Frequent Symptom Mining

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Improving Healthcare Outcomes

[illegible]

Quotes

- “In God we trust, all others bring data.” - W. Edwards Deming
- “Data mining is not about finding the right answers, it’s about asking the right questions.” - Anonymous
- “Data mining is the process of finding needles in haystacks, and then finding the other needles that are hidden in those needles.” - Anonymous
- “You didn’t know? You better call somebody!” - Road Dogg, WWE

Outline

- Background of the Problem
- Background of the Method
- R packages
- Basic example(s)
- The crux of the matter
- Symptom mining

Neonatal Abstinence Syndrome (NAS)

- In utero opiod exposure
- Characterized by withdrawal symptoms
- ICD-9 779.5
- ICD-10 P96.1
- Number of diagnoses increasing
- Control costs (lengthy stays)
- Detection is essential for health of infant
- Treatment is pharmacological therapy with morphine, methadone, or phenobarbital

Finnigan NAS Score (FNASS)

- 21 symptoms scored
- 5 gastronintesinal (e.g., vomit)
- 7 Centrial nerous system (e.g., tremors)
- 9 Respiratory (e.g., stuffiness, flaring)
- Scored every 4 hours
- Many scoring systems
  - *Lipsitz (Lipsitz, 1975)*
  - *Neonatal Withdrawal Inventory (Zahorodny et al., 1998)*
  - *FNASS (Finnegan et al., 1975)*

Goal

- Reduce the number of items
- ESC (Curran et al., 2020)
- Mine frequent (assocaiated) symptoms

Research Team

- Tina Holt, M.D., Maine Medical Center
- Meg Curran, M.D., Maine Medical Center
- Michael Arciero, Ph.D. University of New England
- Curran, M., Holt, C., Arciero, M., Quinlan, J., Cox, D., & Craig, A. (2020). Proxy Finnegan component scores for eat, sleep, console in a cohort of opioid-exposed neonates. *Hospital Pediatrics, 10*(12), 1053-1058.

Itemset & Rule Mining

- Find (useful) patterns in a database
- *Frequent* co-occurrence
- Frequent Itemset Mining
- Sequence Mining
- Market Basket Analysis
  - *Modern parlance*

Applications

- Retail sales (MBA)
- Web usage (data information brokers)
- Congressional Voting Records
- Law enforcement profiling
- Recommender systems
- Supply chain analysis
- Extract information hidden in DNA sequences
- Gene ontology
- Concussion symptims (sleep, light sensitivity)

Terminology

- **Items** are denoted by $\mathcal{I} = \{i_1, i_2, \ldots, i_n\}$ and **transactions** (a.k.a. events, observations, records) as $T = \{t_1, t_2, \ldots, t_N\}$ where $N > n$ and $N \gg 1$.
  - *"Items" are symptoms in our case*
- **Itemset** is any group of one or more items, also called **basket** or **cart**.
  - e.g., $X = \{i_3, i_{17}, i_{1325}\}$
- **Frequent item set** is an itemset that meets (some) criteria.
- Let X be a subset of items, then the **support count** is the number of transactions containing X.

$$\sigma(X) = |\{t_i | X \subset t_i \in T\}|$$

- **Association Rule** is an implication of the form $X \Rightarrow Y$ where $X \cap Y = \emptyset$.

Measures of Strength and Interest

The following measure the strength of an association or frequency of an itemset.

- The **support** (how often the rule applies)

  $$S(X \Rightarrow Y) = \frac{\sigma(X \cup Y)}{N}$$

  where N is the total number of transactions in the database.

- **Confidence** how frequently items in Y appears in transactions that contain X.

  $$C(X \Rightarrow Y) = \frac{\sigma(X \cup Y)}{\sigma(X)}$$

- **Lift** (Brin et al., 1997), ratio of combined support from expected independence

  $$L(X \Rightarrow Y) = \frac{N\sigma(X \cup Y)}{\sigma(X) \cdot \sigma(Y)} = \frac{C(X, Y)}{S(Y)}$$

Example

1	Milk	Eggs	Diapers	Beer
2	Milk		Diapers	
3		Eggs	Diapers	Beer
4	Milk	Eggs		
5	Milk		Diapers	Beer

Consider the transaction database with $X = \{\text{Diapers}\}$ and $Y = \{\text{Beer}\}$.

- Support, $S(X, Y) = 3/5 = 0.6$
- Confidence, $C(X, Y) = 3/4 = 0.75$
- Lift, $L(X, Y) = (5 \cdot 3)/(4 \cdot 3) = 1.25$

Binary Database

tid	Milk	Eggs	Diapers	Beer
1	1	1	1	1
2	1	0	1	0
3	0	1	1	1
4	1	1	0	0
5	1	0	1	1

Rule Mining / Itemset Selection

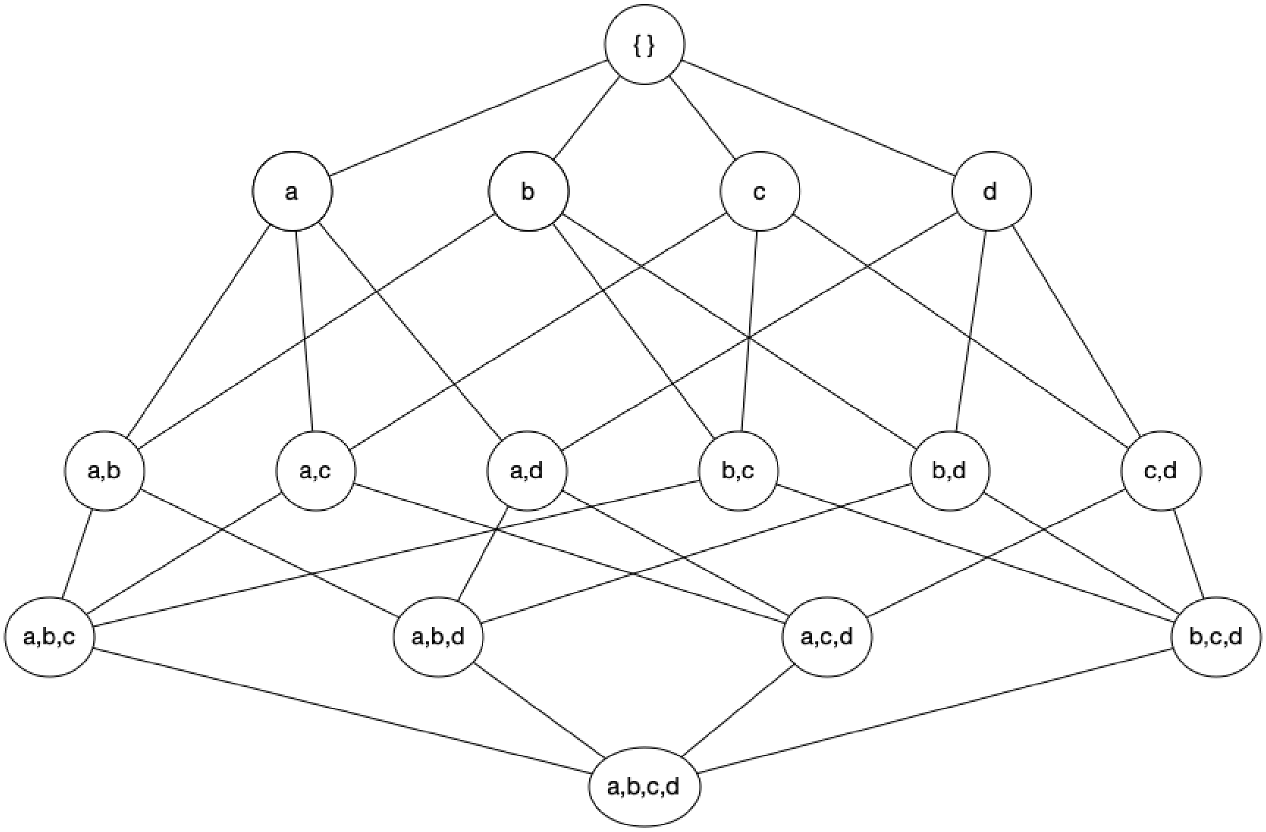
- **Frequent item set** is an itemset that meets minimum support criteria.
- Given d items, exclude the 0 element set and the d element set.
- For each subset k-element subset X, we consider the $d-k$ element subsets Y.

