Applied experimental psychology and psychophysics

PROBABILISTIC CHOICE MODELS

- PREFERENCE TREE ON HEALTH RISK OF DRUGS -

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Introduction

The purpose of this article is to analyse data about the perceived health risk of six different drugs, using either the probabilistic choice model BTL or Preference Tree. It will be tested which one of the two models that fits the best. The data that will be analysed is shown in Table 0.1, where the absolute frequencies used in a cumulative preference matrix is presented. The scores denote how many participants voted the drug in question as being of the highest health risk.

Drugs	No.	1	2	3	4	5	6
Alcohol	1	0	28	35	10	4	7
Tobacco	2	20	0	18	2	0	3
Cannabis	3	13	30	0	3	1	0
Ecstasy	4	38	46	45	0	1	17
Heroin	5	44	48	47	47	0	44
Cocaine	6	41	45	48	31	4	0

Table 0.1. The cumulative preference matrix of the health risk of the drugs. The absolute frequency denotes how many participants judged the drug as being of the highest health risk.

Method

In order to know whether or not the BTL model and the Preference Tree-model can be applied to the data shown in Table 0.1, it is first necessary to check for transitivity in the data. In other words how reliable and consistent the data is. The cumulative preference matrix is a pooled data matrix meaning it contains data from all the participants deemed sufficiently consistent. This is typically done using a *Chi-square*-test. Now a problem could arise because it is unknown whether the pooled subjects have shown an opposite decision behaviour or not eg. chosen high risk where others low risk. If that is the case, then the preference matrix becomes inconsistent. Before it is possible to do the transitivity check, it is necessary to calculate the probability of a stimulus being rated as high risk. See Equation 1.

$$p = \frac{freq}{n} \tag{1}$$

Here *freq* is the frequency that a drug has been rated as having the highest health risk (the pooled preference matrix, Table 0.1) and n is the number of test subjects. Thereafter it is needed to check every combination of the stimuli for transitivity violations. There are no set rules but a rough estimate of when the probabilistic choice models holds is shown in Table 0.2:

Transitivity violations	Expected
None or few SST violations	BTL may fit
Some SST violations and few MST violations	Preference Tree might fit (Not BTL)
Considerable SST and MST but few WST violations	Possible to rank order (no model will fit)

Table 0.2. General estimates of the outcome of probabilistic choice models considering the amount of weak (WST), moderate (MST) and strong (SST) transitivity violations.

Consider three stimuli: a, b, and c. If it is observed that $p_{ab} \geq 0.05$ and $p_{bc} \geq 0.05$, in other words if the probability of a being rated as more unpleasant compared to b and b more unpleasant compared to c. Then *Weak Stochastic Transitivity* (WST) holds when $p_{ac} \geq 0.05$. It is considered a WST violation if $p_{ac} < 0.05$. The same logic applies to MST and SST. If p_{ac} is bigger than or equal to the minimum value in p_{ab} and p_{bc}, MST holds ($p_{ac} \geq min(p_{ab}; p_{bc})$. It is a violation if not. For SST, p_{ac} is compared to the maximum value of both p_{ab} and p_{bc}. If p_{ac} is not bigger or equal to these values, it counts as an SST violation ($p_{ac} < max(p_{ab}; p_{bc})$.

Luckily, with the help of *Matlab* it is not needed to perform every single comparison by hand. A loop was written which identified the number of WST, MST and SST violations respectively:

```
WST = 0;
MST = 0;
SST = 0;
Count = 0;

for a = 1:6;
   for b = 1:6;
      for c = 1:6;
```

```
if (a =b)&&(b =c)&&(a =c); %avoids comparing diagonal (0)
   if p_model(a,b)>=0.5 && p_model(b,c) >=0.5;
      Count = Count+1;
      if p_model(a,c)<0.5; %checks for WST violations
            WST = WST+1; %counts number of violations
         end
               %checks for MST violations
            if p_model(a,c) < min(p_model(a,b),p_model(b,c));
               MST = MST+1; %counts number of violations
            end
               %checks for SST violations
               if p_model(a,c) < max(p_model(a,b),p_model(b,c));
                  SST = SST+1;%counts number of violations
               end
            end
         end
      end
   end
end
```

Bradley-Terry-Luce (BTL)

The probabilistic method used called the BTL-model has a simple model structure, where only one attribute distinguish the stimuli. The model checks for transitivity in data containing pairwise comparisons and is able to predict the outcome of the comparison. See Equation 2.

$$P_{ab} = \frac{v(a)}{v(a) + v(b)} \tag{2}$$

P_{ab} is the probability of drug a being rated to be of higher health risk than drug b. *v(a)* and *v(b)* denotes the scale values of drug a and b.

