



Building curated knowledge-bases for Target Identification and Prioritization

- Therapeutic Area: Fibrotic Diseases (IPF)
- **Context:** Provide automated curation for annotating genetic variants and gene-drug-disease relationships from published literature in the TA
- **Objective:** High-throughput genomics research primarily aims to map disease genetics by clinically annotating the genome, linking genotypes to diseases. The absence of standardized reporting requires automated curation (ECM) for transforming relevant data into structured annotations for preclinical and clinical application

Method

2

Flow

<u>Graph Analytics Implementation:</u> Deploy graph analytics to pinpoint potential targets through their connectivity and influence within disease-relevant networks





LLM Enhancement: Employ LLMs to

enrich the knowledge graph with the

latest biomedical research findings

and to refine predictive models for

target identification



Solution

- 1. Employ advanced **NLP/ML** technologies, tailored specifically to unique datasets, to construct comprehensive databases that map the relationships between **Genes**, **Diseases**, and **Biomarkers**, leveraging extensive genomics and proteomics big data analysis
- 2. Utilize bioinformatics tools to develop specialized gene chips that serve as signatures for cancer diagnostics, enhancing precision and reliability in detection
- 3. Implement NLP/ML to design and develop a backend platform solution specifically for a novel prevention laboratory, facilitating advanced research and development efforts





Results

- 1. Combining **knowledge graphs** and **LLMs** identified key targets within disease networks
- 2. Refined by LLM insights, machine learning models revealed targets with new disease links, offering novel therapeutic avenues for in silico studies
- 3. Targets prioritized this way showed greater validation success,



proving the effectiveness of integrating knowledge graphs and LLMs in drug target discovery







