	Name	Size
<input type="checkbox"/>	 simplebasket.csv	65 Bytes
<input type="checkbox"/>	 simplebasket-test.csv	50 Bytes
<input type="checkbox"/>	 msnbc-seqformat-sample.txt	3.80 KB
<input type="checkbox"/>	 buildandtestAssociationRules.r	3.56 KB
<input type="checkbox"/>	 buildSequenceRules.r	675 Bytes

The MSNBC data - I have converted into the various formats already

Files / Lecture Notes / barry / MSNBC-workshop

MSNBC-workshop

Please select the file(s) or folder which you want to manage.

<input type="checkbox"/>	Name	Size
<input type="checkbox"/>	 msnbc990928-originalformat.txt	12 MB
<input type="checkbox"/>	 msnbc990928-RSpadeformat.txt	64.62 MB
<input type="checkbox"/>	 msnbc990928-tabularformat.txt	39.54 MB
<input type="checkbox"/>	 msnbc990928-transactionformat.csv	49.92 MB