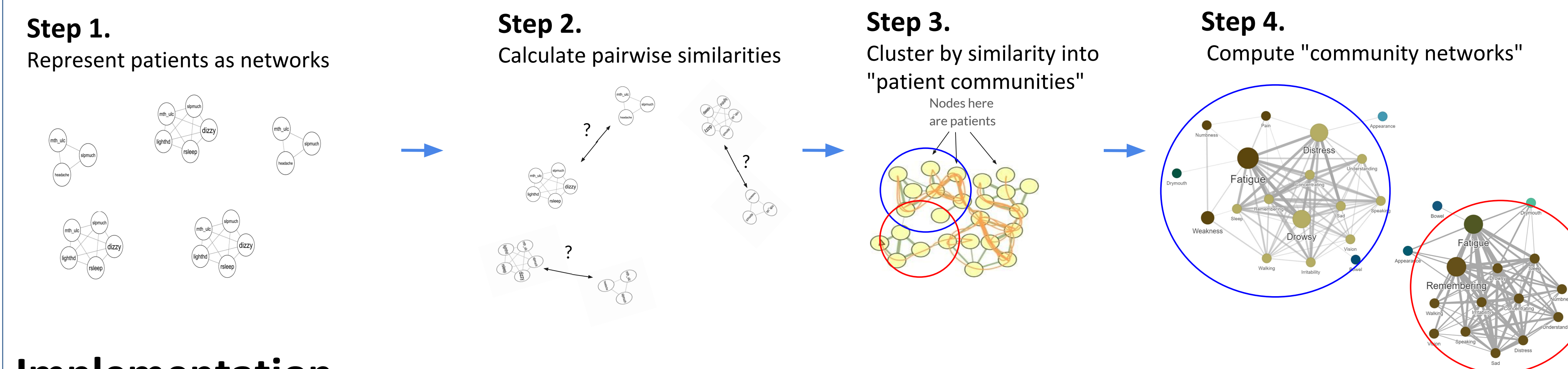


Abstract

The multitude of symptoms that cancer patients experience necessitates better understanding and prioritization of symptoms for clinical targeting. Computational approaches, and in particular network based approaches enable characterizing and uncovering relationships between symptoms and can potentially help outcomes research. We have implemented a web application that enables analysis and exploration of cancer symptomology data for outcomes researchers and clinicians with little bioinformatics expertise. The computational approach builds on a network-based approach, first described by Henry et. al. We demonstrate the functionality and features in a case study of the Brain Tumor Natural History Study of patient symptoms.

