

# ***KinBN* v1.1.2 user manual**

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## 1. What is *KinBN*?

*KinBN* is a free software (GNU General Public License v3.0) for kinship analysis based on a Bayesian network. It can be applied to short tandem repeat (STR) markers commonly used in forensic genetics and calculates likelihood ratio (LR) considering linkage between loci and mutation. The software is graphical-user-interface written in R language. The software has been validated under various conditions.

The current version of *KinBN* has the following capabilities:

- Based on a Bayesian network, it calculates an LR value for kinship analysis.
- It considers the effects of linkage and mutation that influence kinship determination.
- The user can assume complex relationships such as incest.
- Users can also simulate LR distribution of computationally generated DNA profiles according to the assumed relationship.
- *KinBN* generates a report of calculation results. The user can save it and check the results.

*KinBN* has been developed by Morimoto et al. in Department of Forensic Medicine, Kyoto University Graduate School of Medicine. Questions regarding the software should be addressed to [morimoto@fp.med.kyoto-u.ac.jp](mailto:morimoto@fp.med.kyoto-u.ac.jp).

## 2. Changes in v1.1.2

- The required package (*Rgraphviz*) was added for R version 4.0.
- The version of *tkRplotR* package was specified (version 1.1.0).

### 3. Tutorial

#### A) Starting software

*KinBN* is compatible with R language that is available from the R Development Core Team website (<http://www.R-project.org>). The current version of *KinBN* (v1.1.2) is freely available at GitHub repository (<https://github.com/ChieMorimoto/KinBN/releases>). In the repository, there are R Workspace data including source code (KinBN v1.1.2.Rdata), R source code (KinBN v1.1.2 source code.R), example files (Allele data in Caucasian.csv, Mutation rates.csv, and Example of STR genotypes.csv), and this user manual (KinBN v1.1.2 user manual.pdf). The user needs to install R language and the current version of *KinBN* prior to use the software.

The user opens KinBN v1.1.2.Rdata with R language and enter the below code at R console.

```
> KinBN()
```

Then the required packages (*bnlearn*, *RGBL*, *BiocManager*, *BiocGenerics*, *graph*, *Rgraphviz*, *gRbase*, *gRain*, *tcltk2*, *tkRplotR* (version 0.1.1), and *kinship2*) will be installed automatically and the top screen of *KinBN* will be opened (Fig. 1).

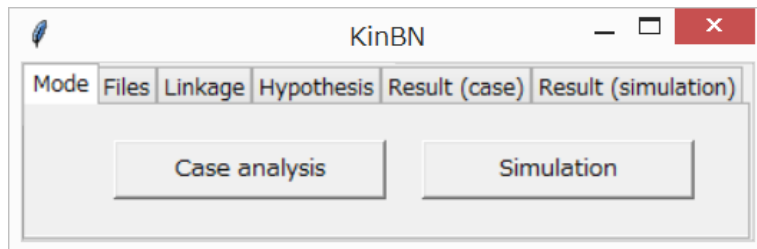


Fig. 1 Top screen of *KinBN*.

## B) Preparation of input files

*KinBN* has two functions; case analysis and simulation. For case analysis, the user prepares three csv files; observed numbers of alleles in each locus at the population (Fig. 2), mutation rates in each locus (Fig. 3), and STR profiles of the case (Fig. 4). Any locus set can be accommodated by the software. Locus name should be unified between these files. For simulation, the user prepares two csv files; observed numbers of alleles in each locus at the population (Fig. 2) and mutation rates in each locus (Fig. 3).

Example files are in the GitHub repository (<https://github.com/ChieMorimoto/KinBN/releases>).

