



## Abstract Submission

14. Myeloma and other monoclonal gammopathies - Clinical

EHA-3531

### **PATIENT SIMILARITY ANALYSIS AND VISUALIZATION IN MULTIPLE MYELOMA**

Joane Joseph\*<sup>1</sup>, Hans Verstraete<sup>2</sup>, Lars Halvorsen<sup>3</sup>, Michel Van Speybroeck<sup>2</sup>

<sup>1</sup>Janssen Pharmaceuticals Inc, Springhouse, United States, <sup>2</sup>Janssen Pharmaceutica N.V., Beerse, <sup>3</sup>EdenceHealth, Kontich, Belgium

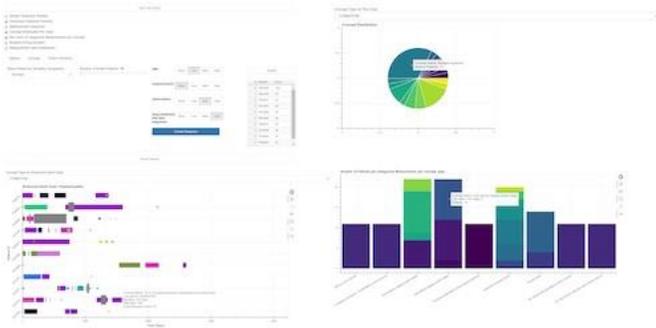
**Background:** Haemato-oncology and multiple myeloma patients in particular are subject to complex, time-varying therapies and clinical outcomes that are difficult to analyze or even visualize. Visualizing these high-dimensional datasets can provide a wealth of insight that cannot be fully captured in a list of summary statistics. These visualizations can be used to highlight the relationships between patient histories in a way that is easier to interpret for investigators with varying backgrounds in statistical data analysis. Furthermore, investigators often want to use these datasets to identify patients that exhibit similar characteristics, which is a function that cannot be performed through ordinary summary statistical methods, since there is no well-defined way to determine the distances between patients.

**Aims:** Herein, we present the specifications of an interactive patient visualization tool, designed to calculate similarities between patients based on an adjustable patient distance determination heuristic and allow for user-friendly dynamic interaction with the summarizing charts generated by the tool.

**Methods:** We first use a two-step heuristic based on drug components to determine the similarity between individual drugs, followed by a similarity score on the drug regimens. The result is an extensive correlation matrix for hematology-related drugs within the HONEUR network. For the visualization of different regimens, we applied further dimensionality reduction approaches such as PCA to ensure that the coloring patterns were indicative of the similarity of treatment regimens. The actual patient similarity score was built using the treatment regimen similarity

score, similarity of the treatment response as an ordinal variable and time invariant variables such as age at diagnosis, and presence of cytogenetic variants.

**Results:** The visualization tool shows the timeline of treatments received by patients, utilizing symbols and color patterns to indicate the degree of similarity. The coloring patterns are determined through principal component analysis of the drug similarity correlation matrix. The tool also generates several other types of charts that can be easily interpreted to show clear clustering patterns based on spatial layouts. The interactive qualities allow investigators to make selections and subcategorize the data as they see fit, as well as calculate scores for the level of similarity between patients. The investigator can specify a set of criteria that would define a metric for similarity between patients and create an ordered list of most similar patients for any given target patient. The dimensions of the similarity space can be augmented based on selections that can be made within the tool. Image/Pictures:



**Summary/Conclusion:** This interactive tool is equipped to accurately depict complex patient similarities, based on several factors within their patient history, and turn these relationships into a quantifiable similarity score. The implementation of this new patient visualization and similarity calculation tool will enhance the identification of patterns within the drug treatment and response timeline and highlights potential patients of interest for medical investigators in all fields of research.

**Keywords:** Multiple myeloma, Patient