



## Patient-Drug mapper

### What's new

We have design and implemented a deep learning framework that, given the genetic and/or the clinical data of patients, it can classify *ex-ante* the best molecule/treatment profile based on their predictive responsive capacity.

### Key insights

A significant number of hi-potential drugs end up falling through the cracks given their testing on patients with incompatible individual profiles. Topazium's analytics allow the mapping of genetic and clinical patient's conditions to a whole universe of experimental and approved drugs. Also, it can be used to produce a rank of matching alternative drugs given a patient's profile, aiming both to increasing treatment efficiency whilst lowering its costs.

### How it works

Patient's genetic and/or clinical data is uploaded into a platform specifically engineered and calibrated for the task. A non-linear algorithmic framework predicts the probability for a patient of being a "super-responder" or a "super-survivor" to a particular treatment and/or drug.

### Results

Topazium's framework can predict treatment results by mapping genetic/clinical characteristics to specific molecules.

### Why it matters

Treatments usually disregard the hidden state dependency on significant combined genetic and clinical features. By combining the patient's genetic imprint and clinical profile, Topazium's analytics potentially increases the identification of "super-responders" and "super-survivors" leading into a potentially higher success ratio of clinical trials. It also allows for reprofiling of vintage failed projects.