

Genetic Association Analysis with R (II)

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Key Features of the Template



- YAML Front Matter: Set metadata like the title, author, theme, and transitions.
- Headings: Use # for slide titles, ## or ### for smaller headers.
- Horizontal Slide Separation: Use --- to separate individual slides.
- Code Blocks: Wrap code in triple backticks for syntax highlighting.
- Others: Title page image, icon on title, embedded image, citation¹, colored URLs, numbered figures and tables, multiple columns, PDF bookmarks.

Slide with Image





Figure 1: physalis

Code/Math Example



Sample Python code
def hello_world():
 print("Hello, world!")

$$\phi(x,y) = \phi\left(\sum_{i=1}^{n} x_i e_i, \sum_{j=1}^{n} y_j e_j\right) = \sum_{i=1}^{n} \sum_{j=1}^{n} x_i y_j \phi(e_i, e_j) =$$

$$(x_1, \dots, x_n) \begin{pmatrix} \phi(e_1, e_1) & \cdots & \phi(e_1, e_n) \\ \vdots & \ddots & \vdots \\ \phi(e_n, e_1) & \cdots & \phi(e_n, e_n) \end{pmatrix} \begin{pmatrix} y_1 \\ \vdots \\ y_n \end{pmatrix}$$

A Numbered Table



Table 1: A summary of files

File	Description
nature-genetics.csl	style
premeable.tex	premeable
REFERENCES.bib	reference library
slides.html	.html output
slides.md	markdown file
slides.pdf	.pdf output
slides.sh*	Bash command file
sunflower.jpg*	sunflower as a logo

Two Columns



Bullet points

- Point 1
- Point 2
- Point 3

Figure 1 can be referred, too!

Ordered list

- 1. First item
- 2. Another item
- 3. A third item

Tools to Render Markdown Slides



Four of them are indicated here,

- Pandoc: Convert Markdown to various formats, including slides in HTML5 or LaTeX Beamer. The current presentation is rendered with v2.18.
- Marp: A tool for creating slides directly from Markdown and the .html in this presentation is rendered with v4.1.1.
- Reveal.js: Use Reveal.js for beautiful web-based presentations. A wonderful demo is by quarto below.
- quarto: Contain comprehensive facilities for rendering presentations including support for pandoc/Reveal.js, see https://quarto.org/.

References



1. Zhao, J. H. & Tan, Q. Integrated analysis of genetic data with R. Hum Genomics 2, 258–65 (2006).