

# ggpedigree: Visualizing Pedigrees with ‘ggplot2’ and ‘plotly’

S. Mason Garrison <sup>1</sup>✉

<sup>1</sup> Department of Psychology, Wake Forest University, North Carolina, USA ✉ Corresponding author

DOI: [10.xxxxxx/draft](https://doi.org/10.xxxxxx/draft)

## Software

- [Review](#) 
- [Repository](#) 
- [Archive](#) 

Editor: [Open Journals](#) 

## Reviewers:

- [@openjournals](#)

Submitted: 01 January 1970

Published: unpublished

## License

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

## Summary

Pedigree diagrams underpin research and practice across genetics, animal breeding, genealogy, forensics, and counseling. They help medical geneticists trace the inheritance of Mendelian diseases and identify at-risk relatives; enable dairy breeders to plan matings that improve milk yield; support genealogists in reconstructing ancestry; assist forensic scientists in establishing familial connections in criminal investigations; and facilitate family therapists and counselors in understanding their clients’ relationships (McGoldrick, Gerson, & Petry, 2020). Early R tools such as kinship2 (Sinnwell, Therneau, & Schaid, 2014) plot simple nuclear families effectively, but they do not scale to today’s pedigrees that can exceed 1,000s of individuals. As datasets have grown, researchers now work with increasingly complex family structures, including large-scale plant breeding pedigrees (Shaw, Graham, Kennedy, Milne, & Marshall, 2014), web-based pedigree management systems (Ranaweera, Makalic, Hopper, & Bickerstaffe, 2018), interactive pedigree editors (Carver et al., 2018), and behavior genetic studies of extended family structures (Garrison et al., 2023; Hunter, Garrison, Burt, & Rodgers, 2021). That complexity exposes the limitations of existing tools, which often struggle with large and complex datasets. ggpedigree addresses this need by combining a vectorised layout algorithm, ggplot2 output, and optional plotly interactivity.

## Statement of need

Pedigree visualization has traditionally relied on proprietary software (e.g., Progeny, GenoPro, Pedigree Viewer) or R packages like kinship2 (Sinnwell et al., 2014), pedtools (Vigeland, 2021a), or pedtricks (J. Martin, Wolak, Johnston, & Morrissey, 2025). While these tools are functional for many use cases, their limitations become pronounced when working with complex, modern pedigree datasets or when more detailed customization is required. Most R packages focus on base graphics or simple ggplot2 implementations.

Existing R solutions face three main challenges. First, current solutions are often poorly integrated with tidyverse workflows and do not expose the full theming and layering capabilities familiar to ggplot2 users (Wickham, 2016). In animal-focused workflows, rapid rendering seems to take precedence over aesthetic flexibility. I suspect that this is because users tend to work with more uniform data and fewer phenotypes. By contrast, human-focused workflows—particularly in behavior genetics and genetic epidemiology (Garrison et al., 2023; Lyu et al., 2025; McArdle & McDonald, 1984)—require closer integration with tidyverse pipelines and more flexible plotting systems to accommodate complex pedigree structures and harmonization of phenotypes across data sources. In other words, the needs are different.

Second, most R-based tools offer no interactivity. Static graphics are often sufficient for publication, but interactivity improves exploration and communication during model development or data cleaning. A notable exception is pedtools (Vigeland, 2021b), which offers a sister shiny

41 app, QuickPed (Vigeland, 2022). While the R ecosystem includes libraries, like plotly, that  
42 support interactive plotting, these features have yet to be integrated into pedigree functions.

43 Third, scalability and extensibility remain limited across existing tools. Several R packages  
44 attempt to address these challenges with built-in pedigree plotting functions. kinship2  
45 (Sinnwell et al., 2014) remains widely used but produces static base graphics and relies on non-  
46 vectorized recursive layout functions that do not scale well to large families. A partial ggplot2  
47 implementation exists in a modernized kinship2 (called Pedexplorer, Le Nézet, Sinnwell,  
48 Letko, André, & Quignon, 2025), but is non-vectorized and incompatible with other ggplot2  
49 layers. pedtricks, a revival of pedantics (Morrissey & Wilson, 2010), provides a ggplot2-  
50 based implementation for large animal pedigrees but lacks extensibility and interactivity. The  
51 geneHapR (Zhang, Jia, & Diao, 2023) package focuses on haplotype visualization rather than  
52 general pedigree structure. The pedgene package (Schaid & Sinnwell, 2024) offers some  
53 plotting functions but is primarily designed for association testing. The pedigreejs package  
54 (Carver et al., 2018) provides an interactive pedigree editor but does not integrate with R or  
55 ggplot2, limiting its utility for R users.

