ggpedigree: Visualizing Pedigrees with 'ggplot2' and 'plotly'

S. Mason Garrison [iD] [1]¶

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

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 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

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

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

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

Software Architecture

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

Features

I describe the main features of the `ggpedigree` package below. More detailed descriptions of features and usage is available in the package vignettes, including examples of how to create static and interactive pedigree plots, customize aesthetics, and visualize relatedness matrices. Additional example data include squirrel data from the Kluane Red Squirrel Project (McFarlane et al., 2014, 2015) and Targaryen family data from the Song of Ice and Fire universe (G. R. R. Martin, 1997, 2018).
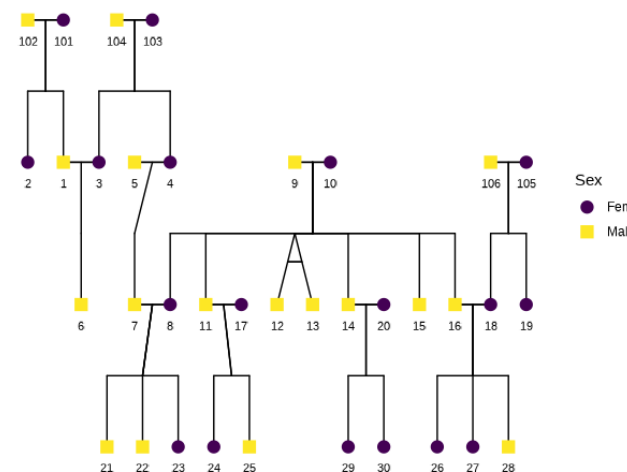
- Data Standardization and Family Structure Analysis: `ggPedigree()` integrates with BGmisc functions like `ped2fam()` to organize individuals by family, `recodeSex()` to standardize sex coding, and `checkParentIDs()` to validate pedigree structures. The function handles consanguineous relationships and individuals appearing in multiple pedigree positions.

- Coordinate Calculation: `calculateCoordinates()` computes optimal positioning for individuals using algorithms adapted from `kinship2::align.pedigree`, with enhancements for large multi-generational pedigrees and complex family structures. These steps are vectorized as much as possible to ensure computational efficiency and compatibility with ggplot2.

89 ▪ Relationship Connection Mapping: `calculateConnections()` generates connection paths
90 between family members, mapping parent-child, sibling, spousal, and twin relationships.
91 The function determines midpoints for line intersections and handles overlapping con-
92 nections with specialized curved segments. These calculations are optimized for large
93 datasets by using vectorized operations rather than the loop-based approaches used in
94 kinship2.

95 ▪ Layer-based Plot Construction: `ggPedigree()` constructs plots using ggplot2 geometry
96 functions, returning standard ggplot2 objects that integrate with existing R workflows.
97 `ggPedigreeInteractive()` extends plots into interactive plotly widgets. A config system
98 allows customization of over 100 aesthetic and layout parameters.

99 ▪ Individual Highlighting: Advanced functionality to highlight specific individuals and their
100 relatives based on additive genetic, mitochondrial, or other relationship matrices.

101 ▪ Specific Visualization Functions: `ggPedigree()` creates static pedigree plots using
102 ggplot2. `ggPedigreeInteractive()` generates interactive pedigree plots using plotly.
103 `ggRelatednessMatrix()` creates customizable heatmaps for relatedness matrices with
104 support for hierarchical clustering, and seamless integration with `BGmisc` relatedness
105 calculations. `ggPhenotypeByDegree()` visualizes phenotypic correlations as a function
106 of genetic relatedness, including confidence intervals and statistical summaries for
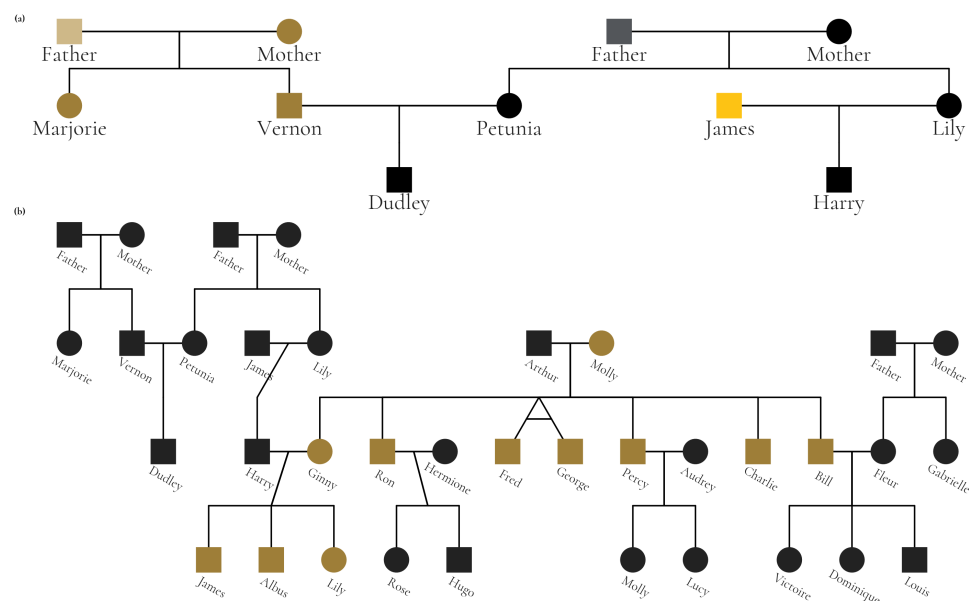107 quantitative genetic analysis.

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.

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


111 This code produces the following pedigree plot:

112 I demonstrate several advanced features by restyling a figure from (Hunter et al., 2025), to
113 follow the Wake Forest brand identity guidelines. The source code for transforming these
114 potter data is available in the package documentation on . The resulting figure appears below:

I have combined two figures using patchwork (Pedersen, 2025): 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.

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 at https://github.com/R-Computing-Lab/ggpedigree and the Comprehensive R Archive Network (CRAN) at https://cran.r-project.org/package=ggpedigree. It is licensed under the GNU General Public License.

Acknowledgments

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