Genetic Association Analysis with R (II)

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31 January 2025

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Slide 1 Title

Content for the first slide.

- Point 1
- Point 2
- Point 3

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

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

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

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

Key Features of the Template

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[1], color URLs, number tables.

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).