

Building, Importing, and Exporting GEXF Graph Files with rgexf

George G Vega Yon¹

1 Department of Preventive Medicine, University of Southern California

DOI: 10.21105/joss.03456

Software

- Review 🗗
- Repository 🗗
- Archive ♂

Editor: Fabian Scheipl ♂ **Reviewers:**

- @jonjoncardoso
- @corneliusfritz

Submitted: 13 June 2021 Published: 12 August 2021

License

Authors of papers retain copyright and release the work under a Creative Commons Attribution 4.0 International License (CC BY 4.0).

Summary

First introduced in 2012, the **rgexf** package for the R programming language was the first effort to make the Graph Exchange XML Format (GEXF) (Heymann et al., 2009) specification available to the **R** world. With more than 500,000 downloads¹, it is one of the most popular ways to incorporate GEXF files into the R programming language environment.

Developed by the Gephi Core Group (Bastian et al., 2009), the GEXF specification is a flexible and widely used format to describe graphs. Although it has not been updated since 2009, the GEXF format has been introduced to several tools and programming environments. A few examples include:

- The python library networkx (Hagberg et al., 2008)
- The stand-alone software **Cytoscape** (Smoot et al., 2010)
- The JavaScript library sigma.js https://simga.js
- The java library **gexf4j** https://github.com/francesco-ficarola/gexf4j)
- The JavaScript library **gexf-js** https://github.com/raphy/gexf-js

Besides the **rgexf** package, other R packages provide functions that interact with GEXF files:

- sigmajs: Interface to 'Sigma.js' Graph Visualization Library (Coene, 2018)
- vkR: Access to VK API via R (Sorokin, 2020)
- microeco: Microbial Community Ecology Data Analysis (Liu et al., 2021)
- netCoin: Interactive Analytic Networks (Escobar & Martinez-Uribe, 2020)

Nevertheless, the **rgexf** package continues to be the de-facto tool to interact with GEXF files in **R**.

Statement of Need

This R package has been serving the scientific community for many years now. Scientists and data analysts across the board have been using \mathbf{rgexf} to enhance their analyses by smoothly moving between \mathbf{R} and other applications used for graph visualization. Some concrete examples include gene networks (Kauffman et al., 2018; Starr et al., 2017), interactions among species (Leclerc et al., 2018), and social networks (Alsaedi et al., 2016).

¹According to the https://cranlogs.r-pkg.org/ website, as of June 14, 2021.



Features

Beyond reading and writing GEXF files from within R, the **rgexf** R package has various other features that can help to create beautiful network visualizations, in particular:

- Using gexf objects—the main class implemented in rgexf—users can create GEXF objects from scratch, adding and removing nodes and edges—including features—as needed.
- Users of the igraph package can directly convert objects between gexf and igraph classes
- Thanks to the gexf-js javascript library, users can immediately visualize their network objects in the web browser.

Because of these and other reasons, the **rgexf** package has been featured in many scientific papers, stating the great utility that this R package has provided to the community. The **rgexf** package is available in the Comprehensive R Archive Network (CRAN) and the project repository at https://github.com/gvegayon/rgexf.

References

- Alsaedi, N., Burnap, P., & Rana, O. (2016). Temporal TF-IDF: A High Performance Approach for Event Summarization in Twitter. 2016 IEEE/WIC/ACM International Conference on Web Intelligence (WI), 515–521. https://doi.org/10.1109/WI.2016.0087
- Bastian, M., Heymann, S., & Jacomy, M. (2009). Gephi: An open source software for exploring and manipulating networks. *Proceedings of the International AAAI Conference on Web and Social Media*, 3.
- Coene, J.-P. (2018). Sigmajs: An r htmlwidget interface to the sigma.js visualization library. *Journal of Open Source Software*, *3*(28), 814. https://doi.org/10.21105/joss.00814
- Escobar, M., & Martinez-Uribe, L. (2020). Network coincidence analysis: The netCoin R package. *Journal of Statistical Software*, *93*(11), 1–32. https://doi.org/10.18637/jss.v093.i11
- Hagberg, A., Swart, P., & S Chult, D. (2008). *Exploring network structure, dynamics, and function using NetworkX*. Los Alamos National Lab.(LANL), Los Alamos, NM (United States).
- Heymann, S., Bastian, M., Jacomy, M., Maussang, C., Rohmer, A., Bilcke, J., & Jacomy, A. (2009). GEXF file format. *GEXF Working Group,[online] C2009 [cit. 2013-05-07]. Available at WWW:* < http://Gexf. Net/Format.
- Kauffman, K. M., Hussain, F. A., Yang, J., Arevalo, P., Brown, J. M., Chang, W. K., VanInsberghe, D., Elsherbini, J., Sharma, R. S., Cutler, M. B., Kelly, L., & Polz, M. F. (2018). A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. *Nature*, 554(7690), 118–122. https://doi.org/10.1038/nature25474
- Leclerc, C., Courchamp, F., & Bellard, C. (2018). Insular threat associations within taxa worldwide. *Scientific Reports*, 8(1), 6393. https://doi.org/10.1038/s41598-018-24733-0
- Liu, C., Cui, Y., Li, X., & Yao*, M. (2021). Microeco: An r package for data mining in microbial community ecology. *FEMS Microbiology Ecology*, *97*(2), fiaa255. https://doi.org/10.1093/femsec/fiaa255



Smoot, M. E., Ono, K., Ruscheinski, J., Wang, P.-L., & Ideker, T. (2010). Cytoscape 2.8: new features for data integration and network visualization. *Bioinformatics*, 27(3), 431–432. https://doi.org/10.1093/bioinformatics/btq675

Sorokin, D. (2020). vkR: Access to VK API via r. https://CRAN.R-project.org/package=vkR

Starr, T. N., Picton, L. K., & Thornton, J. W. (2017). Alternative evolutionary histories in the sequence space of an ancient protein. *Nature*, *549*(7672), 409–413. https://doi.org/10.1038/nature23902