

# **Peripheral nervous system responses to food stimuli: *Analysis using data science approaches***

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## **Abstract**

In the field of food, as in other fields, the measurement of emotional responses to food and their sensory properties is a major challenge. In the present protocol, we propose to the reader a step-by-step procedure that will allow a physiological description of odors, aromas and their hedonic properties. The proposed method belongs to the field of data science and especially data mining. It is still little used in the field of food and is based on a descriptive modeling of emotions on the basis of human physiological responses.

**Keywords.** emotions, pleasantness, odors, aromas, food stimuli, data mining, subgroup discovery

## **1. Introduction**

The measurement of emotions is a real challenge for basic and applied research, especially in the field of food. Often, the analysis of emotions in relation to food stimuli is performed in a multimodal manner by combining subjective measures (valence or self-reported hedonic preferences) and more objective measures such as peripheral nervous system activity. Here, the challenge is to measure hedonic preferences related to odors, visual aspects, texture of food products (or of the food as a whole) and to associate to these verbal and declarative responses more objective measures of emotion such as electrodermal or cardiac activity (1–5).

To date, most studies that have attempted to understand these physiological underpinnings of hedonic preferences to food sensory stimuli have used standard statistical approaches, such as comparing psychophysiological responses across different conditions (e.g., pleasant or unpleasant). Statistical methods used primarily included nonparametric tests (e.g., Wilcoxon, Kruskal Wallis) (**6, 7**) and parametric tests (analysis of variance, ANOVA) (**8–11**) depending on study design, data normality, and/or sample size.

Today, complementary approaches from data science can shed different light on these data by allowing researchers in the field to test descriptive and predictive models of the relationship between subjective preferences and psychophysiological responses. These approaches may be particularly well suited to the format of data generated in emotion and food science as they take into account large, heterogeneous and complex data.

Data science is a general term used to describe the various aspects of data processing, with the aim of extracting meaningful information and relevant knowledge (**12**). It includes data pre-processing (cleaning, normalization, discretization, etc.), data modeling, and data visualization. Within data modeling, we distinguish two main families of algorithms: those referring to machine learning, which are often predictive, and those belonging to data mining, which are often descriptive. Thus, whereas machine learning allows us to predict a variable (e.g. hedonic preference) on the basis of one or more variables (e.g. physiological responses) (see Note 1), data mining allows us to build descriptive models. The latter are often explanatory in the sense that they explain by explicit association rules how a pleasant food flavor is characterized physiologically compared to another less pleasant food for example. The present protocol, inspired from a previous study (**13**), aims to provide researchers and students in the field with a framework for using these data mining methods in the context of research on food-related emotions. We will use electrodermal responses (e.g., skin conductance or SC) and ratings of pleasantness collected from human individuals in response

to various olfactory stimuli as an example of data (**I4**). Using this example data, we provide the user with a step-by-step protocol that will allow for a physiological description of odors and aromas characterized by their hedonic value.

## 2. Materials

1. A computer (*Specifications: Windows 7 or later, Mac OS X 10.11 or higher, or Linux RHEL 6/7*)
2. Python 3 SDK software: It is an interpreted, multi-paradigm and multi-platform programming language (see Note 2). It supports structured, functional and object-oriented imperative programming.
3. A Python development environment: Jupyter notebook; to be able to view the notebook created and read it as a tutorial.
4. The following libraries installed on Python:
  - a. sickit-Learn (version = 0.24.1) (**I5**): it is a library that offers various possibilities in terms data science methods
  - b. matplotlib (version = 3.1.1): to handle graphical representation
  - c. pandas (version = 1.2.3): to visualize and to manipulate tabular data
  - d. pysubgroup (version = 0.7.2) (**I6**): offers several datamining algorithms

One can install Jupyter notebook and all of the above libraries by installing a Python distribution named Anaconda and by installing the pysubgroup package with the following command : *pip install pysubgroup*.

