

# Kongoh version 3.2.0 User Manual

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## Information of Kongoh

Kongoh (named after the Japanese word “mixture”) is an open-source software for DNA evidence interpretation based on a quantitative continuous model[1]. The software is a graphical user interface written in R language, and the R-package *Kongoh* is freely available.

## Changes in ver. 3.2.0

**Note** Users are recommended to switch to the version 3.2.0 because of the following important updates and new features.

### Important updates

- Kongoh can be used as the R-package *Kongoh*.
- The file format for Monte Carlo parameters is changed as follows.
  - Names of parameters in each model are explicitly declared in the column.
  - The scale of “Mean” parameters for AE and Hb is changed from logarithmic scale to linear scale.

### New features

- UI design has been changed.
- Project data can be saved and loaded.
- Users can set analysis methods per typing kit and experimental condition in the software.
- Probabilistic genotyping can be performed without reference genotypes (i.e., mixture deconvolution).
- viewAf : Dirichlet auto correct cancel
- Estimated gamma distributions are replaced with the expected peak heights of gamma distributions in the graph of probabilistic genotyping.
- min. AE and so on can be determined by observed data
- The filter of mixture ratio “mrFiltr” is added to exclude unrealistic genotype combinations.

### Minor changes

- Analytical thresholds can be set per locus.
- aeMin, hbMin, and so on can be set.
- mixture ratio -> mixture proportion
- locus set can be checked by the function fileCkPar
- When no seq info of allele Q, message
- Both OK Sample File, Sample Name(CSP)

## Tutorial

### Getting started

1. Ensure that R ( $\geq 4.2.0$ ) is installed. It is available from the R Development Core Team website (<http://www.R-project.org>).
2. Begin an R session.
3. Install package
4. Execute the following commands in R to start GUI.

```
library(Kongoh)  
Kongoh()
```

### Input files

1. Load a crime stain profile.

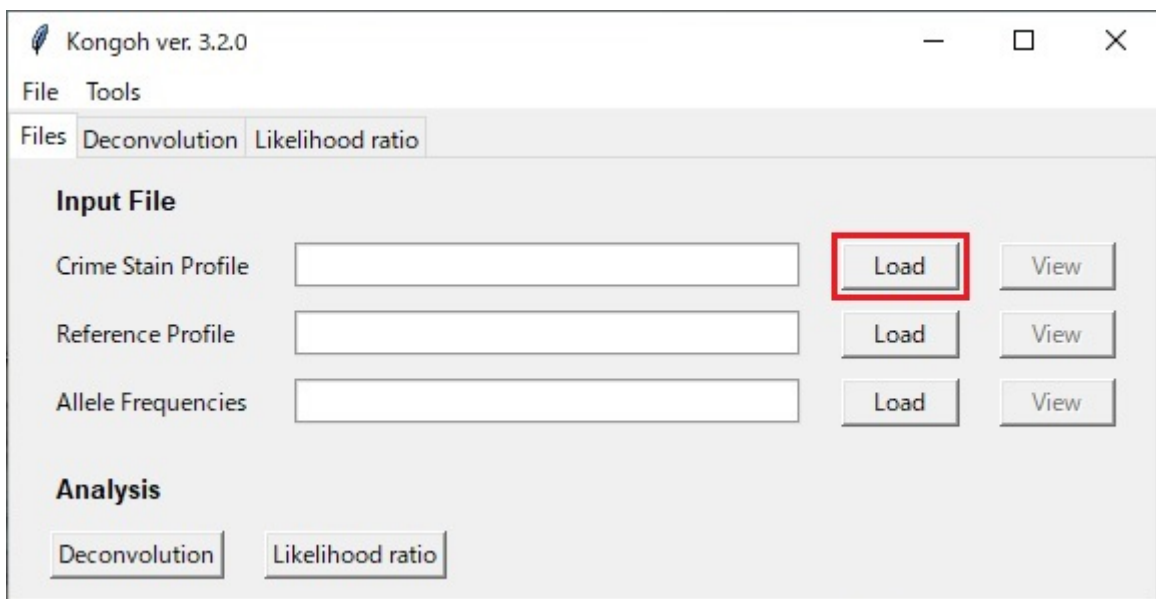


Figure 1: Figure 1

2. Load reference profiles.
3. Load allele frequencies.

### Deconvolution

4. Click the “Deconvolution” button.

## References

- [1] S. Manabe, C. Morimoto, Y. Hamano, S. Fujimoto, K. Tamaki, Development and validation of open-source software for DNA mixture interpretation based on a quantitative continuous model, PLOS ONE. 12 (2017) 1–18. <https://doi.org/10.1371/journal.pone.0188183>.