

# Genetic Association Analysis with R (II)

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Jing Hua Zhao

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## 1. **YAML Front Matter:**

- Set metadata like the title, author, theme, and transitions.

## 2. **Headings:**

- Use # for slide titles, ## or ### for smaller headers.

## 3. **Horizontal Slide Separation:**

- Use --- to separate individual slides.

## 4. **Code Blocks:**

- Wrap code in triple backticks for syntax highlighting.

## 5. **Others:**

- Title page image, icon on titles, multiple columns, embedded images, a citation<sup>1</sup>, colored URLs, numbered figures and tables.



## Bullet points

- Point 1
- Point 2
- Point 3

## Ordered list

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





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

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

Figure 1 is shown on last page.

**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



- **Reveal.js:** Use **Reveal.js** for beautiful web-based presentations. Convert your Markdown using `reveal-md`.
- **Marp:** A tool for creating slides directly from Markdown and exporting them to PDF or PowerPoint.
- **Pandoc:** Convert Markdown to various formats, including slides in HTML5 or LaTeX Beamer.



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