Allele												
A	B	C	D	E	F	G	H	I	J	K	L	M
1 Allele	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA
2	2.2											
3	3.2											
4	4											
5	4.2											
6	5				1						1	
7	6				1						170	
8	6.3											
9	7										140	
10	8		13	4	379	10					69	
11	8.1											
12	9		77	10	92	4			1		86	
13	9.1								1			
14	9.3										249	
15	10		41	159	36	74		6	152	1	6	
16	10.1											
17	10.2											
18	10.3											
19	11	1	227	223	182	55		7	248	4	1	

Fig. 2 Example of observed numbers of alleles in each locus at the population. It is used for estimation of allele frequencies. The first column and row indicate allele number and locus names, respectively.

A1											
	A	B	C	D	E	F	G	H	I	J	K
1	Marker	P (-2)	P (-1)	P (0)	P (+1)	P (+2)	M (-2)	M (-1)	M (0)	M (+1)	M (+2)
2	D3S1358	3.70E-05	0.001424	0.997353	0.001148	3.77E-05	0	0.000193	0.999697	7.56E-05	3.44E-05
3	vWA	0.000146	0.002718	0.994906	0.002201	2.92E-05	0	0.000125	0.999378	0.000445	5.25E-05
4	D16S539	8.41E-05	0.000934	0.997629	0.001353	0	0	0.000484	0.999412	0.000104	0
5	CSF1PO	0	0.002043	0.996111	0.001846	0	0	0.000213	0.999408	0.00038	0
6	TPOX	0	0.000116	0.999697	0.000187	0	0	7.51E-05	0.999849	7.61E-05	0
7	D8S1179	4.82E-05	0.001301	0.99743	0.001196	2.39E-05	0	0.000134	0.999702	0.000142	2.22E-05
8	D21S11	3.70E-05	0.000868	0.998013	0.001082	0	3.60E-05	0.000108	0.999727	0.000129	0
9	D18S51	0.000147	0.000943	0.997459	0.001421	2.98E-05	2.13E-05	0.000117	0.999364	0.000476	2.15E-05
10	D2S441	5.44E-05	0.001167	0.997464	0.001251	6.42E-05	1.49E-05	0.00027	0.999494	0.000212	8.71E-06
11	D19S433	0	0.000958	0.998425	0.000452	0.000164	0	0.000505	0.999435	5.97E-05	0
12	TH01	0	4.48E-05	0.999895	5.97E-05	0	1.70E-05	5.46E-05	0.99992	8.29E-06	0
13	FGA	0.000278	0.001497	0.995438	0.002708	7.94E-05	0	0.000348	0.999358	0.000293	0
14	D22S1045	5.44E-05	0.001167	0.997464	0.001251	6.42E-05	1.49E-05	0.00027	0.999494	0.000212	8.71E-06
15	D5S818	0	0.001421	0.996841	0.001198	0.000541	0	0.000259	0.999462	0.000279	0
16	D13S317	0	0.001369	0.997194	0.001397	3.96E-05	3.33E-05	7.08E-05	0.999657	0.000239	0
17	D7S820	0	0.001303	0.997827	0.00087	0	0	6.22E-05	0.999813	0.000125	0
18	SE33	5.44E-05	0.001167	0.997464	0.001251	6.42E-05	1.49E-05	0.00027	0.999494	0.000212	8.71E-06
19	D10S1248	5.44E-05	0.001167	0.997464	0.001251	6.42E-05	1.49E-05	0.00027	0.999494	0.000212	8.71E-06
20	D1S1656	5.44E-05	0.001167	0.997464	0.001251	6.42E-05	1.49E-05	0.00027	0.999494	0.000212	8.71E-06
21	D12S391	5.44E-05	0.001167	0.997464	0.001251	6.42E-05	1.49E-05	0.00027	0.999494	0.000212	8.71E-06
22	D2S1338	3.70E-05	0.000868	0.998013	0.001082	0	3.60E-05	0.000108	0.999727	0.000129	0

