

# Visual Exploration of Network Meta-Analysis Data

Huan He<sup>1,\*</sup>, Irbaz Bin Riaz<sup>2,\*</sup>, Syed Arsalan Ahmed Naqvi<sup>3</sup>, Rabbia Siddiqi<sup>3</sup>,  
M. Hassan Murad<sup>4</sup>, and Hongfang Liu<sup>1,†</sup>

<sup>1</sup> Division of Digital Health Research, Mayo Clinic, Rochester, MN, USA

<sup>2</sup> Department of Oncology, Mayo Clinic, Rochester, MN, USA

<sup>3</sup> Dow Medical University, Sindh, Pakistan

<sup>4</sup> Department of Internal Medicine, Mayo Clinic, Rochester, MN, USA

## ABSTRACT

Network meta-analysis (NMA) is a widely used approach in ranking a set of treatments when a number of treatment options are available for patient care. Despite efforts in improving the presentation of data, the interpretation of results remains challenging for practicing clinicians. To address this challenge, we propose using interactive visualization techniques to help clinicians visualize and explore the NMA results efficiently.

**Index Terms:** Applied computing - Life and medical sciences - Health informatics; Human-centered computing - Visualization - Visualization application domains - Visual analytics

## 1 INTRODUCTION

Network meta-analysis (NMA) is an approach for quantitatively comparing different set of treatments and synthesizing evidence to provide clinicians with estimates of effect within a single analysis [1]. It can be used to rank a set of treatments for a given disease indication when determining politics and guidelines related to treatments [2]. The NMA has been widely used in a large number of publications in the past decade [3].

To conduct and report NMA, a number of tools have been published, which include software (e.g., ITC, STATA, WinBUGS, OpenBUGS, GeMTC and MetaXL) and R packages (e.g., dmetar, netmeta, and BUGSnet) [2, 3]. Those software and packages provide commands or application programming interfaces for users to perform NMA on a set of studies. However, fully utilizing these tools requires users to setup a compatible computing environment and configure the specified parameters, and the analysis results are usually presented in tables or static images, which makes it difficult to further exploration. As a result, clinicians must have sufficient experiences on computer programming and statistics tool to explore NMA results on their own dataset and meet the requirements of scientific standards.

To address these limitations, we propose using visualization techniques to build an interactive visual analytic system aimed at helping clinicians to explore NMA results efficiently. Our main contributions are, 1) the design and implementation of an interactive visual analytic system for exploring NMA results; and 2) a proof of concept in real NMA project.

## 2 TASK ANALYSIS AND DESIGN REQUIREMENTS

To characterize the design task, we collaborated with domain experts on systematic review and meta-analysis (SRMAs). Two of them (IBR and MHM) are our internal collaborators with rich

\* Those authors contributed equally to this work.

e-mail: He.Huan@mayo.edu

e-mail: riaz.dr@mayo.edu

† e-mail: Liu.Hongfang@mayo.edu

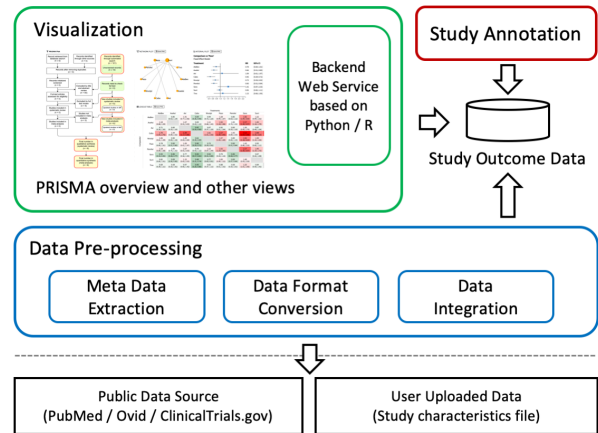


Figure 1: The architecture of our proposed system

experience in SRMAs. The other two external collaborators (SAN and RS) are likewise engaged in a variety of SRMAs. The users of our system would be clinicians and researchers, also including our domain experts.