A database with subjective and psychophysiological data. As an example, we will use a dataset that combines SC responses to pleasant and unpleasant odors (see Licon et al, 2018 (**I4**)). The dataset is downloadable from a public repository (Dataset name: *PsychophysioDataset.xlsx*, available at <https://github.com/mmaelle/Psychophysio-Analysis>). Each dataset row is an observation for a specific odor with its subjective pleasantness (rated using a scale from 1, very unpleasant to 9, very pleasant) and its associated SC response described by four parameters (amplitude, latency, rise time and number of events in a period following stimulus onset). The database contains 2398 observations (109 observations for 22 individuals).

### **3. Methods**

The protocol contains 2 steps developed below: 1/ Preprocessing, and 2/ Data mining analysis.

#### ***1. Preprocessing***

By preprocessing, we mean all the operations that precede the analysis stage. Preprocessing is an important step that should not be neglected: it prepares the dataset so that it is as clean and simple as possible and is adapted to the algorithms that will be used in the following analysis. To do this, noisy, outlier or irrelevant data must be corrected or rejected so as not to bias the study.

##### **1.1. Skin conductance decomposition and data importation**

*In a first step, we start by importing the data — available in the excel file*

*"PsychophysioDataset.xlsx"* — into a python dataframe. The data set contains the following information: participant number, CID (Compound Identification number of the odorant), SC Latency, SC Rise time, SC amplitude, number of events in a time window following stimulus onset (NSSCR), ratings of odor pleasantness. Note that if no peak has been identified, the attributes latency, amplitude and rise time are equal to 0. Moreover, the number of events is calculated by subtracting the number of events before the presentation of the odor from the number of events after the presentation of the odor (the value can therefore be negative).

```
import pandas as pd

data = pd.read_excel(' PsychophysioDataset.xlsx',
sheet_name='Physiol_Raw_data')

print(data.head())
```

	Subject	CID	SC_Latency	SC_Rise_Time	SC_Amplitude	SC_NSSCR	Pleasantness	Intensity
0	1	109	2.980469	3.011719	0.197369	1.0	5	2
1	1	176	0.800781	3.437500	0.083031	0.0	3	6
2	1	998	1.941406	2.687500	0.184974	1.0	5	6
3	1	1032	3.160156	1.953125	0.022002	-1.0	6	5
4	1	2758	3.722656	0.972656	0.010934	0.0	5	6

The preceding command displays the first lines of the Psychophysio dataset.

## 1.2. Feature selection

In a second step, irrelevant data (such as CID) that are not directly helpful to answer our question can be removed as follows.

```
df = data[['Subject', 'Latency', 'Rise_Time', 'Amplitude', 'NSSCR',
'Pleasantness' ]].copy()
```

Incomplete data such as trials for which participants did not provide perceptual scores or for which SC data are missing can also be rejected.

```
df = df.drop(list(df[df['Pleasantness']==0].index))

nan_cols = [i for i in df.columns if df[i].isnull().any()]

for c in nan_cols :

    df = df.drop(list(df[df[c].isnull()].index))
```

Based on your data set, you will decide which variables are of interest and which should not be included or rejected in/from your analysis.

### 1.3. Discretization

In a third step, we seek to label our data as "pleasant odors" and "unpleasant odors" for pleasantness. We will therefore discretize the scores into two classes. The fact of having two discrete classes instead of scores allows to deal with binary responses and to be able to clearly separate pleasant and unpleasant odors on the one hand and weak and strong odors on the other hand. We choose here to discretize the scores using the clustering algorithm called "KMeans" (with k=2) (*17*) because this algorithm allows to get rid of the subjectivity linked to the different scoring strategies (See Note 3).