$$\sum_{k=1}^{d-1} \binom{d}{k} \sum_{i=1}^{d-k} \binom{d-k}{i} = 3^d - 2^{d+1} + 1$$

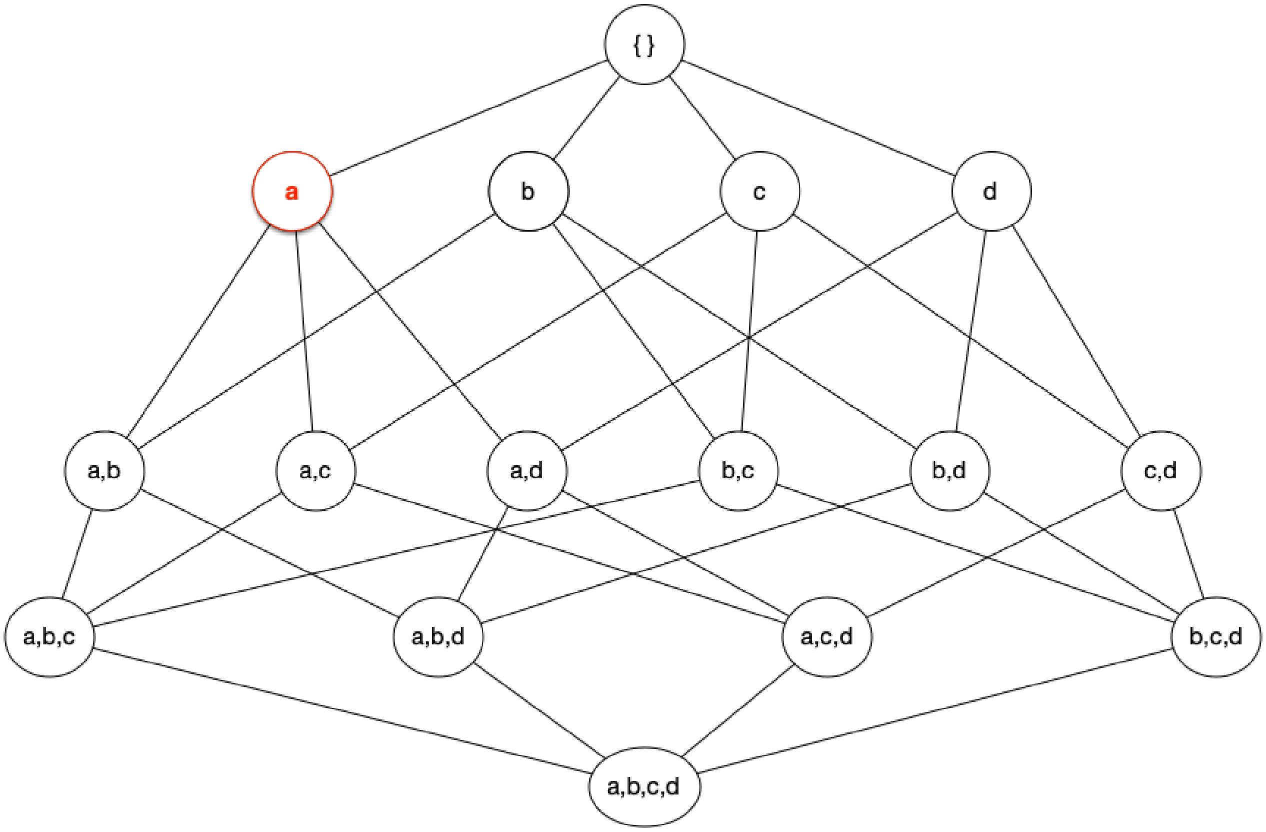
- Brute force is computationally prohibitive
  - *Exponential time,* $O(3^d)$
- Subset reduction needed
  - *Apriori Algorithm*

Aprior Algorithm

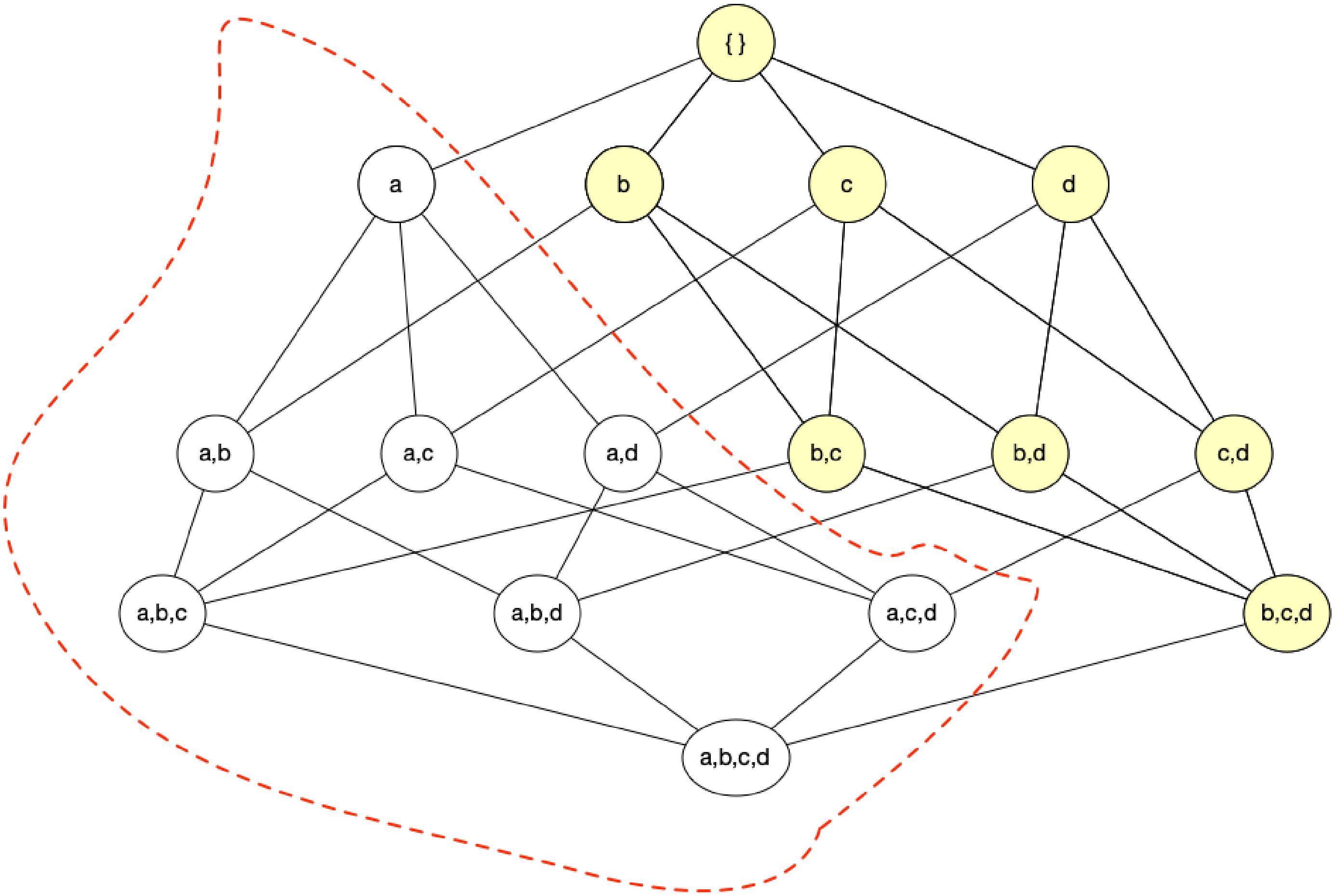
- **Apriori Principle**: If an itemset is frequent, then all its subsets are frequent.
- **Contrapositive**: If a subset is infrequent, then all its supersets are infrequent.