We conducted several rounds of interviews with our domain experts and built a prototype system based on an ongoing NMA project and leverage open source software packages to demonstrate the pipeline of conducting NMA. Then, we summarized the following two tasks as our initial step.

**T.1 What are the statistical results from a given set of studies for a clinical question?** To rank the treatments for a given disease by a set of studies, users need to analyze all the NMA results in an efficient way. Moreover, due to the complexity in the NMA process, the analysis process also needs to be configurable.

**T.2 How are the studies selected to answer the clinical question?** The studies to be analyzed are usually manually screened from a large collection of studies. Users need to check and update the studies of interest dynamically.

Based on these two tasks described above, we identified the following design requirements.

**R.1 Composite visualization of analysis results.** Clinicians usually need to see a variety of statistical analysis for clinical decision making. A design that visualizes all the NMA results in one place can be of great value.

**R.2 Exploration of different settings.** Clinicians would like to know how the NMA result changes according to different variables (e.g., patient characteristics, measure of effects, pooling methods).

**R.3 Interactive exploration.** The visualization of complex results from NMA can be significantly enhanced by presenting the summary results at the use interface with additional details available through interactive tools.

## 3 SYSTEM OVERVIEW

As shown in Figure 1, our proposed system’s architecture consists of three major modules: the data pre-processing module, the data annotation module, and the visualization module.

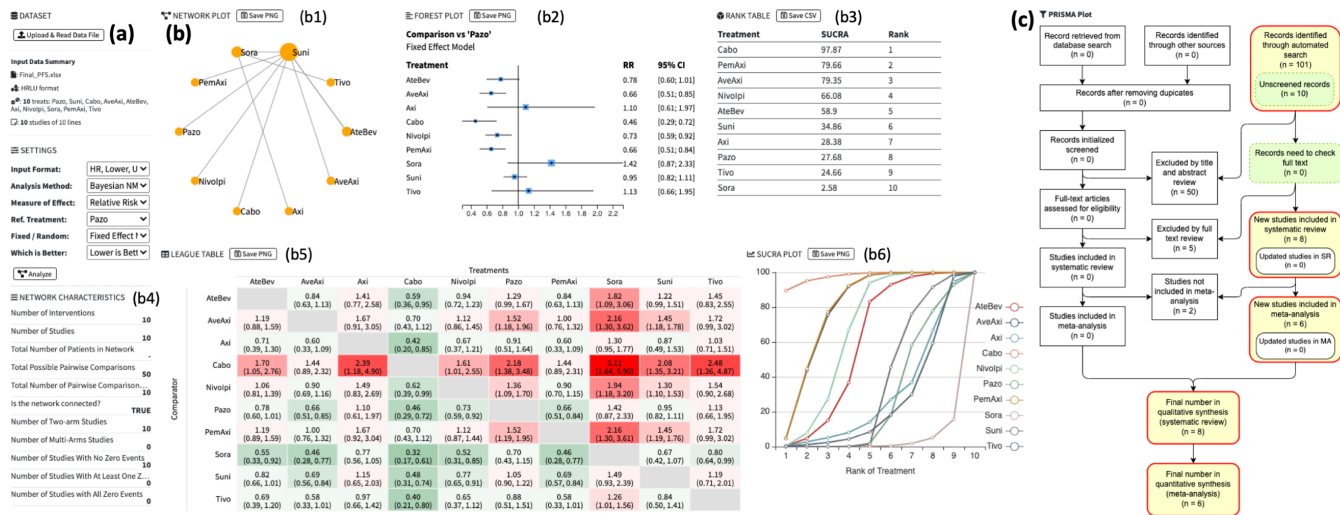


Figure 2: The screenshot of our system that shows: (a) a configuration panel showing the parameters for conducting NMA; (b) an NMA summary view displays the visualized results of an ongoing NMA project, including network plot, forest plot, rank table, network characteristics table, league table, and SUCRA plot; and (c) a PRISMA overview depicting the study selection process.