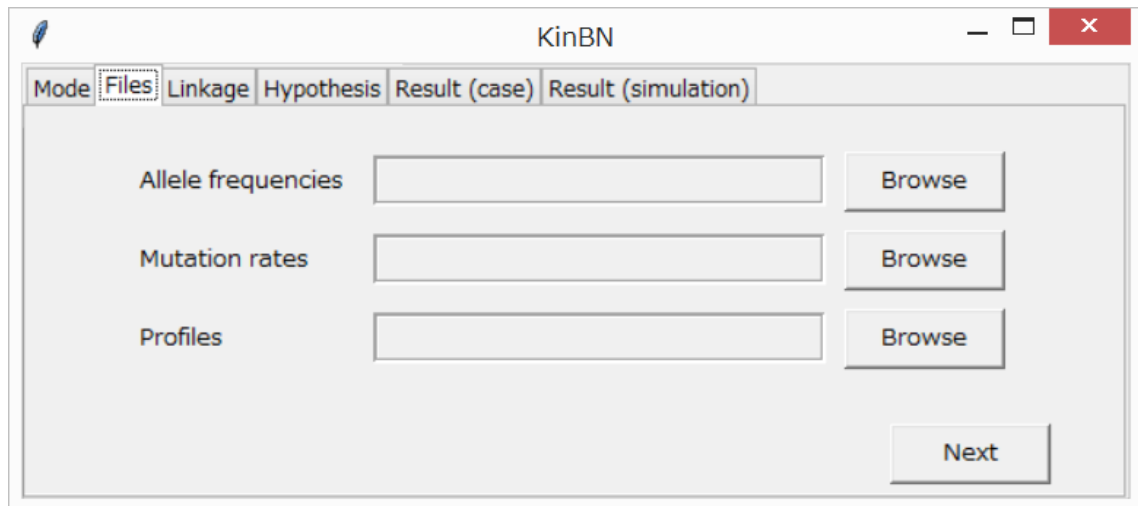
Fig. 3 Example of locus- and sex-specific mutation rates in each locus. The first column indicates locus names. P (x) and M (x) indicate paternal and maternal mutation rates, respectively. X means the distances of mutation.

A1					
	A	B	C	D	E
1	Marker	ID1	ID1	ID2	ID2
2	D3S1358	16	17	16	16
3	vWA	17	17	17	18
4	D16S539	9	9	9	9
5	CSF1PO	12	12	12	13
6	TPOX	8	12	8	10
7	D8S1179	15	15	10	14
8	D21S11	30	30	30	32.2
9	D18S51	13	15	13	14
10	D2S441	10	14	10	14
11	D19S433	13.2	14	14	14
12	TH01	7	8	7	8
13	FGA	23	24	22	24
14	D22S1045	11	15	15	16
15	D5S818	11	12	11	12
16	D13S317	12	13	12	13
17	D7S820	11	11	11	11
18	SE33	18	27.2	18	26.2
19	D10S1248	14	15	14	15
20	D1S1656	12	18	17	17.3
21	D12S391	18	19	18	19
22	D2S1338	23	23	23	25

Fig. 4 Example of STR genotypes of two persons (ID1 and ID2). Note that the user should enter two alleles in homozygotes in each column.

### C) Case analysis

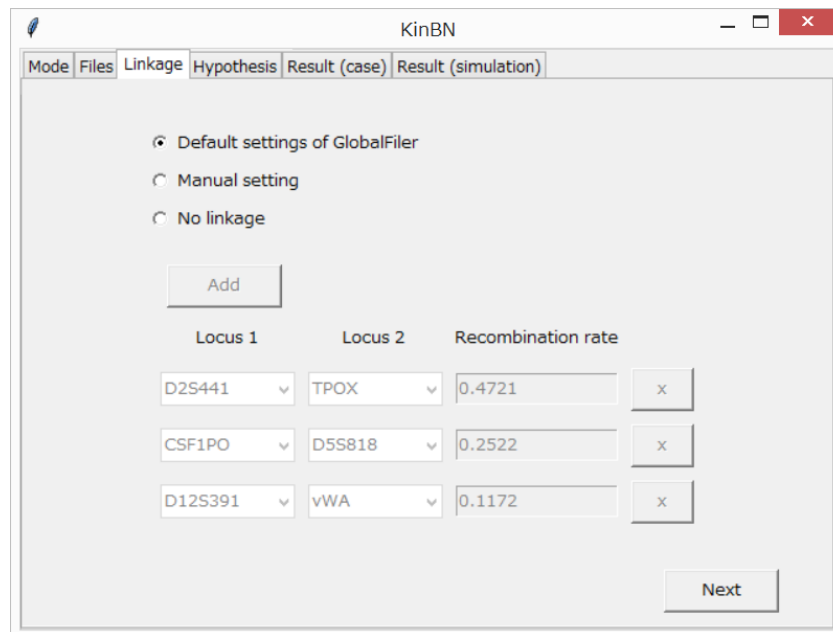
After the user selects *Case analysis* mode in the top screen, Files tab open (Fig. 5).