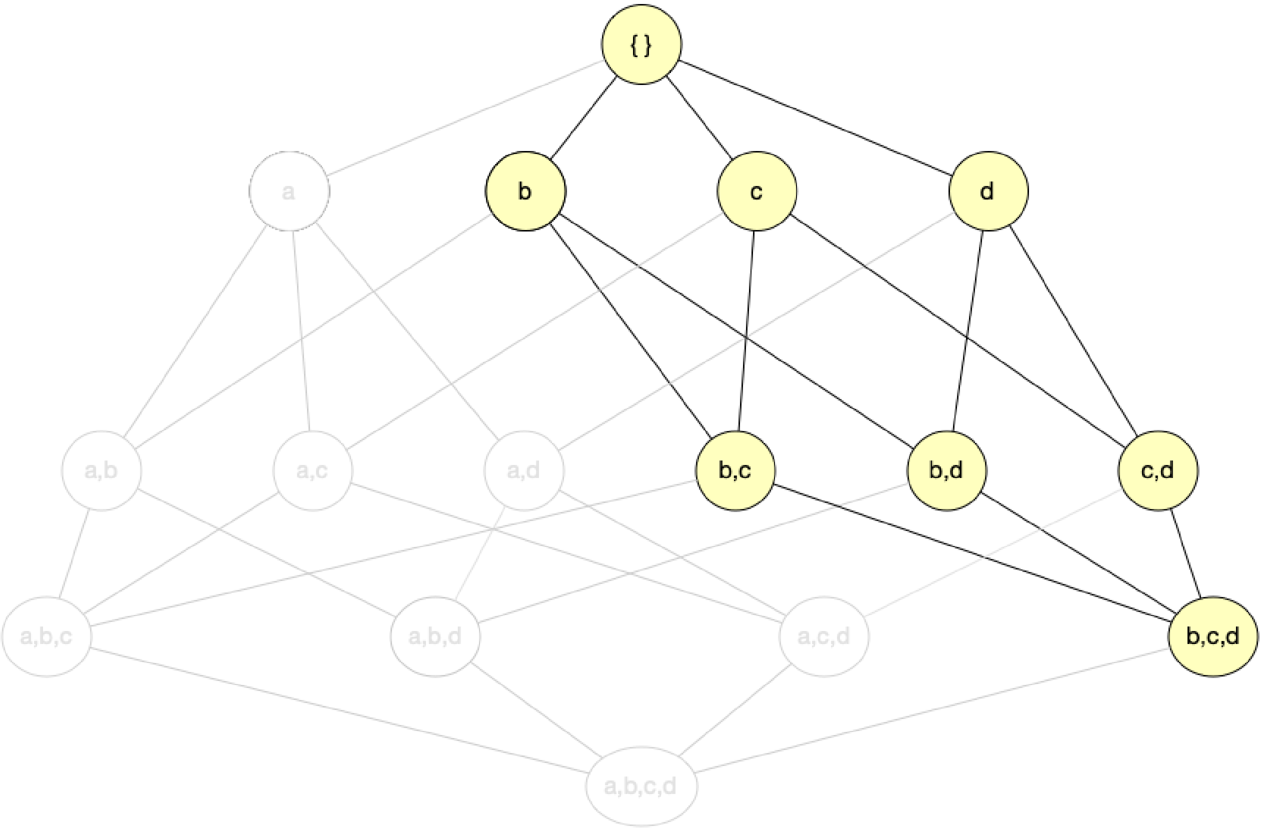
$\mathcal{P}(\{a, b, c, d\})$



Suppose a is infrequent



a and its supersets

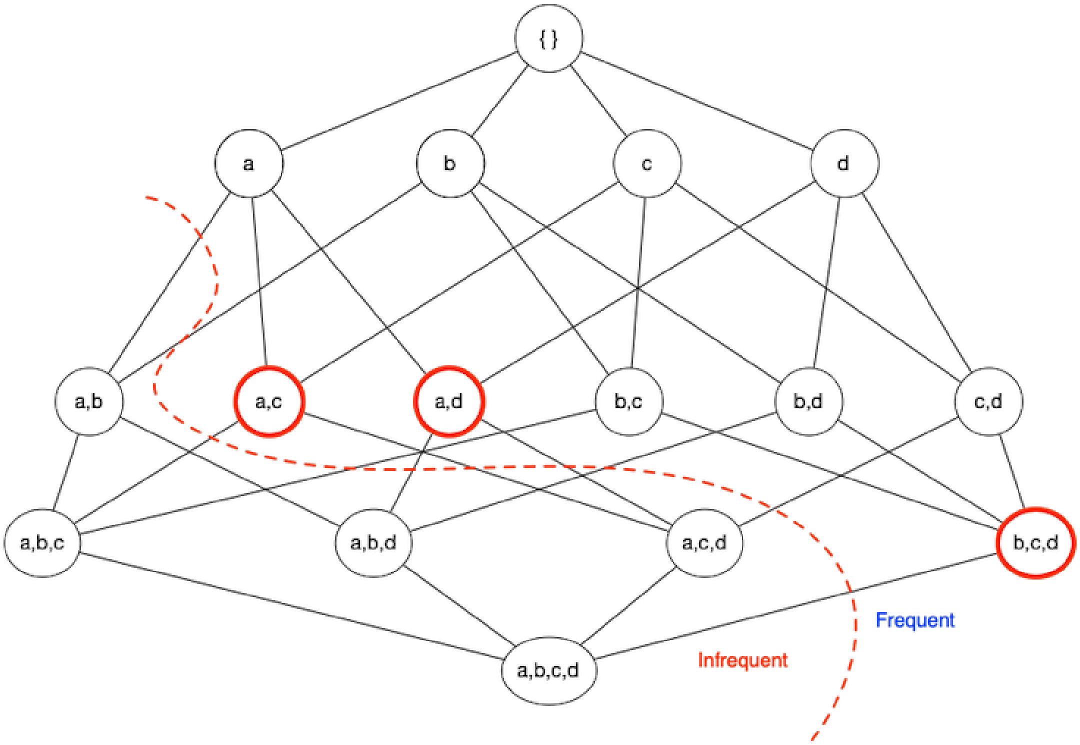


Prune *those* (infrequent) itemsets

Compact representations

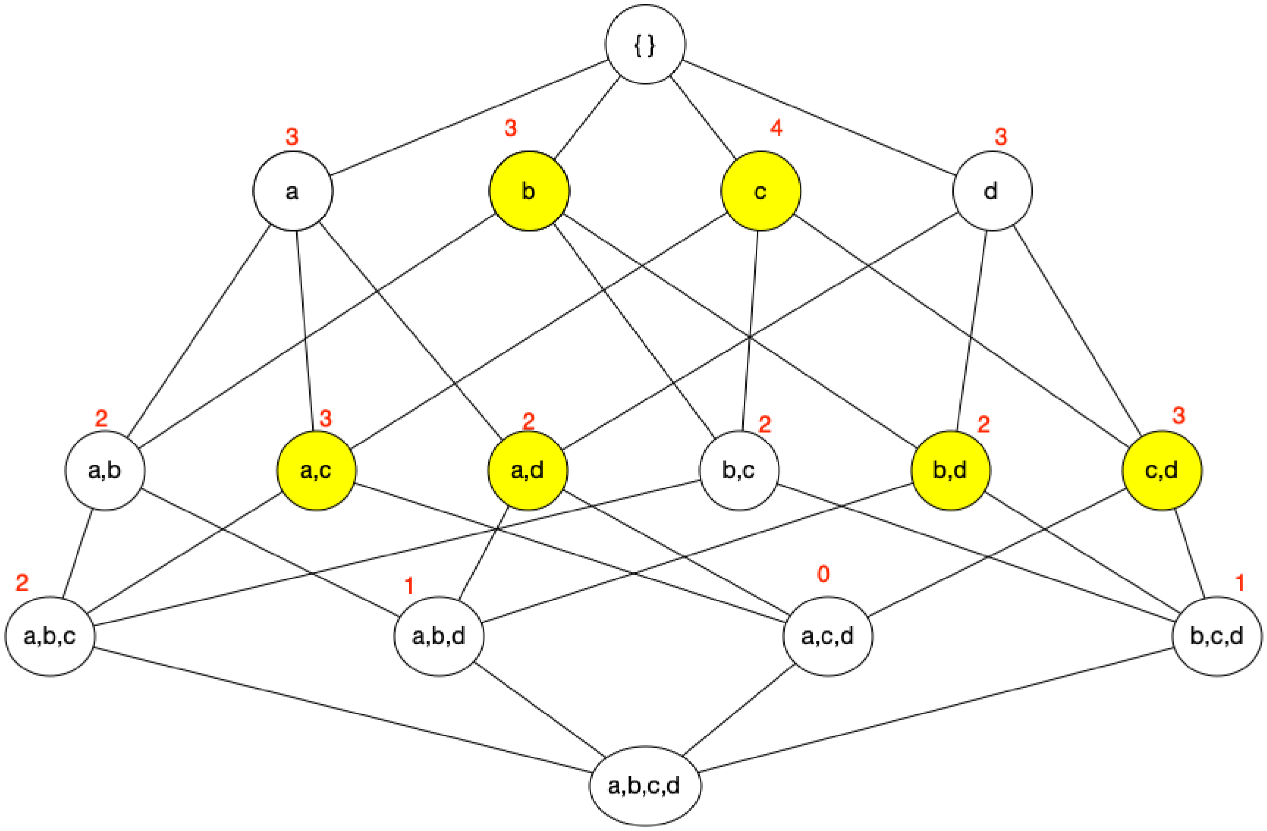
Definition *- A frequent itemset is **maximal** if none of its immediate supersets are frequent.*

All frequent itemsets are a subset of the maximal itemsets.



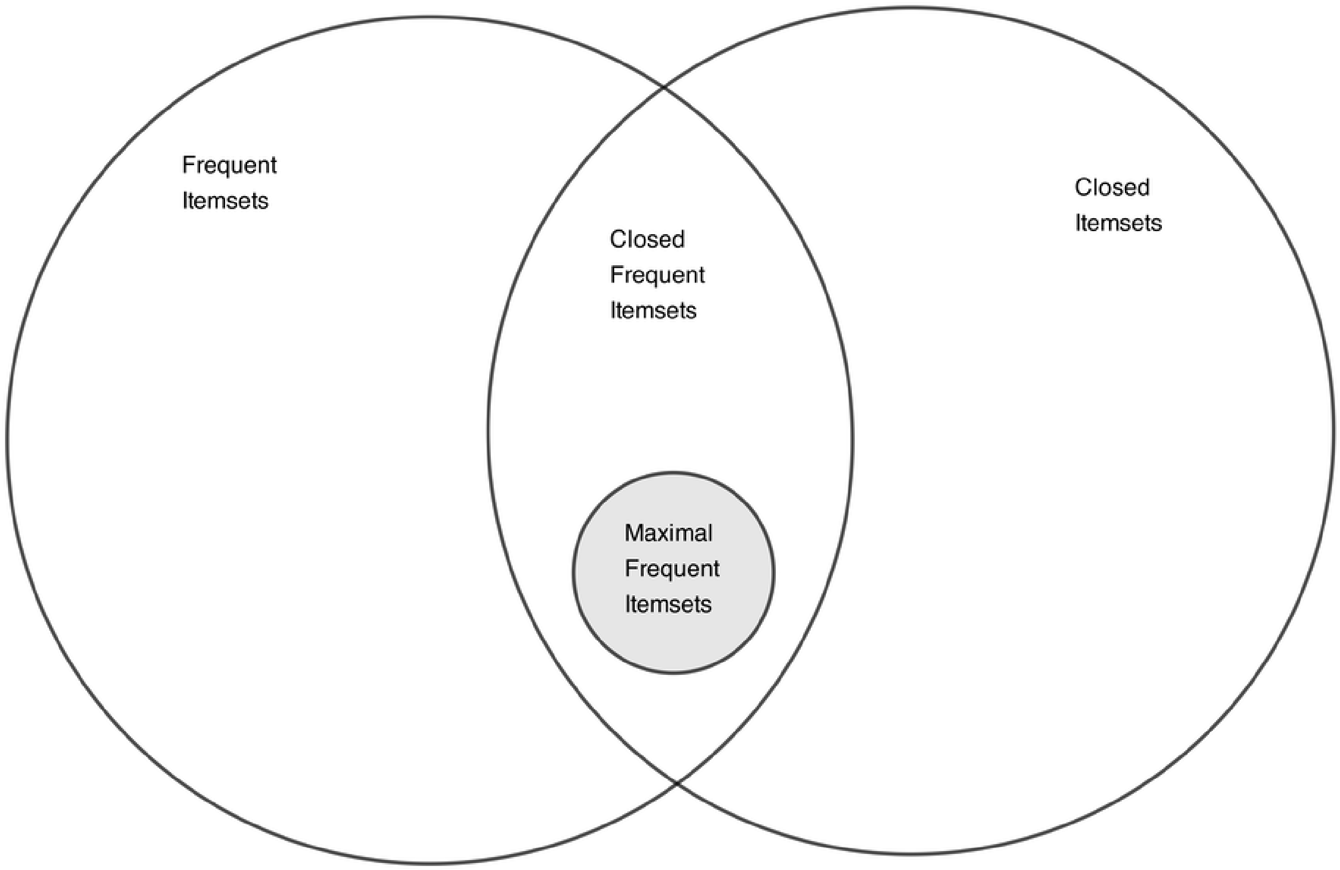
Compact representations (cont)

***Definition** - An itemset X is **closed** if none of its immediate supersets has exactly the same support count as X. An itemset is a **closed frequent itemset** if it is closed and its support is greater than or equal to minimum support.*



Closed itemsets

Compact Representation Diagram



R packages

- `aRules` - Mining Association Rules and Frequent Itemsets
  - *Apriori and eclat algorithms*
- `aRulesViz` - Visualize Association Rules
- `arulesSequences` - Mining Frequent Sequences
- `tidyverse` - Tidy ecosystem