56 None of these packages offers the combination of modern ggplot2 integration, interactive  
57 capabilities, and extensibility that ggpedigree provides. ggpedigree addresses these limitations  
58 by providing a comprehensive visualization framework built on modern R graphics infrastructure.  
59 It leverages the extensive customization capabilities of ggplot2 while adding specialized  
60 functionality for pedigree-specific visualization challenges.

## 61 Software Architecture

62 ggpedigree is built on a modular architecture that separates data processing, layout calculation,  
63 and visualization layers. The core workflow involves: (1) data standardization and family  
64 restructuring using BGmisc functions, (2) coordinate calculation using algorithms adapted  
65 from kinship2, (3) relationship connection mapping, and (4) layer-based plot construction  
66 using ggplot2 geometry functions. This design allows users to customize any aspect of the  
67 visualization while maintaining computational efficiency for large pedigrees. The package  
68 integrates tightly with the broader R ecosystem, particularly the tidyverse (Wickham et al.,  
69 2019) and BGmisc (Garrison, Hunter, Lyu, Trattner, & Burt, 2024). All functions return  
70 standard R objects (ggplot or plotly) that can be further customized.

71 BGmisc, as described in Garrison et al. (2024), is a dependency for its relatedness-heavy  
72 workflows, supplying network-based validation utilities (checkParentIDs()) and relatedness  
73 components, like ped2fam(), ped2paternal(), and ped2maternal(). These components  
74 allow ggpedigree to visualize how related any two individuals are based on additive genetic,  
75 mitochondrial, or other relationship matrices.

## 76 Features

77 I describe the main features of the ggpedigree package below. Detailed descriptions of features  
78 and usage are available in the [package vignettes](#), including examples of how to create static and  
79 interactive pedigree plots, customize aesthetics, and visualize relatedness matrices. Additional  
80 example data include squirrel data from the Kluane Red Squirrel Project (McFarlane et al.,  
81 2014, 2015) and Targaryen family data from the Song of Ice and Fire universe (G. R. R. Martin,  
82 1997, 2018).

- 83 ■ Data Standardization and Family Structure Analysis: ggPedigree() integrates with  
84 network-based functions from BGmisc like ped2fam() to organize individuals by family and  
85 checkParentIDs() to validate pedigree structures. The function handles consanguineous  
86 relationships and individuals appearing in multiple pedigree positions. More details are  
87 in the [complex pedigree data vignette](#), as well as in Garrison et al. (2024), and Hunter,  
88 Garrison, et al (Hunter et al., 2025, 2021).

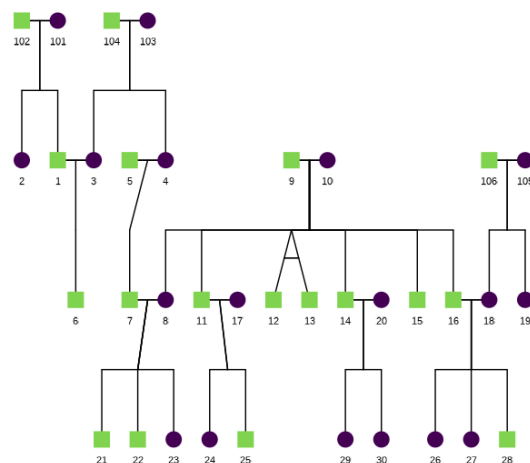
- 89     ▪ Coordinate Calculation: `calculateCoordinates()` computes optimal positioning for indi-  
90     viduals using algorithms adapted from `kinship2::align.pedigree`, with enhancements  
91     for large multi-generational pedigrees and complex family structures. These steps are  
92     vectorized as much as possible to ensure computational efficiency and compatibility with  
93     `ggplot2`.
- 94     ▪ Relationship Connection Mapping: `calculateConnections()` generates connection paths  
95     between family members, mapping parent-child, sibling, spousal, and twin relationships.  
96     The function determines midpoints for line intersections and handles overlapping con-  
97     nections with specialized curved segments. These calculations are optimized for large  
98     datasets by using vectorized operations rather than the loop-based approaches used in  
99     `kinship2`.
- 100    ▪ Layer-based Plot Construction: `ggPedigree()` constructs plots using `ggplot2` geometry  
101    functions, returning standard `ggplot2` objects that integrate with existing R workflows.  
102    `ggPedigreeInteractive()` extends plots into interactive `plotly` widgets. A config system  
103    allows customization of over 150 aesthetic and layout parameters. More details are in  
104    the [configuration vignette](#).
- 105    ▪ Individual Highlighting: Advanced functionality to highlight specific individuals and their  
106    relatives based on additive genetic, mitochondrial, or other relationship matrices.
- 107    ▪ Specific Visualization Functions: `ggPedigree()` creates static pedigree plots using  
108    `ggplot2`. `ggPedigreeInteractive()` generates interactive pedigree plots using `plotly`.  
109    `ggRelatednessMatrix()` creates customizable heatmaps for relatedness matrices with  
110    support for hierarchical clustering, and seamless integration with `BGmisc` relatedness  
111    calculations. `ggPhenotypeByDegree()` visualizes phenotypic correlations as a function  
112    of genetic relatedness, including confidence intervals and statistical summaries for  
113    quantitative genetic analysis.