The screenshot shows the 'Files' tab of the KinBN application. The window title is 'KinBN'. The tabs are 'Mode', 'Files', 'Linkage', 'Hypothesis', 'Result (case)', and 'Result (simulation)'. The 'Files' tab is active. It contains three input fields: 'Allele frequencies', 'Mutation rates', and 'Profiles'. Each field has a 'Browse' button to its right. A 'Next' button is located at the bottom right of the tab area.

Fig. 5 Files tab for importing three input files.

The user imports three input files from *Browse* buttons. Once the user selects *Next*, Linkage tab for setting information about linked loci will open (Fig. 6).



The screenshot shows the 'Linkage' tab of the KinBN application. The window title is 'KinBN'. The tabs are 'Mode', 'Files', 'Linkage', 'Hypothesis', 'Result (case)', and 'Result (simulation)'. The 'Linkage' tab is active. It contains three radio buttons: 'Default settings of GlobalFiler' (selected), 'Manual setting', and 'No linkage'. Below these is an 'Add' button. A table with three columns: 'Locus 1', 'Locus 2', and 'Recombination rate'. The table contains three rows of data. Each row has a dropdown menu for 'Locus 1', a dropdown menu for 'Locus 2', a text input field for 'Recombination rate', and a button with an 'x' icon. A 'Next' button is located at the bottom right of the tab area.

Locus 1	Locus 2	Recombination rate
D2S441	TPOX	0.4721
CSF1PO	D5S818	0.2522
D12S391	vWA	0.1172

Fig. 6 Linkage tab for setting information about linked loci. Default settings of GlobalFiler are shown as an example.

The user can select linkage setting from three modes; *Default setting*, *Manual setting*, and *No linkage*. If the user uses multiplex kits following GlobalFiler (Thermo Fisher Scientific, Waltham, MA, USA), Identifiler (Thermo Fisher Scientific), PowerPlex Fusion (Promega, Madison, WI, USA), PowerPlex 16 (Promega), or NGM SElect (Thermo Fisher Scientific), *Default settings* can be selected. *Manual setting* allows the user to set linked loci and recombination rate freely. The user add and delete pairs of linked loci by *Add* and  $\times$  button, respectively. If the user assumes independence between loci, *No linkage* mode can be used.

After the user selects *Next*, Hypothesis tab for setting hypotheses of LR will open (Fig. 7).

The screenshot shows the KinBN software window with the 'Hypothesis' tab selected. The window contains two main panels, 'Hypothesis1' and 'Hypothesis2', each with a table for defining hypotheses. The tables have columns for Name, Sex, Father, Mother, and founder. The 'founder' column includes a checkbox. Buttons for 'Add', 'Delete', and 'View pedigree tree' are located above each table. A 'Calculate' button is positioned at the bottom right of the window.

Fig. 7 Hypothesis tab. Following imported file, the names of known profiles are displayed automatically.