Install and Load

```r
# install.packages("tidyverse")
# install.packages("arules")
# install.packages("arulesViz")
# install.packages("arulesSequences")

library(tidyverse)
library(arules)
library(arulesViz)
library(arulesSequences)
```

aRules 1.7-5

- `inspect` - display rules in readable form
- `itemFrequency` - Frequency/Support for Single Items
- `itemMatrix` - building block for transactions
- `apriori` - Mine frequent itemsets, association rules
- `eclat` - Mine frequent itemsets with the Eclat algorithm.
  - *equivalence class clustering along with bottom-up lattice traversal.*
- `transactions` - subclass of `itemMatrix`. Note: Data typically starts as a `data.frame` or a `matrix` and needs to be prepared before it can be converted into transactions
- Read the Manual
  - *https://cran.r-project.org/web/packages/arules/arules.pdf*
- Check dependencies (e.g., Matrix $\geq$ 1.4)

Example

```r
# Load Example Data (from aRules package)
data("Groceries")
class(Groceries)
```

```
## [1] "transactions"
## attr(,"package")
## [1] "arules"
```

```r
head(as(Groceries, "data.frame"), 10)
```

```
##                                                                        items
## 1                {citrus fruit,semi-finished bread,margarine,ready soups}
## 2                                          {tropical fruit,yogurt,coffee}
## 3                                                            {whole milk}
## 4                           {pip fruit,yogurt,cream cheese ,meat spreads}
## 5   {other vegetables,whole milk,condensed milk,long life bakery product}
## 6                        {whole milk,butter,yogurt,rice,abrasive cleaner}
## 7                                                            {rolls/buns}
## 8  {other vegetables,UHT-milk,rolls/buns,bottled beer,liquor (appetizer)}
## 9                                                            {pot plants}
## 10                                                   {whole milk,cereals}
```

```r
freqItems <- apriori(Groceries,
                 parameter = list(
                   supp   = 0.01,
                   conf   = 0.5,
                   target = "frequent itemsets",
                   minlen = 3,
                   maxlen = 5)
                 )
```

```
## Apriori
## 
## Parameter specification:
##  confidence minval smax arem  aval originalSupport maxtime support minlen
##          NA    0.1    1 none FALSE            TRUE       5    0.01      3
##  maxlen            target  ext
##       5 frequent itemsets TRUE
## 
## Algorithmic control:
##  filter tree heap memopt load sort verbose
##     0.1 TRUE TRUE  FALSE TRUE    2    TRUE
## 
## Absolute minimum support count: 98 
## 
## set item appearances ...[0 item(s)] done [0.00s].
## set transactions ...[169 item(s), 9835 transaction(s)] done [0.00s].
## sorting and recoding items ... [88 item(s)] done [0.00s].
## creating transaction tree ... done [0.00s].
## checking subsets of size 1 2 3 4 done [0.00s].
## sorting transactions ... done [0.00s].
## writing ... [32 set(s)] done [0.00s].
## creating S4 object  ... done [0.00s].
```

```r
head(as(freqItems,"data.frame") %>% arrange(desc(count)),10)
```

```
##                                                items    support count
## 1     {root vegetables,other vegetables,whole milk} 0.02318251   228
## 2              {other vegetables,whole milk,yogurt} 0.02226741   219
## 3          {other vegetables,whole milk,rolls/buns} 0.01789527   176
## 4      {tropical fruit,other vegetables,whole milk} 0.01708185   168
## 5                    {whole milk,yogurt,rolls/buns} 0.01555669   153
## 6                {tropical fruit,whole milk,yogurt} 0.01514997   149
## 7  {other vegetables,whole milk,whipped/sour cream} 0.01464159   144
## 8               {root vegetables,whole milk,yogurt} 0.01453991   143
## 9                {other vegetables,whole milk,soda} 0.01392984   137
## 10          {pip fruit,other vegetables,whole milk} 0.01352313   133
```

```r
rules <- apriori(Groceries,
                 parameter = list(
                   supp   = 0.01,
                   conf   = 0.5,
                   target = "rules",
                   minlen = 1,
                   maxlen = 10)
                 )
```

```r
head(as(rules,"data.frame") %>% arrange(desc(count)))
```

```
##                                                    rules    support confidence
## 1            {other vegetables,yogurt} => {whole milk} 0.02226741  0.5128806
## 2              {tropical fruit,yogurt} => {whole milk} 0.01514997  0.5173611
## 3 {other vegetables,whipped/sour cream} => {whole milk} 0.01464159  0.5070423
## 4             {root vegetables,yogurt} => {whole milk} 0.01453991  0.5629921
## 5         {pip fruit,other vegetables} => {whole milk} 0.01352313  0.5175097
## 6       {root vegetables,yogurt} => {other vegetables} 0.01291307  0.5000000
##     coverage     lift count
## 1 0.04341637 2.007235   219
## 2 0.02928317 2.024770   149
## 3 0.02887646 1.984385   144
## 4 0.02582613 2.203354   143
## 5 0.02613116 2.025351   133
## 6 0.02582613 2.584078   127
```

```
summary(rules)
```

```
## set of 15 rules
##
## rule length distribution (lhs + rhs):sizes
##  3
## 15
##
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##       3       3       3       3       3       3
##
## summary of quality measures:
##     support           confidence        coverage             lift
##  Min.   :0.01007   Min.   :0.5000   Min.   :0.01729   Min.   :1.984
##  1st Qu.:0.01174   1st Qu.:0.5151   1st Qu.:0.02089   1st Qu.:2.036
##  Median :0.01230   Median :0.5245   Median :0.02430   Median :2.203
##  Mean   :0.01316   Mean   :0.5411   Mean   :0.02454   Mean   :2.299
##  3rd Qu.:0.01403   3rd Qu.:0.5718   3rd Qu.:0.02598   3rd Qu.:2.432
##  Max.   :0.02227   Max.   :0.5862   Max.   :0.04342   Max.   :3.030
##      count
##  Min.   : 99.0
##  1st Qu.:115.5
##  Median :121.0
##  Mean   :129.4
##  3rd Qu.:138.0
##  Max.   :219.0
##
## mining info:
##       data ntransactions support confidence
##  Groceries          9835    0.01        0.5
##
call
##  apriori(data = Groceries, parameter = list(supp = 0.01, conf = 0.5, target = "rules", minlen = 1,
maxlen = 10))
```

```r
inspect(rules[1:10], by ="lift")
```