We thus obtain the following data set:

```
print(data.head())
```

	<b>Latency</b>	<b>Rise_Time</b>	<b>Amplitude</b>	<b>NSSCR</b>	<b>Pleasantness_class</b>	<b>Intensity_class</b>
<b>0</b>	2.980469	3.011719	0.197369	1.0	pleasant	weakly_intense
<b>1</b>	0.800781	3.437500	0.083031	0.0	unpleasant	very_intense
<b>2</b>	1.941406	2.687500	0.184974	1.0	pleasant	very_intense
<b>3</b>	3.160156	1.953125	0.022002	-1.0	pleasant	very_intense
<b>4</b>	3.722656	0.972656	0.010934	0.0	pleasant	very_intense

The preprocessed dataset is then available in csv format in the file

'PsychophysioPreprocessed.csv'.

## *2. Data mining analysis (Subgroup discovery analysis)*

### 2.1. General information

We propose to use a data mining approach based on a subgroup discovery (SD) algorithm (18). SD allows to find patterns that are discriminating for a target class. Indeed, it finds population subgroups that are statistically "most interesting" from a population of individuals (or items). These subgroups are identified by conditions on the descriptive attributes. In this regard, we seek to obtain the largest possible subpopulations that have the most unusual statistical distributional characteristics.

For example, we obtain a pattern described by the rule "*NSSCR==0.0 AND Rise\_Time>=5.35 → unpleasant*". The conditions on the physiological attributes form the property of interest "*NSSCR==0.0 AND Rise\_Time>=5.35*". This property describes the subgroup identified as having exceptional behavior, which is to perceive the odor as "unpleasant." This means that having a rise time greater than or equal to 5.35 seconds and at the same time a constant number of skin conductance peaks is significantly more present for the "unpleasant" trials than for the other so-called "pleasant" trials. This pattern is illustrated by the toy dataset depicted in Figure 1. The subgroup consists of the rows in the dataset that verify the conditions present in the rule (framed). In the dataset, rows belonging to the target class are called "positive" (in bold) and other rows are called "negative" (in italics).

### 2.2. Processing

First, we import the necessary libraries and the data set.

```
import pandas as pd
import pysubgroup as ps
df = pd.read_csv("PsychophysioPreprocessed.csv", sep=',')
```

Next, we define the search space in which the algorithm should search. We remove the target column 'Pleasantness\_class', so that it is not considered as a feature and does not give us the rule "Pleasant implies pleasant". Setting the nbins parameter to 20 means that the algorithm must discretize the variable values into 20 classes.

```
searchspace = ps.create_selectors(df, nbins=20,
ignore=['Pleasantness_class'])
```

We now need to specify the target class: in our case, it is the 'Pleasantness\_class' column, and we will start with the "unpleasant" odorants.

```
target = ps.BinaryTarget('Pleasantness_class', 'unpleasant')
```

Then we create a Subgroup Discovery Task. Here, we want to know the 5 best patterns (*result\_set\_size*), have a maximum of 4 conditions present in the description of the subgroup (*depth*) and use WrAcc as a quality measure (*qf*). There is also the possibility to add the minimum accepted quality with the *min\_quality* parameter.

```
task = ps.SubgroupDiscoveryTask (df, target, searchspace,
result_set_size=5, depth=4, qf=ps.WrAccQF())
```

Now, we can extract the patterns. The algorithm, by default, is the 'BEAM' search which allows to perform a beam search exploration.

```
result = ps.BeamSearch().execute(task)
```

Finally, we can examine the results:

```
unpleasant = result.to_dataframe()
print(unpleasant)
```

	quality	subgroup	size_sg	size_dataset	positives_sg	positives_dataset	size_complement	relative_size_sg	relati
0	0.006387	SC_Rise_Time>=5.35	114.0	2278.0	72.0	1148.0	2164.0	0.050044	
1	0.003314	SC_Amplitude>=0.50	114.0	2278.0	65.0	1148.0	2164.0	0.050044	
2	0.003282	SC_NSSCR==2.0	259.0	2278.0	138.0	1148.0	2019.0	0.113696	
3	0.002875	SC_Latency: [1.84:2.11[	114.0	2278.0	64.0	1148.0	2164.0	0.050044	
4	0.002751	SC_NSSCR==0.0 AND SC_Rise_Time>=5.35	59.0	2278.0	36.0	1148.0	2219.0	0.025900	