In this tab, Hypothesis 1 (H1) and Hypothesis 2 (H2) can be set by making pedigrees manually. In regard to each person, the sex, father, and mother are required. *Add* and *Delete* buttons mean adding and deleting extra persons in the assumed pedigree. If the person is founder, the user checks *founder*. For example, when the user tests pairwise sibship between ID1 and ID2, the setting is shown as Fig. 8. User can confirm pedigrees from *View pedigree tree* button (Fig. 9). This software has a restriction on the number of family members (up to 25).

The screenshot shows the KinBN software interface with two panels for setting hypotheses. The 'Hypothesis1' panel contains a table with the following data:

Name	Sex	Father	Mother	founder
ID1	Male	UK1	UK2	<input type="checkbox"/>
ID2	Male	UK1	UK2	<input type="checkbox"/>
UK1	Male			<input checked="" type="checkbox"/>
UK2	Female			<input checked="" type="checkbox"/>

The 'Hypothesis2' panel contains a similar table with the following data:

Name	Sex	Father	Mother	founder
ID1	Male			<input checked="" type="checkbox"/>
ID2	Male			<input checked="" type="checkbox"/>

Buttons for 'Add', 'Delete', and 'View pedigree tree' are present above each table. A 'Calculate' button is located at the bottom right of the interface.

Fig. 8 Example of hypotheses setting at pairwise sibship analysis. In hypothesis 1, UK1 and UK2 are extra persons.

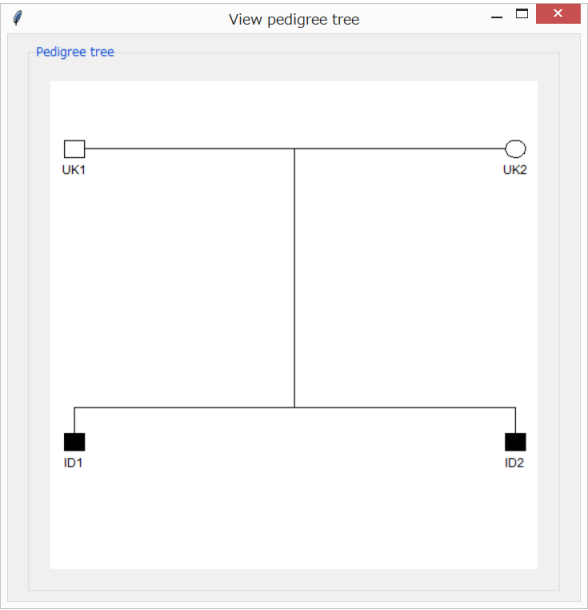


Fig. 9 Pedigree tree of H1 in Fig. 8.



Once the user click *Calculate*, LR calculation will be started. The result will be displayed in Result (case) tab (Fig. 10).