In order to get estimates of the scale values, one has to maximise the likelihood of the data seen in Table 0.1. This is done given the model in Equation 3:

$$L(D|\Theta_{model}) = \prod_{i<j} p_{ij}^{n_{ij}} \cdot (1 - p_{ij})^{n - n_{ij}} \tag{3}$$

Where n is the number of comparisons, which is equal to the amount of test subjects in this case (n=*48*) and n_{ij} is the frequency of how many times the drug in row i was rated as being of higher health risk than the drug in column j. P_{ij} is the preference probability and is estimated using Equation 2.

Preference Tree

The Preference Tree has a more complex structure than the BTL-model, where it has subgroups of attributes. The model assumes the relationship shown in Equation 4 between scale values and the probability the stimuli *v(a)* is chosen over *v(b)*.

$$P_{ab} = \frac{v(a' - b')}{v(a' - b') + v(b' - a')} \tag{4}$$

P_{ab} is the probability of drug a being rated to be of higher health risk than drug b. *v(a'-b')* is the scale value for the attribute(s) that a does not share with b and last is *v(b'-a')* which is the scale value for the attribute(s) that b does not share with a.

In order to get estimates of the scale values, one has to maximise the likelihood (L) of the data seen in Table 0.1. This is done given the model in Equation 3 and this is exactly like it was done for for the BTL-model.

For estimation of the likelihood the *fOptiPt.m* Matlab function has been developed by Florian Wickelmaier and Christian Schmid (Wickelmaier and Schmid 2004). The function requires two mandatory input, M and A, where M is the paired comparison matrix shown in Table 0.1, and A is a cell array with length corresponding to the number of stimuli, which is 10. Further there is an optional input, s, which denotes the starting values for the estimation routine. The search algorithm starts at $\frac{1}{k}$ for each parameter value, where k is the number of parameters, if s is not specified. In the case with both the BTL-model and Preference Tree, s is not specified nor is it used.

Results

The probability of choosing one stimuli over another is calculated for each comparison as explained in Equation 1. The results for the probabilities are shown in Table 0.3.

Drugs	No.	1	2	3	4	5	6
Alcohol	1	0	0.58	0.73	0.21	0.08	0.15
Tobacco	2	0.42	0	0.38	0.04	0	0.06
Cannabis	3	0.27	0.63	0	0.06	0.02	0
Ecstasy	4	0.79	0.96	0.94	0	0.02	0.35
Heroin	5	0.91	1	0.98	0.98	0	0.92
Cocaine	6	0.85	0.94	1	0.65	0.83	0

Table 0.3. The probability that one stimulus is chosen over another stimulus.

To find out how many times the stochastic transitivities are violated, each of the three types are investigated and the number of times there is a violation it is counted. The results are shown in Table 0.4.

Stochastic transitivity	Violations
WST	0
MST	1
SST	5

Table 0.4. Results for the number of violations of the three stochastic transitivities out of 20 possible.

BTL-model

To check how good a fit the BTL-model is, a *Chi-square*-test is conducted and the results are shown in Table 0.5.

χ^2	Df	p-value
24.9423	10	0.0055*

Table 0.5. Results from the *Chi-square*-test. The p-value of 0.0055 suggests that the BTL model does not fit.

The results from the *Chi-square*-test shows a p-value at 0.0055 and therefore the conclusion is that this model is significant worse at predicting the data than the statistic model. The model is not accepted and instead the Preference Tree will be used.

Preference Tree

The way it is determined how the Preference Tree should be structured is by drawing the tree by looking at the types of drugs and conducting a *Chi-square*-test on the model to estimate if it fits. Many different Preference Trees were drawn and tested, the first that fits is illustrated in Figure 0.1.

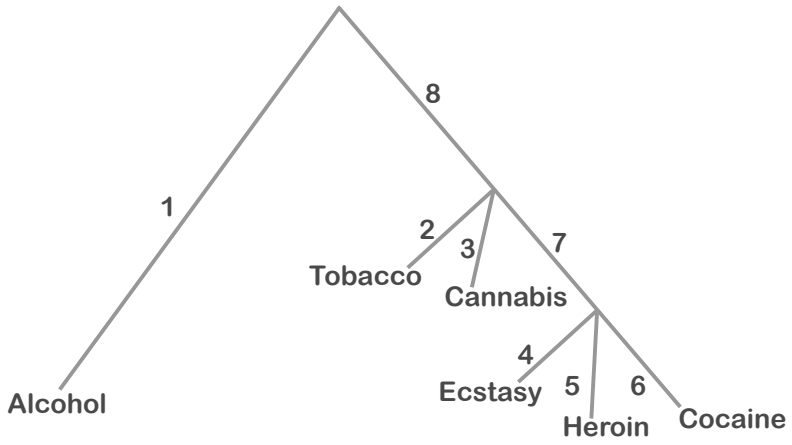

Figure 0.1. Structure of the first Preference Tree that fits the data.