Once a clinical question is selected, our platform supports the process of NMA in several ways. In the data pre-processing module, there are three components to help users get detailed information of studies and ease the burden of data collection, including: 1) meta data extraction, which can import relevant studies from PubMed, Ovid and ClinicalTrials.gov; 2) data format conversion, which helps convert the data format to those formats supported by analysis packages; 3) data integration, which links the user uploaded data with the data extracted from public data sources (e.g., PDF full-text files). After these steps, the pre-processed data is saved for further annotation.

The study annotation module is used to identify and extract detailed information to 1) summarize the results of studies (characteristics of studies involved in NMA, patient characteristics in involved studies), and 2) extract data for analysis.

The visualization module provides users with coordinated interactive views to conduct real-time NMA, which is built on D3.js and Vue.js. The backend web services are based on R packages for conducting NMA on a given set of studies and parameters.

#### 4 VISUALIZATION DESIGN

The main interface our system, as shown in Figure 2, incorporates a configuration panel (Fig. 2(a)), an NMA summary view (Fig. 2(b)) and a PRISMA overview (Fig. 2(c)).

The configuration panel is a dynamic form providing the coordinated options for users to decide parameters for NMA (R.2). Once the parameters are sent to the backend, the NMA results will be returned and the NMA summary view shows the results by several plots and tables (T.1). To best fulfill R.1 and R.3, we use a combination of widely used plots and tables in NMA field to show all the results, including 1) a network plot and a characteristic table (Fig. 2(b1) and (b4)) show the overall structure of comparisons in the treatment network to understand which treatments are compared with each other in the selected studies; 2) a forest plot (Fig. 2(b2)) shows the uncertainty in the network with specified treatment as comparison; 3) a rank table and a line plot (Fig.2(b3) and (b6)) show the surface under the cumulative ranking (SUCRA) score to answer which treatment performs the best; and 4) a league table (Fig. 2(b4)) shows the pooled effect sizes of both direct and indirect comparison. The effect size is color-encoded to help users identify which treatment performs better (the darker red indicates greater effect size, while the darker green indicates opposite). In this view, each plot is coordinated with other plots by treatment.

The PRISMA overview (Fig. 2(c)) is a popup panel that depicts the number of studies identified, included, and excluded in a flow chart (T.2). Moreover, we extend the basic PRISMA according to our own data flow and add interaction designs on this view.

#### 5 DISCUSSION

To adequately address the analysis task, we iteratively designed the system with the weekly feedback from our domain experts. We tested the designs with the dataset from an ongoing NMA project of first line treatment of metastatic kidney cancer and cancer associated thrombosis during the development. Although we did not carry out formal user tests because of its still early stage, our domain experts appreciated the interactive designs and were able to effectively use the configuration panel to explore the results in the NMA summary view.

#### 6 CONCLUSION AND FUTURE WORKS

In this work, we present a visual analytic system to facilitate NMA by leveraging interactive visualization techniques. Although the system is still in the early development stage, the visualization and interaction designs that have been implemented show its potential to help clinicians perform NMA more efficiently. In the future, we keep developing the core functions and plan to extend our system with the following features: First, enhancing the study selection and annotation process with natural language processing techniques to promote the annotation efficiency; second, we would like to capture and visualize the temporal changes in NMA results to help users identify trends and patterns in treatment performance.

#### REFERENCES

- [1] A. W. Lee, "Review of mixed treatment comparisons in published systematic reviews shows marked increase since 2009," *Journal of Clinical Epidemiology*, vol. 67, no. 2, pp. 138–143, Feb. 2014.
- [2] F. S. Tonin, I. Rotta, A. M. Mendes, and R. Pontarolo, "Network meta-analysis: a technique to gather evidence from direct and indirect comparisons," *Pharm Pract (Granada)*, vol. 15, no. 1, 2017.
- [3] A. Béliveau, D. J. Boyne, J. Slater, D. Brenner, and P. Arora, "BUGSnet: an R package to facilitate the conduct and reporting of Bayesian network Meta-analyses," *BMC Medical Research Methodology*, vol. 19, no. 1, p. 196, Oct. 2019.