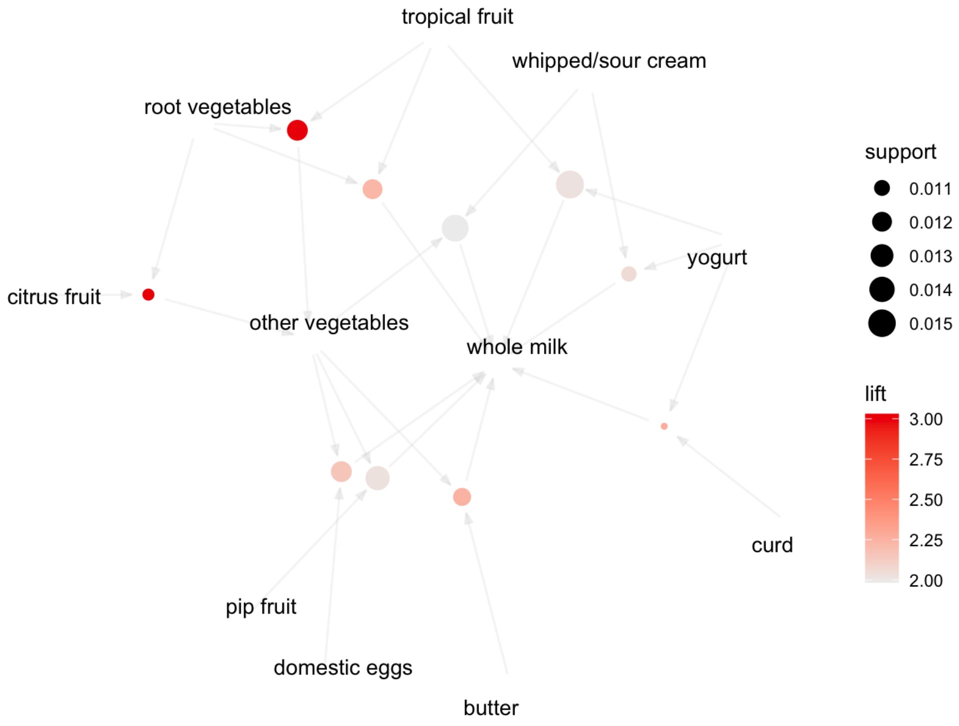
```
##      lhs                                        rhs                support
## [1]  {curd, yogurt}                          => {whole milk}       0.01006609
## [2]  {other vegetables, butter}              => {whole milk}       0.01148958
## [3]  {other vegetables, domestic eggs}       => {whole milk}       0.01230300
## [4]  {yogurt, whipped/sour cream}            => {whole milk}       0.01087951
## [5]  {other vegetables, whipped/sour cream} => {whole milk}       0.01464159
## [6]  {pip fruit, other vegetables}           => {whole milk}       0.01352313
## [7]  {citrus fruit, root vegetables}         => {other vegetables} 0.01037112
## [8]  {tropical fruit, root vegetables}       => {other vegetables} 0.01230300
## [9]  {tropical fruit, root vegetables}       => {whole milk}       0.01199797
## [10] {tropical fruit, yogurt}                => {whole milk}       0.01514997
##      confidence coverage   lift     count
## [1]  0.5823529  0.01728521 2.279125  99
## [2]  0.5736041  0.02003050 2.244885 113
## [3]  0.5525114  0.02226741 2.162336 121
## [4]  0.5245098  0.02074225 2.052747 107
## [5]  0.5070423  0.02887646 1.984385 144
## [6]  0.5175097  0.02613116 2.025351 133
## [7]  0.5862069  0.01769192 3.029608 102
## [8]  0.5845411  0.02104728 3.020999 121
## [9]  0.5700483  0.02104728 2.230969 118
## [10] 0.5173611  0.02928317 2.024770 149
```

`arulesViz` 1.5-2

Visualizing Association Rules and Frequent Itemsets

- https://cran.r-project.org/web/packages/arulesViz/arulesViz.pdf
- `plot(rules, method="graph")`
- See also `ggraph` package for graph and network visualizations

```
plot(rules[1:10], method = "graph")
```



Frequent Sequences

Mining frequent sequential patterns with the cSPADE algorithm

- SPADE (**S**equential **PA**ttern **D**iscovery using **E**quivalence classes)
- Temporal transactions (grouped by customer)
- "If a customer buys X then in the next purchase will they buy Y"?
- Web logs ($a \rightarrow b \rightarrow c \rightarrow d$)
- `arulesSequences` 0.2-28
- `cspade(transactions)`

```r
# create binary matrix of items
data <- data.frame(sequenceID = as.factor(c(1, 1, 1, 1, 2, 2, 3, 4, 4, 4)),
                   eventID = as.factor(c(1, 2, 3, 4, 1, 1, 1, 1, 2, 3)),
                   A = c(0, 1, 1, 1, 1, 0, 1, 0, 0, 1),
                   B = c(0, 1, 1, 0, 1, 0, 1, 0, 1, 0),
                   C = c(1, 1, 0, 1, 0, 0, 0, 0, 0, 0),
                   D = c(1, 0, 0, 0, 0, 0, 0, 1, 0, 0),
                   E = c(0, 0, 0, 0, 0, 1, 0, 0, 0, 0),
                   F = c(0, 0, 1, 1, 1, 0, 1, 0, 0, 1),
                   G = c(0, 0, 0, 0, 0, 0, 0, 1, 1, 0),
                   H = c(0, 0, 0, 0, 0, 0, 0, 1, 0, 1))

db <- pivot_longer(data, cols = c(3,4,5,6,7,8,9,10)) %>% filter(value > 0)
```

```
sequences <- db %>%
  group_by(sequenceID, eventID) %>%
  summarize(
    SIZE = n(),
    items = paste(as.character(name), collapse = ';')
  )
```

```
## `summarise()` has grouped output by 'sequenceID'. You can override using the
## `.groups` argument.
```

```
names(sequences) = c("sequenceID", "eventID", "SIZE", "items")

sequences <- data.frame(lapply(sequences, as.factor))
sequences <- sequences[order(sequences$sequenceID, sequences$eventID),]

# Convert to transaction matrix data type
write.table(sequences, "seqs.txt", sep=";", row.names = FALSE, col.names = FALSE, quote = FALSE)
trans_matrix <- read_baskets("seqs.txt", sep = ";", info = c("sequenceID","eventID","SIZE"))
```

```
s1 <- cspade(trans_matrix, parameter = list(support = 0.6, maxlen=5), control = list(verbose = TRUE))
```

```
summary(s1)
```

```
## set of 7 sequences with
## 
## most frequent items:
##       A       B       F (Other) 
##       4       4       4       4 
## 
## most frequent elements:
##     {A}     {B}     {F}   {A,F}   {B,F} (Other) 
##       1       1       1       1       1       2 
## 
## element (sequence) size distribution:
## sizes
## 1 
## 7 
## 
## sequence length distribution:
## lengths
## 1 2 3 
## 3 3 1 
## 
## summary of quality measures:
##     support      
##  Min.   :0.7500  
##  1st Qu.:0.7500  
##  Median :1.0000  
##  Mean   :0.8929  
##  3rd Qu.:1.0000  
##  Max.   :1.0000  
## 
## includes transaction ID lists: FALSE 
## 
## mining info:
##          data ntransactions nsequences support
##  trans_matrix             9          4     0.6
```

```
s1.df <- as(s1, "data.frame")
s1.df
```

```
##    sequence support
## 1     <{A}>    1.00
## 2     <{B}>    1.00
## 3     <{F}>    1.00
## 4   <{A,F}>    1.00
## 5   <{B,F}>    0.75
## 6 <{A,B,F}>    0.75
## 7   <{A,B}>    0.75
```

Crux(es)

- Data frame must be converted to a **transaction**
- For `arulesSequences`
  - *`pivot_longer`*
  - *`write_table`*
  - *`read_baskets`*

