Visualizing HIV Treatment Patterns with Network Models

Will Bridewell¹ PhD, Wei-Nchih Lee¹ MD MPH, Amar K. Das¹ MD PhD ¹Center for Biomedical Informatics Research, Stanford University, Stanford, CA

Abstract

Network visualization of temporal data offers insights into the practical application of treatment guidelines. Using publicly available data on sequential HIV treatments, we apply network models to visualize switches in regimens and to understand when and if guideline-recommended regimens were used.

Introduction

Identifying variability in patterns of care and guideline adherence can indicate fruitful areas for clinical research. By visualizing changes in treatment, we can uncover effective alternative therapies and assess overall quality of care.¹ We use network visualization tools to uncover patterns of treatment for patients with HIV.

Methods

To explore variability of care, we constructed a network of data from the HIV Drug Resistance Database (HIVdb; <u>http://hivdb.stanford.edu</u>), which includes de-identified information on patients seen at two outpatient clinics and from clinical trials. Focusing on the 2002 guidelines from the U.S. Department of Health and Human Services (DHHS), we extracted treatment histories for the patients who received first-line treatment between 2002 and 2004 within the United States. Using Cytoscape (<u>http://www.cytoscape.org/</u>), we created a network where the nodes are treatment episodes consisting of a regimen and the order in which it was received. Edges indicate that a patient moved from one regimen to the next.

Additionally, we associated other information with each treatment episode. The number of patients indicates the prevalence of the regimen, the number of drugs indicates its complexity, and guideline adherence records whether the regimen is recommended as first-line treatment by DHHS.

Results and Discussion

In total, we had detailed drug information for 141 patients, with fewer patients as the number of treatment episodes increased (Table 1). One patient was prescribed atazanavir monotherapy, but all others were on multidrug regimens.

1	2	3	4	5	6	7
141	111	48	18	10	5	3

Table 1. Treatment episode and number of patients receiving a known treatment at that stage. One patient changed treatment nine different times.

Figure 1 shows a view of the network. Nodes in black indicate an unknown treatment, nodes in white indicate a drug-free period, otherwise the darker the shade, the more drugs in the regimen. Triangular nodes reflect adherence to the 2002 guidelines. And larger nodes indicate more patients.

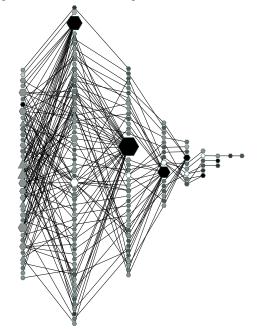


Figure 1. Network model of HIV treatment episodes.

This view of the data suggests that most patients did not receive guideline specific therapy at the outset and only four were moved to a recommended regimen after first-line treatment. Also, variability increases in the second episode, and there are more regimens in the third episode than the first although the number of patients has decreased by almost 70%.

Conclusion

We have introduced a method for viewing the trajectory of patients through the healthcare system as they receive care for chronic conditions. Although the contents, sample distribution, and other factors limit the knowledge derivable from HIVdb, we anticipate applying this approach to visualize treatment variability and guideline adherence in other clinical areas, linking the findings to clinical outcomes.

References

¹Bhavnani SK, Carini S, Ross J, Sim I. Network analysis of clinical trials on depression: implications for comparative effectiveness research. Proceedings of the AMIA Annual Symposium. 2010. 51–55.