# "How can we generate counterfactual explanations for ML models that predict the number of contributors to DNA samples?".

## What do experts look at when determining the NOC?

In forensic work, DNA evidence is often analyzed using *Short Tandem Repeats (STR)*. These STR are specific tracks of repeated short DNA sequences of about two to six base pairs long, that have been proven to show high variability between individuals. These parts of the DNA or *loci* have been defined by CODIS, which is the United States national DNA database. One individual can have two different amounts of repeats for a single locus; one inherited from the mother, and one from the father. These thus represent the alleles for this certain region of the DNA. These STR are measured by a process called electrophoresis, which produces an electropherogram. An example can be seen in Figure 1. We will not go into detail about the measuring process, but will provide information about how these results are interpreted. In Figure 1, we only see the locus TH01 with two clear peaks at six and nine repeats. The repeat sequence for TH01 is AATG, so one of chromosome of this individual the AATG sequence is repeated six times on that location, while on the other chromosome it is repeated nine times. The y-axis represents the quantity of information found, measured in Relative Fluorescence Units (RFU). This is also referred to as peak height.

The first step of DNA STR profile interpretation is to determine whether a sample has originated from a single source, or if the sample is a mixture [1, 2]. This is usually easily discerned by looking at the Maximum Allele Count (MAC), which is a measure of the locus with the most alleles present. If this number is bigger than 2, the sample could be considered a mixture since a single human has at most 2 alleles at a given locus; one from the mother and one from the father. Determining the exact number of contributors is difficult, since most DNA profiles are not as clear cut. There are many factors that can obscure the number of contributors.

* Allele sharing: If two donors have the same allele at a locus, we speak of allele sharing. This frequently occurs when donors are relatives, since brothers and sisters share a lot of DNA. It might be difficult to distinguish if an allele is shared between donors, or if a single donor simply is homozygous for this allele; in both cases, the peak height for that allele is higher.
* Allele drop-out: If the DNA was degraded, for example due to sunlight, some parts of the DNA might not be present in the sample to measure. It is also possible that the amount of the DNA available is so small, that the alleles fall below a certain noise filter. Because of this low quality or quantity of DNA, some allele fragments might not show up in the profile at all, which is called drop-out.

These factors can decrease the number of alleles found in a certain profile, which could lead to an underestimation of the number of contributors. There are also factors that could lead to an overestimation of alleles present in a sample:

* Stutter or drop-in: During the process of measuring the STRs, a STR fragment can “slip” from the template. This could cause the electropherogram to measure this strand to have one repeat fewer, since the slipped part of the fragment is not correctly measured. In this way, a small stutter peak is found in the profile just before the valid peak.
* Other noise: The measuring process is not perfect, so some random noise or blobs might show up in the electropherogram, that do not contain any information about the DNA.

Stutter peaks and noise are often filtered out using certain thresholds. As a result, some DNA information might also be lost due to a low-quantity donor.

In general, it is more difficult to discern the NOC, when the number of donors increases.

It is important to make a correct assumption of the number of contributors, since the following steps rely on this number to determine correct evidence in criminal cases. When an incorrect NOC is used for further analysis involving the investigation of the DNA profiles, the results are unreliable [3]. It is possible to rerun the software with a different number of contributors, but

The Maximum Allele Count approach to determine the NOC is quite simple, but it is unreliable due to the factors discussed prior. Performance in general is quite poor, especially with 3 or more contributors [1, 4, 5]. On average, when assessing mixtures between 2-5 contributors, the MAC cannot obtain correct predictions for more than 70% of samples [6]. When looking at 4-person mixtures, more than 70% of the samples are characterized as 2-, or 3-person mixtures using only the MAC approach [5].

Often experts use MAC in combination with the Total Allele Count (TAC), which measures the total number of alleles across all loci. However, this measure suffers from the same obscuring factors as the MAC.

**nC-tool [7]:** Estimates the NOC by simulations performed on the TAC. This achieves better results than using the MAC only, obtaining correct predictions for roughly 76% of 2-5 person mixtures [6].