We can also export the results to a csv file.

```
unpleasant.to_csv('unpleasant_result.csv', index=False, sep=',')
```

Then we can do the same search for “pleasant” odorants.

```
target = ps.BinaryTarget('Pleasantness_class', 'pleasant')
task = ps.SubgroupDiscoveryTask(df, target, searchspace,
    result_set_size=5, depth=4, qf=ps.WRaccQF())
result = ps.BeamSearch().execute(task)
pleasant = result.to_dataframe()
```

```
pleasant.to_csv('pleasant_result.csv', index=False, sep=',')
```

### 2.3. Example of results

The top 5 results obtained for the attribute pleasantness and its targets can be viewed in Table

1. The best model for unpleasant has the following rule: "Rise\_Time >= 5.35 → unpleasant".

The subgroup size is 114 (size\_sg) which corresponds to 5% of the dataset (relative\_size\_sg or size\_sg / size\_dataset). Of these 114 odors, 72 are classified as "unpleasant" (positive\_sg) and

42 as "pleasant" (size\_sg - positive\_sg). So we see that we do not get a 100% exact rule, but

information like "if we have a Rise\_Time >= 5.35, then the smell is more likely to be unpleasant". To know how correct this rule is, we use quality measures.

The quality of the model is calculated as the frequency of the rule in the subgroup relative to

the frequency of the rule in the entire data set. The score generally used is the Weighted

Relative Accuracy (WRAcc) value. The WRAcc value is the probability of having the target

in the subgroup minus the probability of having the target in the data set, multiplied by the

probability of the target in the data set.

$$WRAcc = size\_sg / size\_dataset \times (positives\_sg / size\_sg - positives\_dataset / size\_dataset)$$

WRAcc is between -0.25 and 0.25. The higher this value, the more exceptional the description

feature in the subgroup compared to the rest of the data. 0.25 corresponds to the case where

the classes are balanced and 50% of the data of the target class are in the subgroup with no

data of the other classes in this group, so it is very rare to obtain such a high score. Another

measure of quality is shown in these results: the lift. The lift is the probability of having the

target in the subgroup divided by the probability of having the target in the whole dataset.

$$\text{lift} = (\text{positive\_sg} / \text{size\_sg}) / (\text{positive\_dataset} / \text{size\_dataset})$$

If it is less than 1, the rule is not interesting because the target is less frequent in the subgroup than outside. If we obtain a lift of 3, it means that the target is 3 times more frequent in the subgroup than in the whole data set.

We have data with a positive WRAcc and a lift greater than 1, which means that trends are found. One way to be sure that a pattern is meaningful and not due to chance is to perform a bootstrap validation (see Note 4).

## 2.4. Conclusions

Subgroup discovery methods have had very little application in olfaction and food science, but when they have (*13, 19–21*), they have provided descriptive models linking physicochemical or physiological parameters to hedonic odor and aroma perceptions. This approach is promising and will be useful when seeking to describe perceptual phenomena and emotional reactions related to food perception from a physiological perspective.

## **Notes**

### *1. Machine learning analysis*

To analyze the link between physiological and emotional responses, it is possible to use other data science methods such as predictive approaches called supervised machine learning.

Supervised machine learning can be used to achieve two goals. The first is to automate a process, for example, to learn directly about a person's perceived emotions without having to ask them. The second is to know how the classifier separated the different groups in order to

better understand the underlying neural or physiological process. To do this, the algorithm must be intelligible or, if it is a black box, a method must be found to allow for explanation (Lundberg, 2017). The algorithm must also have a high prediction score, which can be difficult when trying to relate 2 unstable dimensions such as physiological responses and emotional responses. These dimensions are not stable because they are highly subject to individual variability. To make predictions, the scikit learn library available on Python is complete and offers you great possibilities in terms of learning methods and algorithms. In R, there are libraries corresponding to the classifier to be used (e.g. e1071, rpart, klaR, kernlab, CORElearn, Rweka, tree, caret randomForest, nnet, glmnet, gbm, rath, ipred, ROCR, mboost). In KNIME (menu Analytics/Mining), you can find a series of learning algorithms including neural network, decision tree, logistic regression. In Orange, you can find classification algorithms in the Model menu (Logistic Regression, KNN, Random Forest, SVM...).

