

Genetic Association Analysis with R (II)

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- **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.



Figure 1: physalis



Sample Python code

```
def hello_world():  
    print("Hello, world!")
```

$$\phi(x, y) = \phi \left(\sum_{i=1}^n x_i e_i, \sum_{j=1}^n y_j e_j \right) = \sum_{i=1}^n \sum_{j=1}^n x_i y_j \phi(e_i, e_j) =$$
$$(x_1, \dots, x_n) \begin{pmatrix} \phi(e_1, e_1) & \cdots & \phi(e_1, e_n) \\ \vdots & \ddots & \vdots \\ \phi(e_n, e_1) & \cdots & \phi(e_n, e_n) \end{pmatrix} \begin{pmatrix} y_1 \\ \vdots \\ y_n \end{pmatrix}$$



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



Bullet points

- Point 1
- Point 2
- Point 3

Ordered list

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

Figure 1 can be referred, too!



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/>.



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