excelra

Where data means more

CASE STUDY

Personalized Psoriasis Treatment: A Case Study On How AI Accelerated Biomarker Discovery

Client's challenge and goal

A leading pharmaceutical company based out of Europe, sought to optimize treatment for psoriasis patients using their blockbuster drug, Cosentyx (Secukinumab). While Cosentyx was successful, the client aimed to identify patient-specific biomarkers to predict treatment response and personalize therapy. Traditionally, this process relied on manual analysis, leading to:

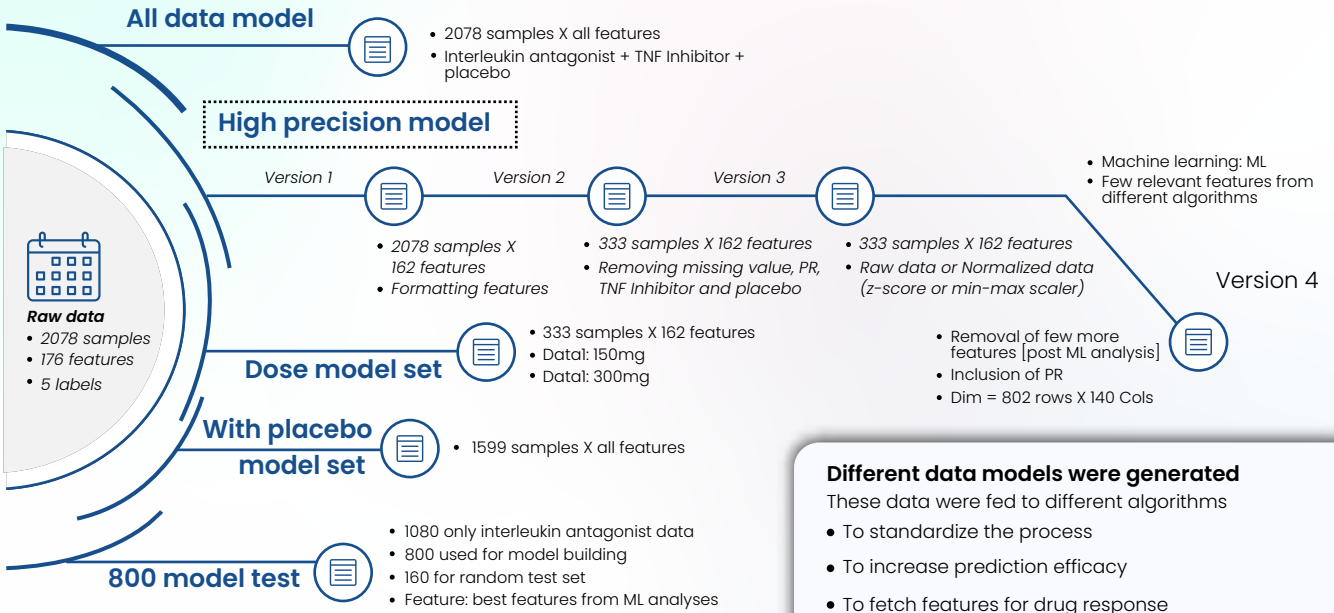
Time-consuming data analysis	Manually sifting through large, heterogeneous clinical trial data sets was laborious and prone to human error.
Limited insights	Traditional methods often miss hidden patterns and potential biomarkers
Inconsistent results	Subjectivity in analysis could lead to inconsistent biomarker selection across studies.

Our Approach

Excelra partnered with a leading pharmaceutical company to leverage advanced AI and machine learning (ML) for biomarker identification. We closely collaborated with the client's scientists to understand their needs and develop a custom approach:

Stage 1: **Data Preprocessing:** We meticulously cleaned and normalized heterogeneous data from two clinical trials, including blood diagnostics, patient history, and genotypes.

Data processing and normalization



***Details on datasets are for representation purposes only**

Different data models were generated

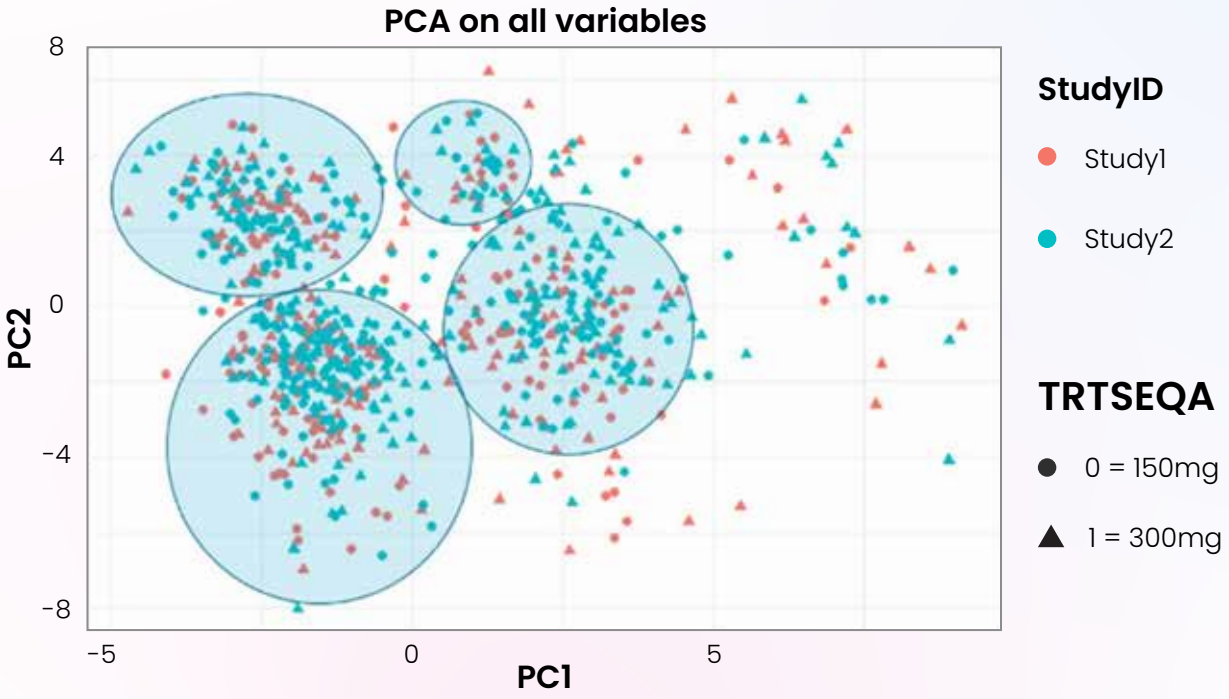
These data were fed to different algorithms