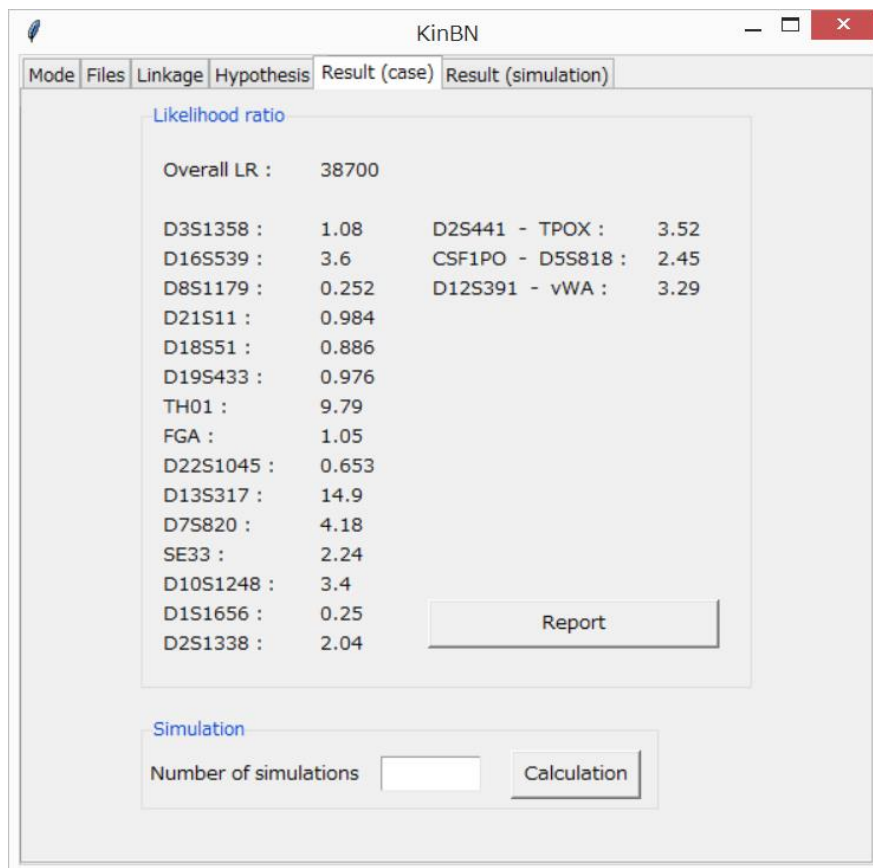
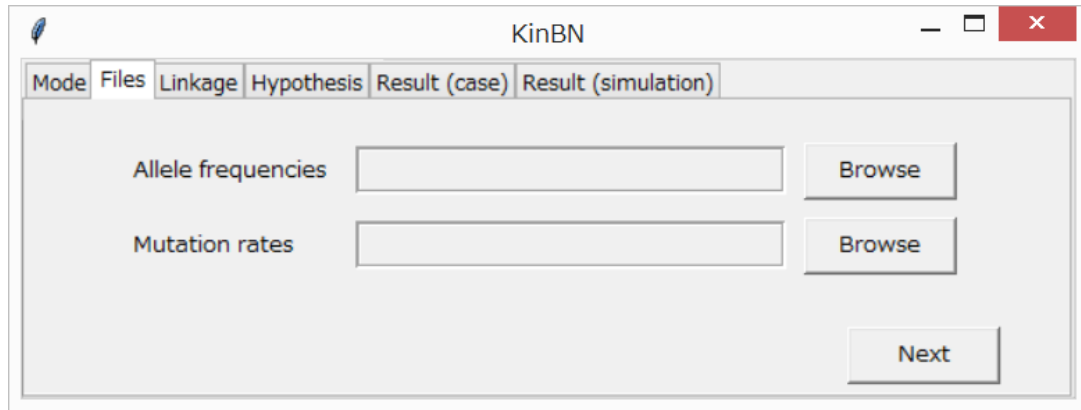


Fig. 10 Example of calculation result of case analysis mode. Overall LR is combined value of all loci. LR value of two linked loci is calculated as one value.

The user can save a report of the case (csv file) from *Report* button. Moreover, by entering *number of simulations*, simulation of LR values in the assumed relationship can be done similar to simulation mode.