#### 114    Code example

115    This example shows how to use `ggpedigree` to visualize a pedigree. The potter dataset  
116    includes several wizarding families from the Harry Potter series.

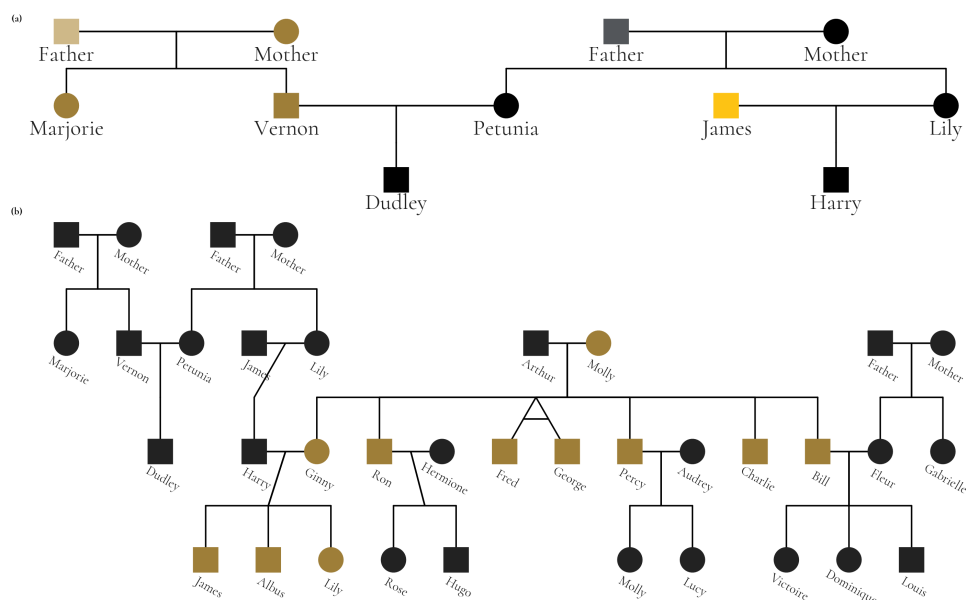
```
ggPedigree(potter,  
  famID = "famID",  
  personID = "personID"  
)
```

117    This code produces the following pedigree plot:



118

The package supports extensive customization of visual aesthetics. The following example is a figure from Hunter et al. (2025) that used the Potter pedigree data. The figure has been restyled according to Wake Forest University brand identity guidelines to demonstrate ggpedigree's customization capabilities. The figure combines two panels: panel (a) highlights unique mitochondrial lines in the Dursley and Evans families, while panel (b) shows the full pedigree with Molly Weasley's mitochondrial descendants in gold.



The complete source code for this example is available in the package documentation [website](#). Collectively, these tools provide a valuable resource for behavior geneticists and others who work with extended family data. They were developed as part of a grant and have been used in several ongoing projects, presentations (Garrison, 2024; Hunter, Garrison, Lyu, Good, & Burt, 2024), and forthcoming papers (Burt et al., 2025; Hunter et al., 2025; Lyu et al., 2025).

## Availability

The ggpedigree package is open-source and available on both [GitHub](#) and the [Comprehensive R Archive Network \(CRAN\)](#). It is licensed under the GNU General Public License.

## Acknowledgments

The current research is supported by the National Institute on Aging (NIA), [R01-AG073189](#). The author would like to thank Michael Hunter for his enthusiasm for the development of this package.