In 2019, a Machine Learning (ML) model was created that derived the NOC with an accuracy of roughly 82% [6]. This Random Forest (RF) model was trained based on 590 profiles of 2-5 person mixtures, obtained from **TODO:find how many**  donors. The data used for training was not the original electrophoresis results, but consists of 19 features such as the MAC, locus-specific information, and other statistical features of the data.

Allowing stutter peaks to be counted as alleles [8].

How relatives influence the LR [9]

More contributors, more likely to be estimated to have fewer NOC [10].

**Decision Tree [11]**

Derive NOC from

* Decision tree with

Tested various ML approached (RF / MLP / LDA), showing similar performance to the RF19 model. They obtained very high performance (96%) with a RFC 35 model.

Difference with [2] is “Benschop et al. used 1174 unique donors to construct 590 profiles [20], whereas the PROVEDIt dataset only had 26 unique donors within the 766 profiles used”

This means that the classifiers probably overfit to certain donors.

“In conclusion, the decision tree method for NoC assignment has been shown to be over 77% accurate, with increasing performance with improved stutter and artefact filters”

They used a decision tree to classify peaks as stutter or allele.

**Background STR mixture interpretation [12]**

Information about how statistical analysis is done to determine the LR with the Hd and Hp. Showing that the LR is still the de-facto standard method.

“The peak height information is of benefit for analyzing mixed profiles.”

“The effect of incorrect estimation of the number of donors (caused by allele sharing) to the LR value was examined by Benschop (…) and was illustrated to exert a great effect on the LR” [3]

**Background about NFI-used software for LR calculation DNAStatistX**

Shows the importance of correct NOC estimations: under-assigned number of contributors can cause the model the fail calculating the LR because the observed peaks cannot be well explained.

Also includes the NOC model + the generic RF11 model (with a lower accuracy of ~

Also includes the LoCIM method for inferring the major contributor.

## Counterfactuals [13]

“MOC returns a Pareto set of counterfactuals that represents different trade-offs between our proposed objectives, and which are constructed to be diverse in feature space.”

* Low number of feature changes (sparse explanations)
* Close to nearest observed data points (plausible explanations)

Dependence between features must be visualized in explanations

The quality of explanations is sometimes evaluated by performing a quantitative evaluation of a user study. Users are asked to perform a certain task and the explanations help support this task. How well and how fast the humans can accomplish the task is measured as accuracy and efficiency respectively [14, 15]. Subjectively, users were asked for their preference of explanation type in a 1 versus 1 fashion and asked to provide reasons.

Explanations should have few features, as humans pick usually just a few reasons. They should be specific to the problem at hand, and every instance should be explained in the same deterministic way [16]. Deterministic, or consistent feature attributions [17].

Exploration using several visual aids [18].

Research into XAI has shown the need for comparison and evaluation of methods [19-25], and the recent interest in the implementation of counterfactual explanations [19-23]. Although there are a few key components highlighted by these surveys, they also mention that the evaluation must be done specifically to certain applications [23]. One could specify a specific goal to be achieved by the explanations which should be tested [24]. Also the relevance of explanations to a certain audience [25].

What does the NOC machine learning problem look like?

The dataset consists of 590 samples of mixtures between 1 and 5 contributors.

Any machine learning model learns to map the profile to a single output .

Where are the input features of a profile, which are all continuous variables. Currently in the RFC19 model. The target constitutes a multi-class classification problem in the current model, and for any classifier. The target could be changed to be to correspond to a regression model.

Which model-agnostic counterfactual explanation techniques exist and what assumptions do they make on the data?

One of the first papers on counterfactual explanations was written to bring up discussion on the “right to explanation” in automated decisions made by black-box algorithms [26].

