

¹ `ggpedigree`: Visualizing Pedigrees with ‘`ggplot2`’ and ² ‘`plotly`’

³ **S. Mason Garrison**  

⁴ 1 Department of Psychology, Wake Forest University, North Carolina, USA  Corresponding author

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⁵ 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.

²² 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 takes 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 `Pedixplorer`, [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 `ggpeditree` provides. `ggpeditree` 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 `ggpeditree` 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 structure analysis 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, S. M., Hunter, Michael D., Lyu, X., Trattner, J. D., & Burt,
70 S. A., 2024](#)). All functions return standard R objects (`ggplot` or `plotly`) that can be further
71 customized.

72 Features

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

- 79 ▪ Data Standardization and Family Structure Analysis: `ggPedigree()` integrates with
80 `BGmisc` functions like `ped2fam()` to organize individuals by family, `recodeSex()` to
81 standardize sex coding, and `checkParentIDs()` to validate pedigree structures. The
82 function handles consanguineous relationships and individuals appearing in multiple
83 pedigree positions.
- 84 ▪ Coordinate Calculation: `calculateCoordinates()` computes optimal positioning for indi-
85 viduals using algorithms adapted from `kinship2::align_pedigree`, with enhancements
86 for large multi-generational pedigrees and complex family structures. These steps are
87 vectorized as much as possible to ensure computational efficiency and compatibility with
88 `ggplot2`.

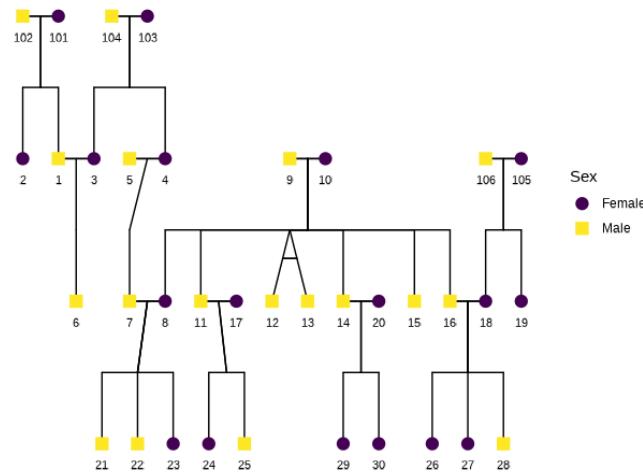
- Relationship Connection Mapping: `calculateConnections()` generates connection paths between family members, mapping parent-child, sibling, spousal, and twin relationships. The function determines midpoints for line intersections and handles overlapping connections with specialized curved segments. These calculations are optimized for large datasets by using vectorized operations rather than the loop-based approaches used in `kinship2`.
- Layer-based Plot Construction: `ggPedigree()` constructs plots using `ggplot2` geometry functions, returning standard `ggplot2` objects that integrate with existing R workflows. `ggPedigreeInteractive()` extends plots into interactive `plotly` widgets. A config system allows customization of over 100 aesthetic and layout parameters.
- Individual Highlighting: Advanced functionality to highlight specific individuals and their relatives based on additive genetic, mitochondrial, or other relationship matrices.
- Specific Visualization Functions: `ggPedigree()` creates static pedigree plots using `ggplot2`. `ggPedigreeInteractive()` generates interactive pedigree plots using `plotly`. `ggRelatednessMatrix()` creates customizable heatmaps for relatedness matrices with support for hierarchical clustering, and seamless integration with `BGmisc` relatedness calculations. `ggPhenotypeByDegree()` visualizes phenotypic correlations as a function of genetic relatedness, including confidence intervals and statistical summaries for quantitative genetic analysis.