## References

- Burt, S. A., Garrison, S. M., Lyu, X., Rodgers, J. L., Carroll, S. L., Smith, K. R., & Hunter, M. D. (2025). Contributions of inherited mtDNA to longevity: Evidence from extended pedigrees with 176 million kinship pairs. *eBioMedicine*, 119, 105911. doi:10.1016/j.ebiom.2025.105911
- Carver, T., Cunningham, A. P., Babb de Villiers, C., Lee, A., Hartley, S., Tischkowitz, M., Walter, F. M., et al. (2018). Pedigreejs: A web-based graphical pedigree editor.

- 145 *Bioinformatics*, 34(6), 1069–1071. doi:[10.1093/bioinformatics/btx705](https://doi.org/10.1093/bioinformatics/btx705)
- 146 Garrison, S. M. (2024). Charting new paths in behavior genetics: Developing a comprehensive  
147 r visualization atlas. *Behavior Genetics* (Vol. 54, p. 488488). doi:[10.1007/s10519-024-](https://doi.org/10.1007/s10519-024-10197-8)  
148 [10197-8](https://doi.org/10.1007/s10519-024-10197-8)
- 149 Garrison, S. M., Hunter, M. D., Lyu, X., Trattner, J. D., & Burt, S. A. (2024). BGmisc: An r  
150 package for extended behavior genetics analysis. *Journal of Open Source Software*, 9(94).  
151 doi:[10.21105/joss.06203](https://doi.org/10.21105/joss.06203)
- 152 Garrison, S. M., Lyu, X., Hunter, M. D., Rodgers, J. L., Smith, K. R., Coon, H., & Burt, S.  
153 A. (2023). Analyzing extended cousin similarity to unravel the mystery of mtDNA and  
154 longevity. *Behavior Genetics*. doi:[10.1007/s10519-023-10156-9](https://doi.org/10.1007/s10519-023-10156-9)
- 155 Hunter, M. D., Garrison, S. M., Burt, S. A., & Rodgers, J. L. (2021). The Analytic Identification  
156 of Variance Component Models Common to Behavior Genetics. *Behavior Genetics*, 51(4),  
157 425–437. doi:[10.1007/s10519-021-10055-x](https://doi.org/10.1007/s10519-021-10055-x)
- 158 Hunter, M. D., Garrison, S. M., Lyu, X., Good, R., & Burt, S. A. (2024). Tools for  
159 biometric modeling in large population databases. *Behavior Genetics* (Vol. 54, p. 531531).  
160 doi:[10.1007/s10519-024-10197-8](https://doi.org/10.1007/s10519-024-10197-8)
- 161 Hunter, M. D., Garrison, S. M., Lyu, X., Good, R., Carroll, S. L., & Burt, S. A. (2025). *Tracing*  
162 *the right path: Determination of large pedigree segmentation and relatedness. Revise and*  
163 *Resubmit at Behavior Genetics*.
- 164 Le Nézet, L., Sinnwell, J., Letko, A., André, C., & Quignon, P. (2025). Pedexplorer: A  
165 bioconductor package to streamline pedigree design and visualization. *Bioinformatics*,  
166 41(6), btaf329. doi:[10.1093/bioinformatics/btaf329](https://doi.org/10.1093/bioinformatics/btaf329)
- 167 Lyu, X., Hunter, M. D., Burt, S. A., Good, R., Carroll, S. L., & Garrison, S. M. (2025).  
168 Detecting mtDNA effects with an extended pedigree model: An analysis of statistical power  
169 and estimation bias. *Behavior Genetics*. doi:[10.1007/s10519-025-10225-1](https://doi.org/10.1007/s10519-025-10225-1)
- 170 Martin, G. R. R. (1997). *A game of thrones*. Bantam.
- 171 Martin, G. R. R. (2018). *Fire & blood: 300 years before a game of thrones*. New York:  
172 Random House Worlds.
- 173 Martin, J., Wolak, M., Johnston, S., & Morrissey, M. (2025). *Pedtricks: Visualize, summarize*  
174 *and simulate data from pedigrees*. doi:[10.32614/CRAN.package.pedtricks](https://doi.org/10.32614/CRAN.package.pedtricks)
- 175 McArdle, J. J., & McDonald, R. P. (1984). Some algebraic properties of the reticular action  
176 model for moment structures. *British Journal of Mathematical and Statistical Psychology*,  
177 37, 234–251. doi:[10.1111/j.2044-8317.1984.tb00802.x](https://doi.org/10.1111/j.2044-8317.1984.tb00802.x)
- 178 McFarlane, S. E., Boutin, S., Humphries, M. M., McAdam, A. G., Gorrell, J. C., & Colt-  
179 man, D. W. (2015, January 21). Data from: Very low levels of direct additive ge-  
180 netic variance in fitness and fitness components in a red squirrel population. Dryad.  
181 doi:[10.5061/DRYAD.N5Q05](https://doi.org/10.5061/DRYAD.N5Q05)
- 182 McFarlane, S. E., Gorrell, J. C., Coltman, D. W., Humphries, M. M., Boutin, S., & McAdam,  
183 A. G. (2014). Very low levels of direct additive genetic variance in fitness and fitness  
184 components in a red squirrel population. *Ecology and Evolution*, 4(10), 1729–1738.  
185 doi:[10.1002/ece3.982](https://doi.org/10.1002/ece3.982)
- 186 McGoldrick, M., Gerson, R., & Petry, S. (2020). *Genograms: Assessment and Treatment*.  
187 Erscheinungsort nicht ermittelbar: W. W. Norton & Company.
- 188 Morrissey, M. B., & Wilson, A. J. (2010). pedantics: an r package for pedigree-based genetic  
189 simulation and pedigree manipulation, characterization and viewing. *Molecular Ecology*  
190 *Resources*, 10(4), 711–719. doi:[10.1111/j.1755-0998.2009.02817.x](https://doi.org/10.1111/j.1755-0998.2009.02817.x)