Methods

Symptom Network Generation



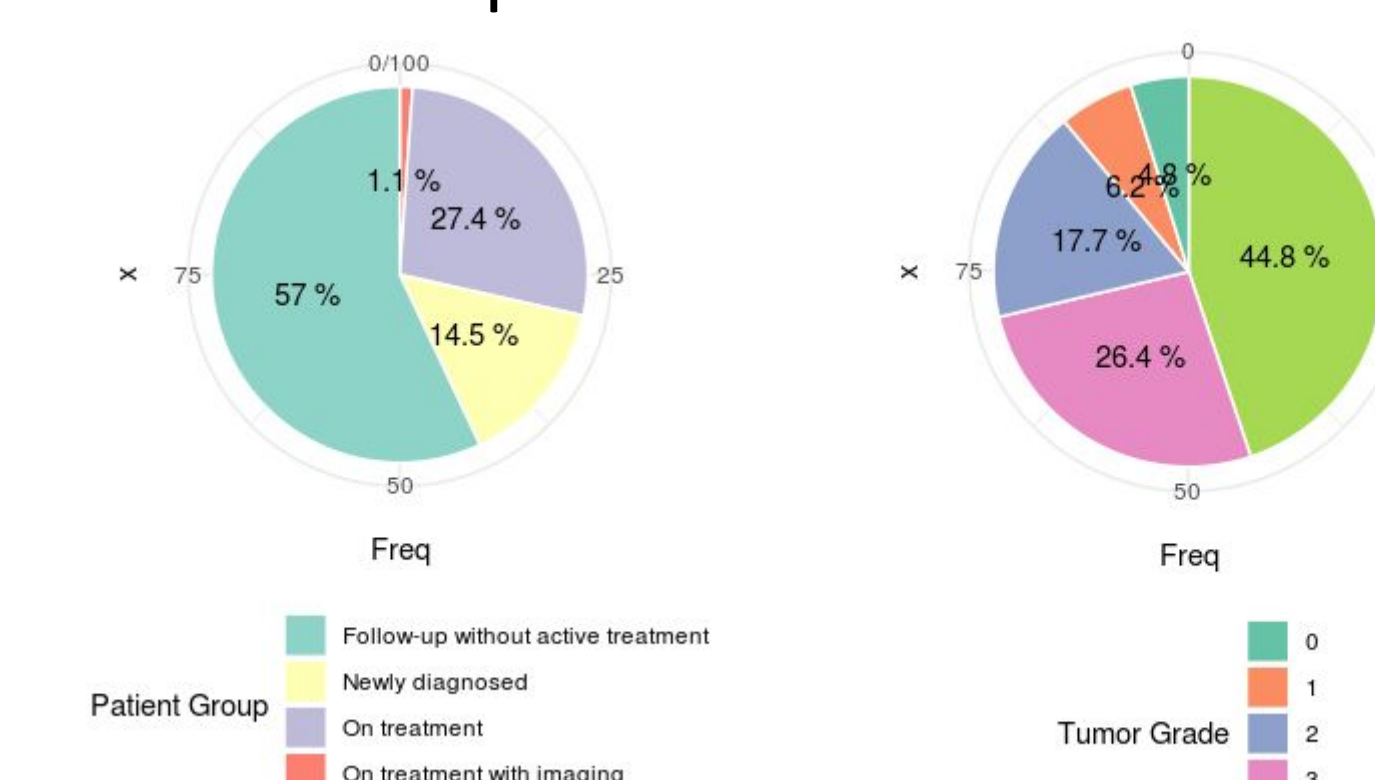
Implementation

- R was used to implement the network algorithm; the implementation is packaged as an R library.
- The igraph and visNetwork packages were used for network analysis and visualization; ggplot2 for graphical summaries.
- The web application portal was implemented using the R Shiny framework.

Dataset

Natural History Study

- Patient-reported symptoms collected as part of the Brain Tumor Natural History Study at NOB
- MD Anderson Symptom Instrument -- Brain Tumor (MDASI-BT) used for reporting 23 symptoms, with severity ranging from 0 to 10.
- Cohort of 435 patients.



Motivation

- Better understanding of symptoms is necessary:
 - Cancer patients experience a large number of symptoms.
 - Symptoms vary across patients and along the disease course.
 - Traditionally, symptoms were considered in isolation. However, how symptoms cluster or co-occur may be more informative.
 - Treating for pivotal symptoms may be more beneficial.
- New datasets collected as part of recent initiatives present unprecedented opportunity for study
 - Brain Tumor Natural History Study collecting longitudinal outcomes and clinical data
 - Molecular profiling is becoming routine
- Computational approaches can be instrumental:
 - Can be used to uncover complex relationships but are hard to use by non-experts.
 - Packaging the algorithms into user-friendly applications can facilitate complex analyses even for non-experts.

Results

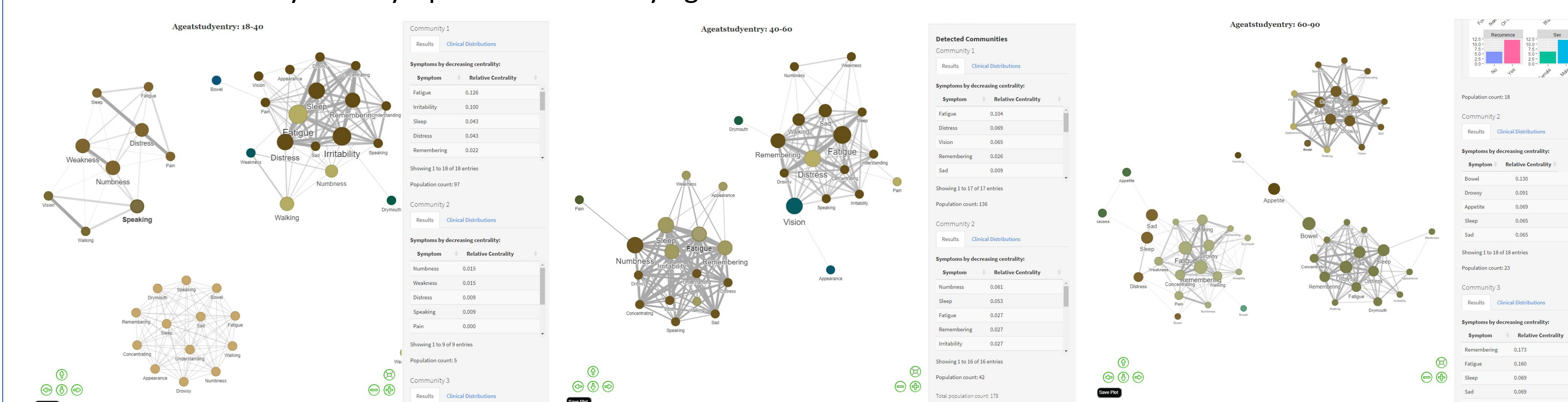
NCI SCOUT: an R Shiny Application

- Users can upload quantitative symptom profiles of patients.
- Users can upload clinical or demographical attributes.
- Users can stratify the data by a selected clinical attribute.
- The user can modify parameters such as symptom presence threshold and centrality measure.
- The user can run the network discovery algorithm, and explore the results interactively as plots.
- The user can download an automatically generated report of the results.



Case study: Brain Cancer Patients

- Distinct community level symptom networks by age:



Parameters used above: stratification = by age group; symptom presence threshold = 1; network sparsification = 70%; centrality measure = betweenness. Larger nodes indicate higher centrality, thicker edges indicate more frequent co-occurrence of the symptom pair, and color indicates symptom cluster membership.

Conclusions

- The NOB symptomology portal allows discovery of patient communities characterized by similarly occurring symptoms.
- Clinical features can be used to stratify patients enabling discovery of symptom patterns characterizing specific subsets of patients.
- Interactive features of the application enable intuitive exploration.
- Our case study of Brain Tumor Natural History Study shows that disease stage gives rise to distinct patterns of symptoms.
- Discovery of such patterns can potentially guide clinical decision making by prioritizing which symptoms to target interventionally.
- The resource's utility would increase if datasets from different trials and or tumor types can be catalogued and compared side by side.

Next Steps

- Addition of analysis and visualization features.
- Deployment of resource for public access.
- Exploration of longitudinal changes of individual symptomology profiles.
- Incorporation of molecular data into the analysis.

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