The results of the *Chi-square*-test for the Preference Tree, illustrated in Figure 0.1, are shown in Table 0.5.

χ^2	Df	p-value
12.7157	8	0.1220

Table 0.6. Results from the *Chi-square*-test on the first Preference Tree. The p-value of 0.1220 suggests that the Preference model fits.

Another Preference Tree was found to fit, and this tree is illustrated in Figure 0.2.

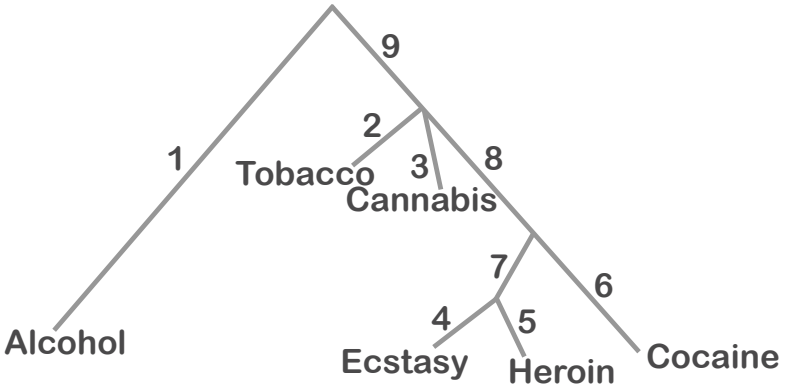

Figure 0.2. Structure of the second Preference Tree that fits the data.

The results of the *Chi-square*-test for the second Preference Tree, illustrated in Figure 0.2, are shown in Table 0.7.

χ^2	Df	p-value
10.9377	7	0.1414

Table 0.7. Results from the *Chi-square*-test on the second Preference Tree. The p-value of 0.1220 suggests that the Preference model fits.

Analysis

Based on the results presented in the previous section it is possible to analyse how well a fit the BTL-model and the Preference Tree are.

The total number of possible stochastic violations in the data is 20, where one MST and five SST violations was found. This amount of violations could most likely be described as *some SST violations and few MST violations* and therefore the expectation, as explained in section (*Method*), will be that the Preference Tree might fit, but the BTL-model will not.

To test if the BTL-model could fit a *Chi-square*-test was conducted. The result from the test is a p-value at 0.0055, which is under the significants level at 0.1, and therefore the conclusion is that the BTL-model is significant worse at predicting the data than the statistic model and therefore the model is not accepted as a fit. Instead a Preference Tree was made.

Different types of Preference Trees were tested, but only two Preference Trees was found to have a p-value above 0.1 in the *Chi-square*-tests and therefore not significant different from the statistic model. The two Preference Trees that are concluded to be a fit are illustrated in section (*Results*) on Figure 0.1 and Figure 0.2 respectively. The value for every line segment of the Preference Tree is calculated. The length of the line segments are presented in Table 0.8 for the first Preference Tree and in Table 0.9 for the second Preference Tree.

Number of line segment	Length of line segment
1	0.1976
2	0.0277
3	0.0376
4	0.0259
5	0.6931
6	0.0509
7	0.8717
8	0.0727

Table 0.8. The length of the line segments for the first Preference Tree.

Number of line segment	Length of line segment
1	$3.36 \cdot 10^{15}$
2	$4.37 \cdot 10^{14}$
3	$5.98 \cdot 10^{14}$
4	$7.66 \cdot 10^{14}$
5	$3.58 \cdot 10^{16}$
6	$4.00 \cdot 10^{15}$
7	$1.39 \cdot 10^{15}$
8	$9.69 \cdot 10^{15}$
9	$1.30 \cdot 10^{15}$

Table 0.9. The length of the line segments for the second Preference Tree.

The scale values for every drug type are calculated by adding all length together for the line segments that leads to the drug. The values are presented in Table 0.10 for the first Preference Tree and in Table 0.11 for the second Preference Tree.

