

# **Explainable Al**



# BIOTECHNOLOGY & PHARMACEUTICAL

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For drugs and medical treatments there is no 'one-size-fits-all'. Patients

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vary greatly in their needs and responses. A treatment that is life-saving for one person might be ineffective or even harmful to another. This has led to the revolution of personalized medicine and drug design.

Fortunately, there is commonality among people. Much can be learned from partitioning the overall population of patients into subpopulations that share certain common features and attributes. However, identifying well-defined patient subpopulations is challenging.

There is no shortage in data to minutely characterize individual patients and the symptoms they exhibit. But these detailed characterizations lead to vast and unwieldy feature spaces where patient data are rarely homogenous and patient subpopulations are often difficult to separate.

Furthermore, many of the features and attributes may not be important but this is difficult to assess beforehand. Analysts are often riddled with the problem of selecting the right features for a specific problem. Unable to cope, feature selection reduces to a guessing game.

There are many application areas in the BioTech/Pharma sector where these critical challenges occur

- Rare diseases: select the most promising treatment for a given patient
- Treatment prognosis: match drug interventions with individual patients
- Drug testing and validation: select the most appropriate candidates for a clinical trial
- Drug repurposing: find new associations of disease progression patterns for a given drug

### Common Challenges:

Knowing a person's membership in a concrete and statistically robust subpopulation is critically important. It is because determining this membership with high confidence drastically reduces risk and uncertainty in the decision's outcome.

Moreover, many times it is not only important to know whether a particular data item will yield a certain outcome in a given response variable. Rather, it can also be important whether it allows certain predictions of the outcome's growth or decline.

#### For example:

- Will a patient experience a drop in blood pressure as the level of medication is increased
- Will a given individual have adverse reactions to an administered drug and if so, how much
- Will a selected trial candidate demonstrate a significant response to the tested drug
- $\cdot$  What is the margin of safety of a certain dose in relation to its benefit

These predictions can be assessed by statistically correlating the target variable with one or more attributes. However, correlation can be sporadic and confined to a certain subpopulation only. It may even vanish and remain undetected when aggregated over loosely defined subpopulations.

Identifying robust and well defined subpopulations in large datasets is hence mission-critical. However, the aforementioned "data fog" in which these subpopulations are typically situated poses tremendous challenges.

Deep neural networks, random forests, etc. circumvent this problem in an elegant manner but this comes at the price of low explainability and subsequent poorly informed decision making. This uncertainty is a fateful adversary in the high stakes effort of personalized medicine and drug design.



## How Explainable AI Can Help:

Akai Kaeru's advanced pattern mining and discovery engine directly decomposes the high-dimensional input data into a reliable set of independent data patterns - the subpopulations - using a sophisticated yet efficient suite of proprietary algorithms.

Each pattern consists of data items that behave similarly in terms of a given target variable and which are succinctly defined by just a small set of attributes. The succinct description of each pattern makes them easy to understand and appeals to the user's domain knowledge – a hallmark of explainable AI.

Our fully interactive visual interface alerts the analyst to a set of concrete and concise regions with unusually high or low target variable values and correlations. The patterns are explained by visualizing them in the context of their relevant attributes.

Our software's causal inference engine can establish true causal relations among the patterns. It provides directional relations such as "smoking causes cancer, but not vice versa". The intricate web of causal relationships is visualized directly on the pattern layout.

Akai Kaeru's software can help analysts and decision makers turn troves of data into actionable insight they can trust, justify and explain to others. Try it out. Schedule a demo.