Two reasons that the authors mention which are also relevant to the current case:

1. Understand why a decision was made
2. Understand how a different decision could me made if certain conditions were changed

In short, a counterfactual explanation is a statement that shows how the instance would have to change to yield a different outcome, or formally:

“Score *p* was returned because variables *V* had values (*v*1, *v*2 , . . .) associated with them. If *V* instead had values (*v*1*'*, *v*2*'*, . . .), and all other variables had remained constant, score *p'* would have been returned.”[26]

For one instance, multiple possible counterfactuals exist, and it is often the question which one is most appropriate. Counterfactuals are purposefully constructed to be minimal, meaning that minimal changes are made to the instance in question. In this way, the changed instance can still be related to the original. It is desirable to present multiple explanations, which correspond to altering different aspects of the original instance. These aspects could also be case-specific.

To generate counterfactuals, we minimize:

Where is the original instance, and is the counterfactual, which we want to find to be as close to as defined by a certain distance function . The outcome of the prediction by the model should be the desired outcome . The desired outcome is balanced to the distance by a weight , where a larger value favors the desired outcome, and a lower value favors less change made to the original instance.

The choice of the distance function is important. The authors found the or Manhattan distance, weighed by the inverse median absolute deviation to be most useful. It is used to normalize each feature, and is robust to outliers. However, the authors recognize that this distance metric should be catered towards specific problems, audiences, and data.

Any suitable optimization algorithm can be used to solve this problem. If access to the gradients of the machine learning model are given, optimization is faster. However, since we aim to look at model-agnostic methods, we disregard this statement.

“Principally, counterfactuals bypass the substantial challenge of explaining the internal workings of complex machine learning systems”

“As the working memory of humans can contain around seven distinct items”

They tested on the LSAT dataset, which is a regression dataset predicting their entrance exam scores (3 input variables).

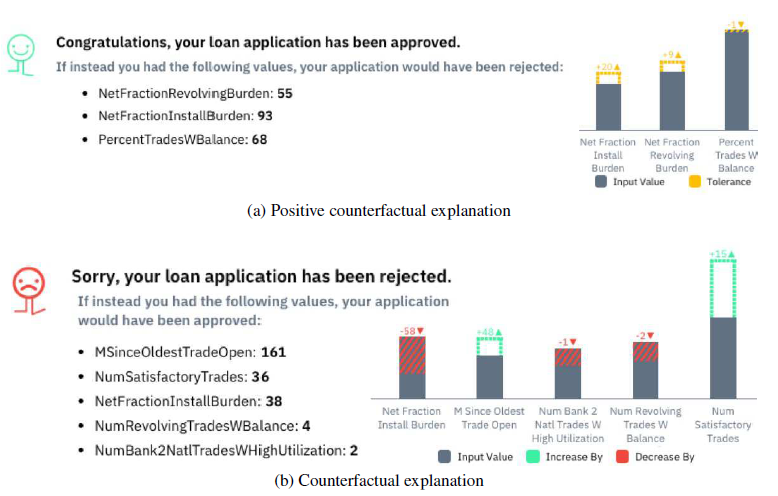
Pima Diabetes Database: whether Pima women are likely to develop diabetes or not (8 input variables).

Since then, many varieties of counterfactual methods have been generated.

One method proposes to expand on Wachter et al. by adding *positive counterfactuals*, which were catered towards the HELOC loan applications dataset [27]. These explanations are created when the desired outcome is already achieved, but a certain margin of value ranges is presented for which the outcome will also hold. They achieve this by setting the target to represent the decision boundary, which would entail .

In our case, that would still yield the same explanations since we have no explicit positive or negative case.

A second change they propose, is to weigh certain features based on their relevance or importance. This is achieved by adding a weight vector to the original distance metric [27]. They use two strategies to obtain a relevance score for each feature. The first is using global feature importance (ANOVA) scores between feature and target, which should result in a smaller set of feature changes. The second is based on K-Nearest Neighbors to find instances close to the original stance, but with the desired result. The changed features can then be weighted according to this local area, giving more value to features that have historically been known to vary (since neighboring points exist).

**Nice visualization **

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