Drug	Scale value
Alcohol	0.1976
Tobacco	0.1004
Cannabis	0.1103
Ecstasy	0.9703
Heroin	1.6376
Cocaine	0.9953

Table 0.10. The scale values of the different drugs for the first Preference Tree.

Drugs	Scale value
Alcohol	$3.36 \cdot 10^{15}$
Tobacco	$1.74 \cdot 10^{15}$
Cannabis	$1.90 \cdot 10^{15}$
Ecstasy	$1.31 \cdot 10^{16}$
Heroin	$4.82 \cdot 10^{16}$
Cocaine	$1.50 \cdot 10^{16}$

Table 0.11. The scale values for the different drugs for the second Preference Tree.

To illustrate how the different drugs are rated, the line segments are drawn and labelled, where the labels are found by looking at the types of drugs and considering what is an appropriate description for these specific drugs. On Figure 0.3 the first Preference Tree is illustrated with labels and on Figure 0.4 the second Preference Tree is illustrated. The interpretation of the figures are that the longer the line the higher health risk the drug is rated to have.

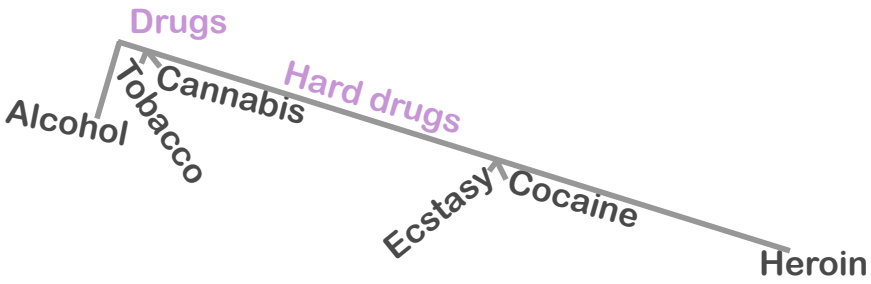

Figure 0.3. The first Preference Tree with correct line length and labels on the line segments.

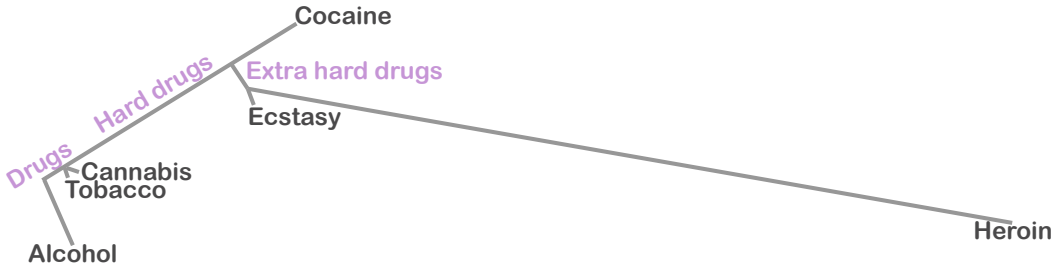

Figure 0.4. The second Preference Tree with correct line length and labels on the line segments.

The scale values for the line segments and their respective confidence interval for the first Preference Tree are represented in Figure 0.5.

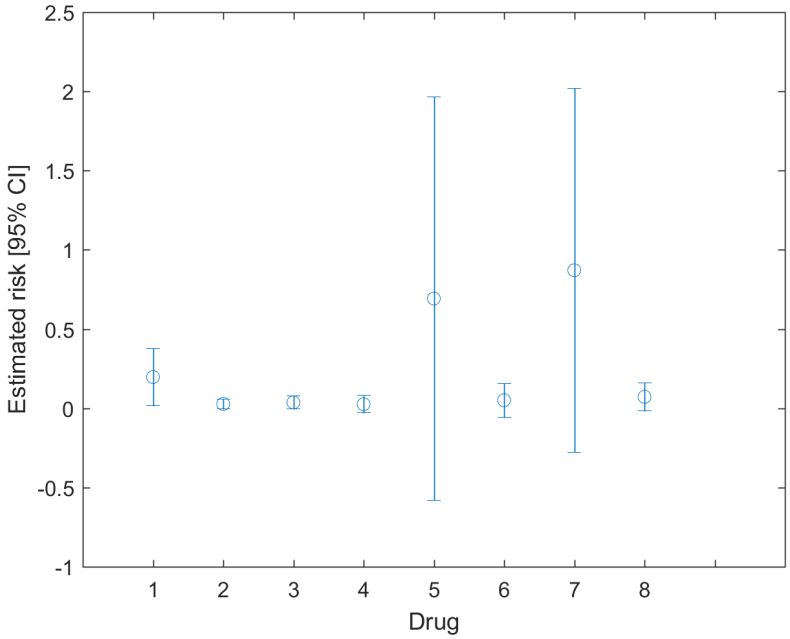

Figure 0.5. Scale values and confidence intervals for the line segments for the first Preference Tree.