108 Code example

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

```
111    ggPedigree(potter,
112       famID = "famID",
113       personID = "personID"
114     )
```

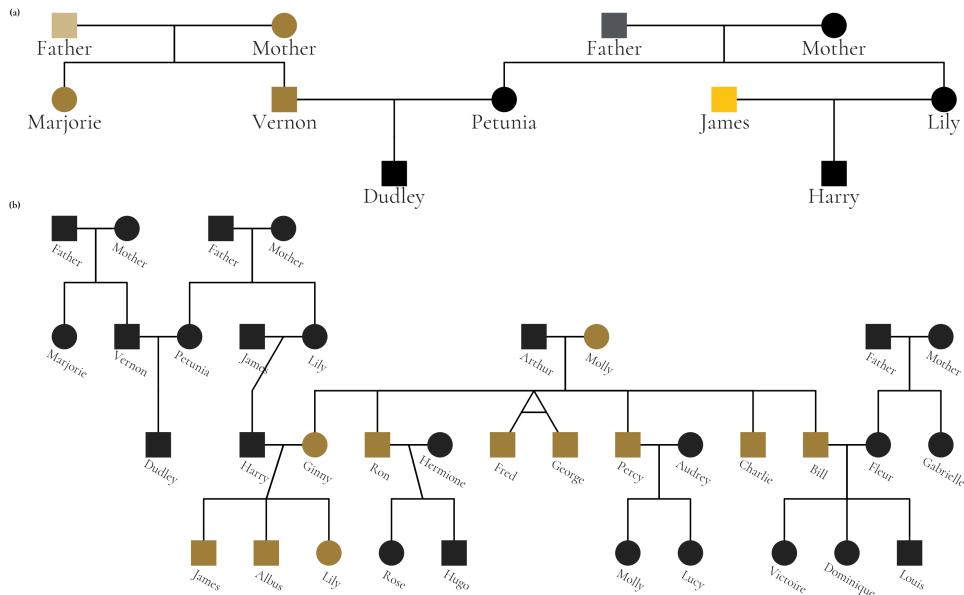
115 This code produces the following pedigree plot:



112

113 The package supports extensive customization of visual aesthetics. The following example
 114 is a figure from Hunter et al. (2025) that used the Potter pedigree data. The figure has
 115 been restyled according to Wake Forest University brand identity guidelines to demonstrate
 116 `ggpedigree`'s customization capabilities. The figure combines two panels: panel (a) highlights

117 unique mitochondrial lines in the Dursley and Evans families, while panel (b) shows the full
 118 pedigree with Molly Weasley's mitochondrial descendants in gold.



119
 120 The complete source code for this example is available in the package documentation at
 121 <https://r-computing-lab.github.io/ggpedigree/articles/>.

122 Collectively, these tools provide a valuable resource for behavior geneticists and others who
 123 work with extended family data. They were developed as part of a grant and have been used
 124 in several ongoing projects, presentations ([Garrison, 2024](#); [Hunter, Garrison, Lyu, Good, &](#)
 125 [Burt, 2024](#)), and forthcoming papers ([Burt et al., 2025](#); [Hunter et al., 2025](#); [Lyu et al., 2025](#)).

126 Availability

127 The ggpedigree package is open-source and available on both GitHub at <https://github.com/R-Computing-Lab/ggpedigree> and the Comprehensive R Archive Network (CRAN) at
 128 <https://cran.r-project.org/package=ggpedigree>. It is licensed under the GNU General Public
 129 License.

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 134 package.

135 References

- 136 Burt, S. A., Garrison, S. M., Lyu, X., Rodgers, J. L., Carroll, S. L., Smith, K. R., &
 137 Hunter, M. D. (2025). Contributions of inherited mtDNA to longevity: Evidence from
 138 extended pedigrees with 176 million kinship pairs. *eBioMedicine*, 119, 105911. doi:<https://doi.org/10.1016/j.ebiom.2025.105911>
- 140 Carver, T., Cunningham, A. P., Babb de Villiers, C., Lee, A., Hartley, S., Tischkowitz,
 141 M., Walter, F. M., et al. (2018). Pedigreejs: A web-based graphical pedigree editor.
 142 *Bioinformatics*, 34(6), 1069–1071. doi:[10.1093/bioinformatics/btx705](https://doi.org/10.1093/bioinformatics/btx705)

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

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