

# Genetic Association Analysis with R (II)

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Content for the first slide.

- Point 1
- Point 2
- Point 3



1. Ordered list item
2. Another item
3. A third item





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

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



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

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

## 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. **Images:**

- Embed images using the standard Markdown syntax: ![alt text](path).

## 6. **Others:**

- Cite a paper<sup>1</sup>, color URLs, number tables.



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- **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).