## *2. Other data mining tools*

Besides Python, different tools and platforms exist to perform data science analysis: graphical interfaces such as Weka (22) and ELKI (23) or software such as KNIME (24) or Orange (25), with which one can compose a specific workflow by assembling one after another modules performing a specific operation. There is also an easy-to-use software with a graphical interface called Cortana (26). Cortana is also available as a plugin for KNIME. For those with good R skills, for subgroup discovery, one can use rsubgroup (27) on R.

## *3. Discretization*

In the literature, ratings are usually discretized by dividing the scale as used into 2 or 3 or by dividing into percentiles of equal size. However, the way in which emotions and preferences

are provided is unique to each person: some people rate using a wide range of nuances, whereas others do not. It is important to separate the notes into several categories while limiting this subjectivity. Therefore, we recommend not discretizing the scores by dividing the scale into equivalent spaces (e.g. 1-3 vs. 4-6 vs. 7-9, for 3 groups and a scale ranging from 1 to 9). We also do not recommend partitioning into median or 33 percentiles because this method does not always reflect one's assessment strategy. Therefore, we propose a partitioning method that is neither equi-depth nor equi-width: use KMeans clustering on each subject independently. This algorithm allows partitioning into  $k$  clusters such that the distance between intra-cluster points is minimized and the inter-cluster distance is maximized allowing the subjective data to be partitioned into categories as different as possible.

#### *4. Bootstrap validation*

To validate the quality of a pattern, one can make a very large number of random draws of the same size as the pattern to be validated and look at the distribution of the quality measure of all the generated draws to verify that the pattern is outside the confidence interval of that distribution. For example, by calculating the WRAcc of 10,000 groups for each pattern discovered, with the same support as the current pattern, drawn at random (with discount between each draw). If its WRAcc is outside the 95% random distribution, then the pattern is validated and can be considered as interesting. This interval validation avoids flagging subgroups indicating a WRAcc likely to be observed by a random subset of entities.

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Unpleasant pattern							
Pattern rank	Quality (WRAcc)	subgroup	size_sg	size_dataset	positives_sg	positives_dataset	lift
1	0.006387	Rise_Time>=5.35	114	2278	72	1130	1.25
2	0.003314	Amplitude>=0.50	114	2278	65	1130	1.13
3	0.003282	NSSCR==2.0	259	2278	138	1130	1.06
4	0.002875	Latency: [1.84:2.11[	114	2278	64	1130	1.11
5	0.002751	NSSCR==0.0 AND Rise_Time>=5.35	59	2278	36	1130	1.21
Pleasant pattern							
Pattern rank	Quality (WRAcc)	subgroup	size_sg	size_dataset	positives_sg	positives_dataset	lift
1	0.005683	Rise_Time: [1.92:2.26[	113	2278	69	1148	1.23
2	0.004285	NSSCR== -1.0	319	2278	168	1148	1.06
3	0.003271	Rise_Time: [3.03:3.41[	114	2278	64	1148	1.13
4	0.003053	Latency>=3.20	115	2278	64	1148	1.12
5	0.002541	Latency: [0.09:0.43[	73	2278	42	1148	1.16

**Table 1.** Top 5 results obtained with *pysubgroup* library (unpleasant and pleasant patterns are depicted separately).

Figure captions :

**Figure 1.** Dataset example for the pattern described by the “NSSCR==0.0 AND

*Rise\_Time>=5.35 → unpleasant” rule.*