Symptom Mining

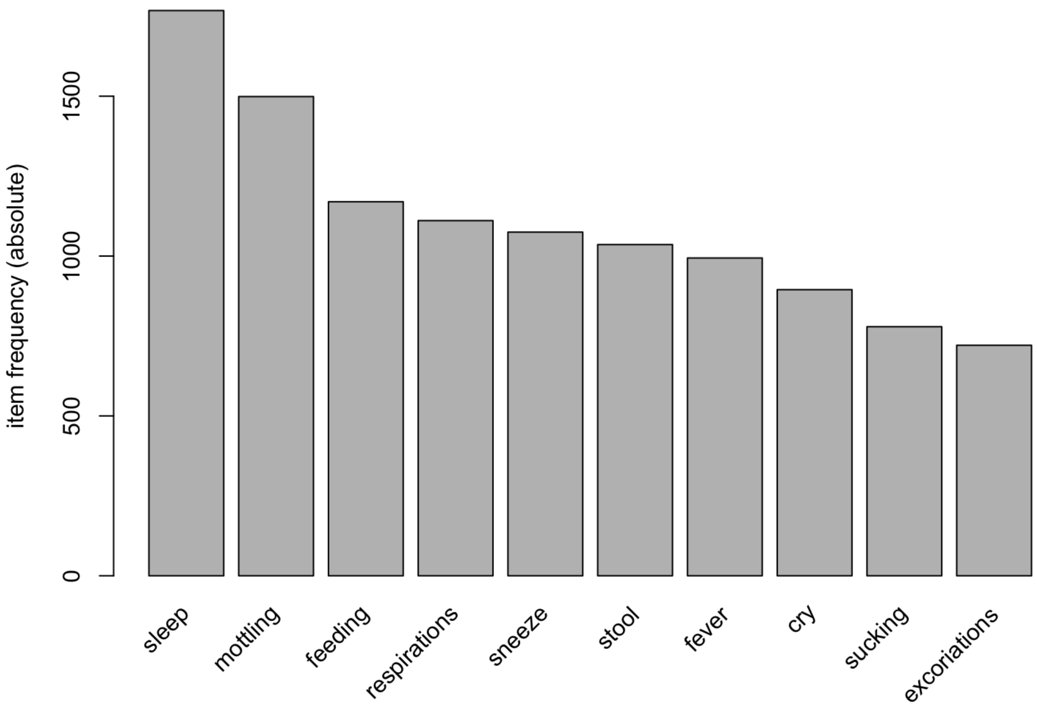
```
# read data
raw = read_csv('nas.csv', show_col_types = FALSE)

# clean
tidset = raw %>% mutate(Tremors = tremors_disturbed + tremors_undisturbed) %>%
          select(-c(tid, bid, oid, nas, num_items, tremors_disturbed, tremors_undisturbed, Tremors, tone))
```

```
# df --> binary matrix --> transactions
transactions = as(ifelse(tidset > 0, 1, 0), "transactions")
```

```
itemFrequency(transactions)
```

```
##    excoriations myoclonic_jerks             cry           sleep            moro 
##     0.144866385     0.004018485     0.179827205     0.355234077     0.137030340 
##           sweat            yawn        mottling      stuffiness          sneeze 
##     0.016073940     0.021097046     0.301185453     0.117942536     0.215993570 
##   nasal_flaring           fever    respirations         sucking         feeding 
##     0.012256379     0.199718706     0.223226843     0.156519992     0.235081374 
##           vomit           stool 
##     0.119750854     0.208157525
```

```r
# Frequency Plots
itemFrequencyPlot(transactions,topN=10,type="absolute")
```



Frequent Itemsets

```
itemsets =  apriori(transactions, parameter = list(supp   = 0.03,
                                                   conf   = 0.7,
                                                   minlen = 3,
                                                   target = "maximally frequent itemsets")
                    )
```

```
inspect(itemsets, by = "lift")
```

```
##      items                             support    count
## [1]  {excoriations, sleep, mottling} 0.03054049 152
## [2]  {cry, respirations, sucking}    0.03576452 178
## [3]  {cry, sleep, sucking}           0.04641350 231
## [4]  {sleep, sneeze, sucking}        0.03275065 163
## [5]  {sleep, respirations, sucking}  0.04098855 204
## [6]  {cry, sleep, fever}             0.03275065 163
## [7]  {sleep, sneeze, fever}          0.04139040 206
## [8]  {sleep, fever, respirations}    0.04560981 227
## [9]  {sleep, mottling, fever}        0.03475990 173
## [10] {cry, sleep, stool}             0.03154511 157
## [11] {sleep, sneeze, stool}          0.03335343 166
## [12] {sleep, respirations, stool}    0.03496082 174
## [13] {cry, sleep, feeding}           0.03134418 156
## [14] {cry, sleep, sneeze}            0.03737191 186
## [15] {cry, sleep, respirations}      0.05123568 255
## [16] {cry, sleep, mottling}          0.03596544 179
## [17] {sleep, sneeze, feeding}        0.03033956 151
## [18] {sleep, sneeze, respirations}   0.04741812 236
## [19] {sleep, mottling, sneeze}       0.03757284 187
## [20] {sleep, mottling, respirations} 0.03697006 184
```

Frequent Rules

```
# Generate and Prune ASSOCIATION RULES
rules <- apriori(transactions, parameter = list(supp = 0.01,
                                               conf = 0.70,
                                               minlen = 1,
                                               maxlen = 5,
                                               target = "rules")
                )
sortedRules <- sort(rules, by="lift", decreasing=TRUE)
```

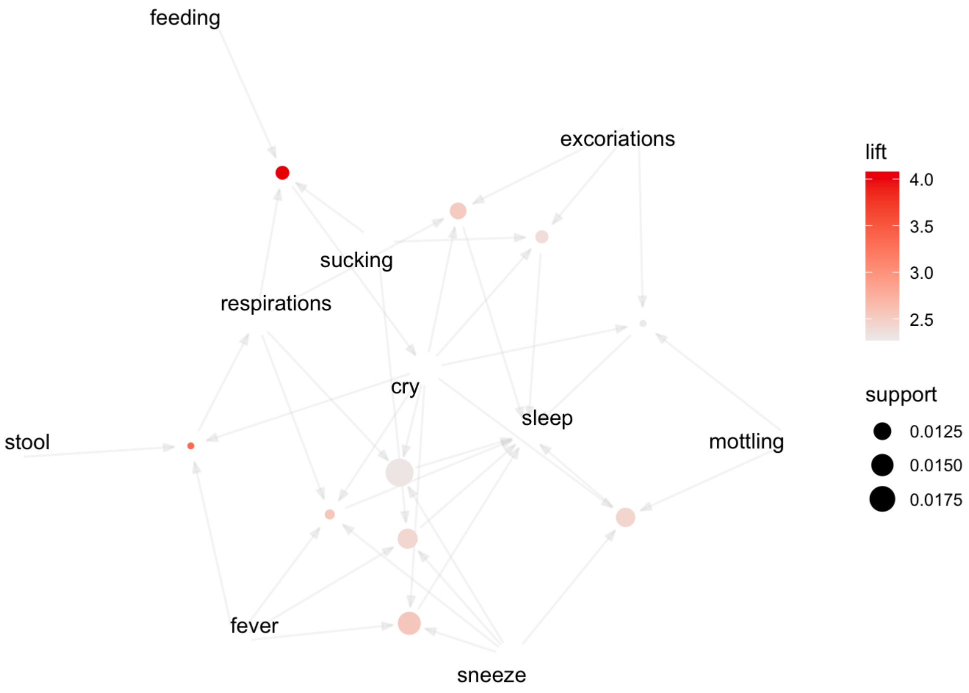
```
summary(sortedRules)
```

```
## set of 42 rules
##
## rule length distribution (lhs + rhs):sizes
##  3  4  5
##  5 36  1
##
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   3.000   4.000   4.000   3.905   4.000   5.000
##
## summary of quality measures:
##     support           confidence        coverage             lift
##  Min.   :0.01005   Min.   :0.7033   Min.   :0.01125   Min.   :1.980
##  1st Qu.:0.01160   1st Qu.:0.7201   1st Qu.:0.01507   1st Qu.:2.027
##  Median :0.01366   Median :0.7489   Median :0.01849   Median :2.141
##  Mean   :0.01598   Mean   :0.7659   Mean   :0.02103   Mean   :2.234
##  3rd Qu.:0.01703   3rd Qu.:0.7865   3rd Qu.:0.02270   3rd Qu.:2.239
##  Max.   :0.03737   Max.   :0.9107   Max.   :0.04842   Max.   :4.078
##      count
##  Min.   : 50.00
##  1st Qu.: 57.75
##  Median : 68.00
##  Mean   : 79.55
##  3rd Qu.: 84.75
##  Max.   :186.00
##
## mining info:
##          data ntransactions support confidence
##  transactions          4977    0.01        0.7
##
call
##  apriori(data = transactions, parameter = list(supp = 0.01, conf = 0.7, minlen = 1, maxlen = 5,
target = "rules"))
```

```
inspect(sortedRules[1:10])
```

```
##      lhs                                  rhs            support    confidence
## [1]  {respirations, sucking, feeding}  => {cry}          0.01105083 0.7333333
## [2]  {cry, fever, stool}               => {respirations} 0.01004621 0.7462687
## [3]  {cry, sneeze, fever, respirations} => {sleep}       0.01024714 0.9107143
## [4]  {cry, sneeze, fever}              => {sleep}        0.01547117 0.9058824
## [5]  {excoriations, cry, respirations} => {sleep}        0.01205546 0.8955224
## [6]  {cry, mottling, sneeze}           => {sleep}        0.01326100 0.8684211
## [7]  {sneeze, fever, sucking}          => {sleep}        0.01366285 0.8607595
## [8]  {excoriations, cry, sucking}      => {sleep}        0.01084991 0.8437500
## [9]  {cry, sneeze, respirations}       => {sleep}        0.01928873 0.8205128
## [10] {excoriations, cry, mottling}     => {sleep}        0.01004621 0.8064516
##      coverage   lift     count
## [1]  0.01506932 4.077989 55
## [2]  0.01346192 3.343096 50
## [3]  0.01125176 2.563702 51
## [4]  0.01707856 2.550100 77
## [5]  0.01346192 2.520936 60
## [6]  0.01527024 2.444645 66
## [7]  0.01587302 2.423077 68
## [8]  0.01285915 2.375194 54
## [9]  0.02350814 2.309781 96
## [10] 0.01245730 2.270198 50
```

```
plot(sortedRules[1:10], method="graph")
```