#### D) Simulation

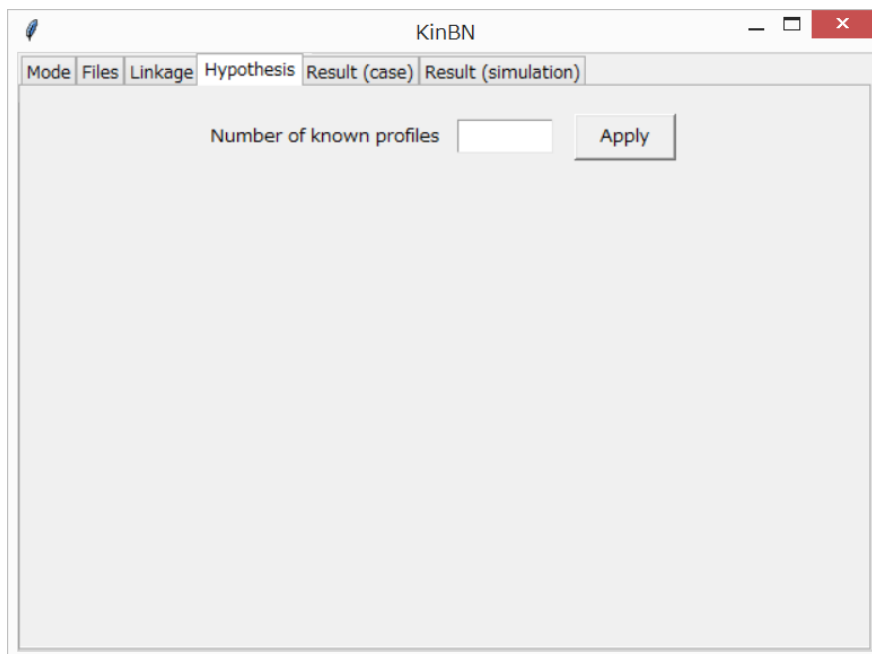
After the user selects *Simulation* in the top screen (Fig. 1), Files tab will open (Fig. 11).



The screenshot shows a window titled "KinBN" with a standard Windows-style title bar (minimize, maximize, close buttons). Below the title bar is a tabbed interface with six tabs: "Mode", "Files", "Linkage", "Hypothesis", "Result (case)", and "Result (simulation)". The "Files" tab is currently selected. The main content area of the "Files" tab contains two input fields. The first is labeled "Allele frequencies" and has a text box next to it, with a "Browse" button to its right. The second is labeled "Mutation rates" and also has a text box and a "Browse" button to its right. At the bottom right of the main content area is a "Next" button.

Fig. 11 Files tab at simulation mode.

The user imports two input files from *Browse* buttons. Once the user selects *Next*, Linkage tab for setting information about linked loci will open (refer to Fig. 6). The user can select linkage setting similar to case analysis. After the user selects *Next*, Hypothesis tab will open (Fig. 12).



The screenshot shows the same "KinBN" window, but now the "Hypothesis" tab is selected. The main content area of the "Hypothesis" tab contains a single input field labeled "Number of known profiles" with a text box next to it, and an "Apply" button to its right.

Fig. 12 Hypothesis tab at simulation mode.

In Hypothesis tab, the user enters the number of known profiles. Once the user clicks *Apply*, the screen of hypothesis setting will be displayed (Fig. 13). As with case analysis, each hypothesis can be set by making pedigrees manually. For starting simulation, the user enters the number of simulation and clicks *Calculate* button. A large number of familial genotypes are computationally generated with considering linkage and mutation according to the user's setting. LR values are calculated based on the genotypes and give the distribution under the targeted family tree. Progress bar indicates the state of simulation (Fig. 14).

The screenshot shows the KinBN software interface. The top menu bar includes Mode, Files, Linkage, Hypothesis, Result (case), and Result (simulation). The Hypothesis tab is selected. Below the menu bar, there is a section for 'Number of known profiles' with a value of 2 and an 'Apply' button. Below this, there are two panels for 'Hypothesis1' and 'Hypothesis2'. Each panel contains buttons for 'Add', 'Delete', and 'View pedigree tree'. Below these buttons is a table with columns for 'Name', 'Sex', 'Father', 'Mother', and 'founder'. The table for Hypothesis1 shows two rows: ID1 and ID2. The table for Hypothesis2 also shows two rows: ID1 and ID2. At the bottom right, there is a 'Number of simulations' field with a value of 1 and a 'Calculate' button.

Fig. 13 Example of hypothesis tab in simulation mode. In this example, the number of known profiles is two (ID1 and ID2).

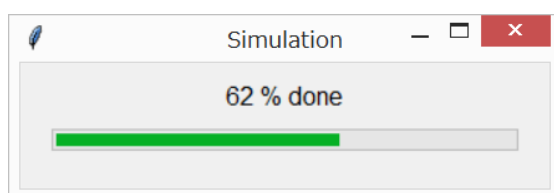


Fig. 14 Progress bar for the state of simulation.