The scale values for the line segments and their respective confidence interval for the second Preference Tree are represented in Figure 0.6.

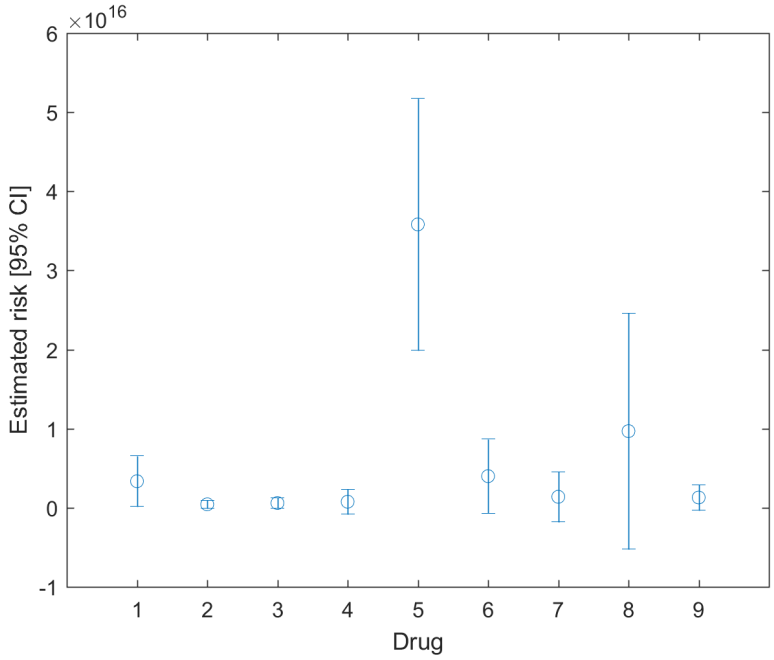

Figure 0.6. Scale values and confidence intervals for the line segments for the second Preference Tree.

When looking at the confidence intervals plotted for the two Preference Trees, it is clear

that the second Tree is a better fit. An example is the placement of number five, heroin, clearly different from the other drugs on the confidence plot for the second tree. This is consistent with the plots of the line segments in Figure 0.3 and Figure 0.4 that illustrated that heroin is rated a higher health risk than the other drugs.

Discussion

The Preference model is used to analyse the data. This kind of model is a bit harder to interpret, but gives a good representation on how the drugs can be compared. It can be difficult to make a Preference Tree which fits the data, especially if the analyst does not have the same mental idea of the health risk of drugs as the participants. A lot of different Preference Trees including branches as legal and illegal, organic and chemically manufactured was suggested, but non of these was a found to be a fit.

The two found Preference Trees only has p-values on 0.12 and 0.14 respectively. These are not particular high p-values and thus it is possible that another Preference Tree might fit better if all possible relations were tested.

As shown in section (*Analysis*) heroin is considered to be of a higher health risk than any other drug in this study. Cocaine and ecstasy is also rated to have a high health risk compared to alcohol, tobacco and cannabis, but not as high as heroin.

As seen on both Preference Trees alcohol has a branch for itself, which indicates that this drug can not be compared with any of the other drugs. The Preference Trees also shows that both tobacco and cannabis, even though grouped with harder drugs, are evaluated to be of lower health risk than alcohol.

Conclusion

The conclusion is that the BTL-model with a p-value at 0.0055 does not fit the data, therefore the Preference Tree is used to analyse the data instead. There were found two different Preference Trees that fitted, with p-values at 0.1220 and 0.1414 respectively. Both trees have alcohol in its own branch which indicates that it is rated different than the other five drugs. Cannabis and tobacco tended to be rated at the same level for both trees. The last three drugs were structured differently between the two trees, the first tree had these three drugs on the same level, whereas the other tree, which were found to be a better fit, had cocaine in one branch and heroin and ecstasy on same level in another.

Bibliography

Wickelmaier, F.; C. Schmid (2004): "A Matlab function to estimate choice model parameters from paired-comparison data". In: *Behavior Research Methods, Instruments, & Computers* 36.1, pp. 29–40. ISSN: 1532-5970. DOI: 10.3758/BF03195547. URL: https://doi.org/10.3758/BF03195547.