- To standardize the process
- To increase prediction efficacy
- To fetch features for drug response

However, once the process is standardized, 800 model set was used to generate uniform model and test on 160 random samples

PCA analysis

PCA analysis was done to understand data architecture and distributions



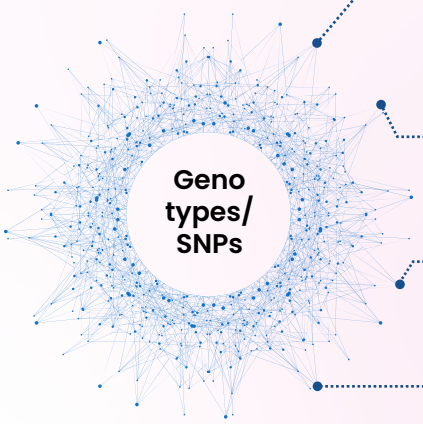
Results

- Four compact clusters
- No significant batch effect
- No clustering based on study 1 & 2
- No clustering in two studios, based on treatment dosage

Stage 2: Multi-Model Exploration: We tested fifteen different AI/ML algorithms across five data models to identify the most effective approach for the specific data set.

	Strategy 1	*Strategy 2*	*Strategy 3*	*Strategy 4*	*Strategy 5*
	All data model	**High precision data model**	**Drug dose model**	**Drug + Placebo model**	**800 Model set**
Artificial neural network					
Correlation attribute ranker					
Elastic net					
Genetic algorithm					
GLM					
K-NN					
LDA					
Logistic regression					
Multilayer perception					
Naive bayes					
PLS					
RandomForest					
Recursive feature elimination					
RPART					
Support vector machine					

Stage 3: Confounding Factor Analysis: We employed sophisticated algorithms to account for placebo effects and identify drug-specific biomarkers. The ML approach summarized 21 attributes that may play a major role in interleukin antagonist response to the auto-immune disease. These features belonged to four different categories, including clinical features, blood related features, and genetic features



rs11045392
Location: Phosphodiesterase 3A (PDE3A) and solute carrier organic anion transporter family member 1C1 (SLCO1C1)

rs1332099
Location: NK2 Homeobox 3 (NKX 2-3)

rs3890745
Location: Membrane metalloendopeptidase Like 1 (MMLE1)

rs39984
Location: Gypsy retrotransposon integrase-like protein 1 (GIN1)

Stage 4: Biomarker Validation: We validated the identified biomarkers against known disease and drug mechanisms of action (MoA) to ensure their biological relevance.

Key conclusions

21 features were identified to be associated with efficacy of interleukin antagonist therapy:

- **9 features** have **strong evidence** of being associated with **drug's MoA and/or disease progression**
- **3 features** could **be linked to the therapy** and/or disease indirectly
- These reflect the **strenght of the algorithms and analyses** used
- 4 Genotypes/SNPs and other identified features appeared as **novel** and hence **direct a new field to study**

Clinical trial design

- **4 clinical parameters** recommended as potential inclusion criteria
- Increased expression **of 4 targets could be potential inclusion criteria**
- The levels of **3 hematological parameters** scan be used for screening psoriatic patients in clinical trial with interleukin antagonist

Combination therapy

- **Comorbidities** associated with the disease were identified that ıse the disease pathogeneiss and ıse treatment response to interleukin antagonist.
- Potential **combination therapy** may be beneficial or warranted in the individuals with comorbidites

Our Solution

Excelra's data-driven approach delivered exceptional results:

Enhanced efficiency: Our automated processes significantly reduced analysis time compared to traditional methods.

Deeper insights: By applying a diverse range of AI/ML algorithms, we uncovered 21 potential biomarkers associated with Secukinumab efficacy.

Strong validation: We identified 9 biomarkers with strong evidence linking them to the drug's MoA and disease progression.

Novel discoveries: Four identified features were novel genotypes/SNPs, opening avenues for further research.

Comprehensive biomarkers: The identified features spanned clinical, blood-related, and genetic data, providing a holistic view of patient response.

Conclusion

This successful collaboration demonstrates the power of AI and ML in biomarker discovery and patient stratification. By leveraging Excelra's expertise and advanced analytics, the client gained valuable insights to personalize treatment for psoriasis patients.

Looking to personalize your drug development strategies?

Excelra offers a suite of AI-powered solutions to accelerate biomarker discovery, optimize clinical trials, and improve patient outcomes. Contact us today to learn more about how we can help you unlock the full potential of your data.

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