- 191 Ranaweera, T., Makalic, E., Hopper, J. L., & Bickerstaffe, A. (2018). An open-source,  
192 integrated pedigree data management and visualization tool for genetic epidemiology.  
193 *International Journal of Epidemiology*, 47(4), 1034–1039. doi:[10.1093/ije/dyy049](https://doi.org/10.1093/ije/dyy049)
- 194 Schaid, D., & Sinnwell, J. (2024). Pedgene: Gene-level variant association tests for pedigree  
195 data. doi:[10.32614/CRAN.package.pedgene](https://doi.org/10.32614/CRAN.package.pedgene)
- 196 Shaw, P. D., Graham, M., Kennedy, J., Milne, I., & Marshall, D. F. (2014). Helium: Visualiza-  
197 tion of large scale plant pedigrees. *BMC Bioinformatics*, 15(1), 259. doi:[10.1186/1471-](https://doi.org/10.1186/1471-2105-15-259)  
198 [2105-15-259](https://doi.org/10.1186/1471-2105-15-259)
- 199 Sinnwell, J. P., Therneau, T. M., & Schaid, D. J. (2014). The kinship2 r package for pedigree  
200 data. *Human Heredity*, 78, 91–93. doi:[10.1159/000363105](https://doi.org/10.1159/000363105)
- 201 Vigeland, M. D. (2021b). *Pedigree analysis in r*. London: Academic Press, an imprint of  
202 Elsevier. Retrieved from [https://shop.elsevier.com/books/pedigree-analysis-in-r/vigeland/](https://shop.elsevier.com/books/pedigree-analysis-in-r/vigeland/978-0-12-824430-2)  
203 [978-0-12-824430-2](https://shop.elsevier.com/books/pedigree-analysis-in-r/vigeland/978-0-12-824430-2)
- 204 Vigeland, M. D. (2021a). *Pedigree analysis in {r}*. doi:[10.32614/CRAN.package.pedtools](https://doi.org/10.32614/CRAN.package.pedtools)
- 205 Vigeland, M. D. (2022). QuickPed: An online tool for drawing pedigrees and analysing  
206 relatedness. *BMC Bioinformatics*, 23(1), 220. doi:[10.1186/s12859-022-04759-y](https://doi.org/10.1186/s12859-022-04759-y)
- 207 Wickham, H. (2016). *ggplot2*. Use R! Cham: Springer International Publishing.  
208 doi:[10.1007/978-3-319-24277-4](https://doi.org/10.1007/978-3-319-24277-4)
- 209 Wickham, H., Averick, M., Bryan, J., Chang, W., McGowan, L., François, R., Golemund, G.,  
210 et al. (2019). Welcome to the tidyverse. *Journal of Open Source Software*, 4(43), 1686.  
211 doi:[10.21105/joss.01686](https://doi.org/10.21105/joss.01686)
- 212 Zhang, R., Jia, G., & Diao, X. (2023). geneHapR: An r package for gene haplotypic statistics  
213 and visualization. *BMC Bioinformatics*, 24(1), 199. doi:[10.1186/s12859-023-05318-9](https://doi.org/10.1186/s12859-023-05318-9)