

# Building, Importing, and Exporting GEXF Graph Files with `rgexf`

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## Software

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## 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 downloads<sup>1</sup>, 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/raphv/gexf-js>

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

- `sigmaj`s: 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-Urbe, 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 `rgexf` to enhance their analyses by smoothly moving between **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](#)).

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<sup>1</sup>According 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](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), fiae255. <https://doi.org/10.1093/femsec/fiae255>

- 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>