Frequent Symptom Sequences

```r
seqDB <- raw %>% mutate(sequenceID = bid, eventID = oid) %>%
          select(-c(tid, bid, oid, nas, num_items, tremors_disturbed, tremors_undisturbed, tone))
seqDB <- pivot_longer(seqDB, c(1:17) ) %>% filter(value > 0)

sequences <- seqDB %>%
  group_by(sequenceID, eventID) %>%
  summarize(
    SIZE = n(),
    items = paste(as.character(name), collapse = ';')
  )
```

```
## `summarise()` has grouped output by 'sequenceID'. You can override using the
## `.groups` argument.
```

```r
names(sequences) = c("sequenceID", "eventID", "SIZE", "items")
sequences <- data.frame(lapply(sequences, as.factor))
sequences <- sequences[order(sequences$sequenceID, sequences$eventID),]
```

```r
write.table(sequences, "seqDB.txt", sep=";", row.names = FALSE, col.names = FALSE, quote = FALSE)
seq_mat <- read_baskets("seqDB.txt", sep = ";", info = c("sequenceID","eventID","SIZE"))

s1 <- cspade(seq_mat, parameter = list(support = 0.4, maxsize = 5), control = list(verbose = TRUE))
# PARAMETERS:
# support: minimum support of a sequence (default 0.1).
# maxsize: (integer) max number of items of an element of a sequence (default 10).
# maxlen: (integer) max number of elements of a sequence (default 10).
# mingap: (integer) min time diff between consecutive elements of a sequence (default none, range >= 1).
# maxgap: (integer) max time diff between consecutive elements of a sequence (default none).
# maxwin: (integer) max time diff between any two elements of a sequence (default none.
s1.df <- as(s1, "data.frame")
summary(s1)
```

```
## set of 30943 sequences with
## 
## most frequent items:
##        sleep       sneeze        fever respirations        stool      (Other) 
##        28271        17044        15417        11055         6928        15716 
## 
## most frequent elements:
##        {sleep}       {sneeze}        {fever} {respirations}        {stool} 
##          25124          14124          12874           8052           5980 
##        (Other) 
##          31648 
## 
## element (sequence) size distribution:
## sizes
##    1    2    3    4    5    6    7    8    9   10 
##   75  818 3448 7437 8946 6422 2809  796  169   23 
## 
## sequence length distribution:
## lengths
##    1    2    3    4    5    6    7    8    9   10 
##   13  199 1323 4560 8189 8931 5518 1806  369   35 
## 
## summary of quality measures:
##     support      
##  Min.   :0.4012  
##  1st Qu.:0.4128  
##  Median :0.4360  
##  Mean   :0.4521  
##  3rd Qu.:0.4709  
##  Max.   :1.0000  
## 
## includes transaction ID lists: FALSE 
## 
## mining info:
##     data ntransactions nsequences support
##  seq_mat          4377        172     0.4
```

```r
head(arrange(s1.df, desc(support)),30)
```

```
##                                      sequence   support
## 1                                   <{sleep}> 1.0000000
## 2                           <{sleep},{sleep}> 0.9941860
## 3                   <{sleep},{sleep},{sleep}> 0.9651163
## 4                                  <{sneeze}> 0.9302326
## 5                                   <{fever}> 0.9127907
## 6                          <{sleep},{sneeze}> 0.9069767
## 7           <{sleep},{sleep},{sleep},{sleep}> 0.9069767
## 8                           <{fever},{sleep}> 0.9011628
## 9                          <{sneeze},{sleep}> 0.8953488
## 10                                  <{stool}> 0.8837209
## 11                 <{sleep},{sleep},{sneeze}> 0.8779070
## 12                           <{respirations}> 0.8662791
## 13                          <{sleep},{stool}> 0.8662791
## 14                 <{sneeze},{sleep},{sleep}> 0.8662791
## 15                  <{fever},{sleep},{sleep}> 0.8662791
## 16 <{sleep},{sleep},{sleep},{sleep},{sleep}> 0.8546512
## 17                                    <{cry}> 0.8430233
## 18                  <{sleep},{sleep},{stool}> 0.8430233
## 19                         <{fever},{sneeze}> 0.8430233
## 20                        <{sneeze},{sneeze}> 0.8430233
## 21                           <{sleep,sneeze}> 0.8372093
## 22                          <{stool},{sleep}> 0.8372093
## 23                 <{sleep},{sneeze},{sleep}> 0.8372093
## 24          <{fever},{sleep},{sleep},{sleep}> 0.8313953
## 25                          <{sleep},{fever}> 0.8313953
## 26                   <{respirations},{sleep}> 0.8255814
## 27                   <{sleep},{respirations}> 0.8255814
## 28         <{sneeze},{sleep},{sleep},{sleep}> 0.8197674
## 29                            <{cry},{sleep}> 0.8139535
## 30         <{sleep},{sleep},{sleep},{sneeze}> 0.8081395
```

```r
# Get induced temporal rules from frequent itemsets
r1 <- as(ruleInduction(s1, confidence = 0.9, control = list(verbose = TRUE)), "data.frame")
head(r1)
```

```
##                                                                   rule   support
## 226         <{respirations},{sleep},{sleep},{sucking}> => <{sucking}> 0.4418605
## 266  <{respirations},{sleep},{respirations},{sucking}> => <{sucking}> 0.4011628
## 1338                                          <{stool}> => <{stool}> 0.7965116
## 1376                                  <{stool,sucking}> => <{stool}> 0.4011628
## 1436                                  <{stool},{stool}> => <{stool}> 0.7267442
## 1441                                    <{sleep,stool}> => <{stool}> 0.6279070
##      confidence     lift
## 226   0.9156627 1.175328
## 266   0.9078947 1.165357
## 1338  0.9013158 1.019910
## 1376  0.9200000 1.041053
## 1436  0.9124088 1.032463
## 1441  0.9000000 1.018421
```