Computation time mainly depends on the assumed pedigree and the number of linked loci. It takes about 4 hours to simulate 10,000 pairwise sibship analyses of 21 STR including three pairs of linked loci by laptop (CPU: Intel Core i7, RAM: 8 GB, storage: 618 GB, OS: Windows 8.1 64 bit). In the case of large family consisted by 21 persons, it takes about 1.5 hours to calculate single LR value of

21 STR including three pairs of linked loci by the same laptop. The calculation time can be reduced to 7 sec by ignoring linkage. If it takes a lot of time to complete the simulation, please consider reducing family members and ignoring linkage. When we performed developmental validation of *KinBN*, considering linkage does not have a general effect on LR distributions in the GlobalFiler 21 loci. In addition, we don't recommend large number of simulations (e.g., > 1,000 times) especially when the user assume a lot of family members and consider linkage.

Result (simulation) tab will be opened by finishing simulation (Fig. 15). Quantiles (minimum, 5%, 25%, 50%, 75%, 95%, and maximum) of LR values are shown for both H1 true testing and H2 true testing.

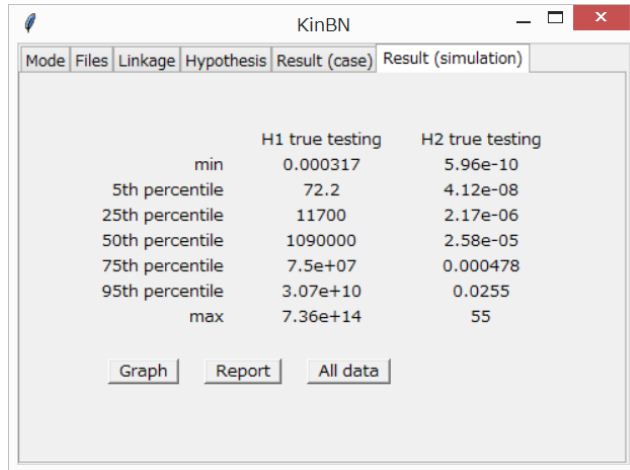


Fig. 15 Example of calculation result of simulation mode.

Graph of LR distributions can be shown from *Graph* button (Fig. 16). The user can save a report of the simulation summary (csv file) from *Report* button. All data of LR values can also be obtained from *All data* button.

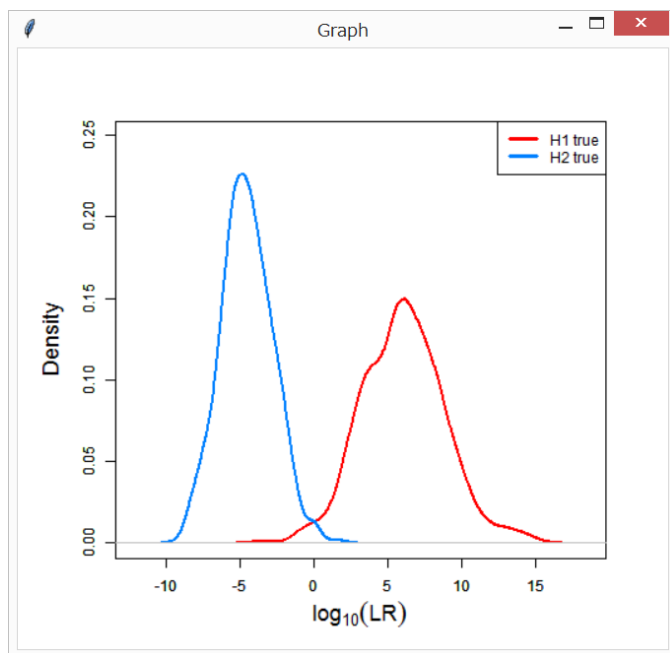


Fig. 16 Example of LR distributions.