

Displaying Genealogy with Various Layouts by Using the WHItEBasE

Seiji Sugiyama¹, Atsushi Ikuta², Daisuke Yokozawa³, Miyuki Shibata⁴ and Tohru Matsuura⁵

¹College of Information Science and Engineering, Ritsumeikan University
1-1-1, Noji-Higashi, Kusatsu, Shiga 525-8577, Japan
seijisan@is.ritsumeik.ac.jp

²Department of Humane Informatics, Faculty of Letters, Otani University
Kamifusa-cho, Koyama, Kita-ku, Kyoto 603-8143, Japan
a.ikuta@sch.otani.ac.jp

³Department of Humane Informatics, Faculty of Letters, Otani University
Kamifusa-cho, Koyama, Kita-ku, Kyoto 603-8143, Japan
dyokozawa@gmail.com

⁴Department of Humane Informatics, Faculty of Letters, Otani University
Kamifusa-cho, Koyama, Kita-ku, Kyoto 603-8143, Japan
neko@res.otani.ac.jp

⁵Department of Clinical Laboratory and Transfusion, Hokkaido University Hospital
Kita 14, Nishi 5, Kita-ku, Sapporo 060-8648, Japan
macchan@med.hokudai.ac.jp

Abstract: In this research, needs of displaying genealogy with various layouts are described and those solutions using our “WHItEBasE” method are proposed. Previous WHItEBasE method can perfectly integrate each relation that includes a married couple and their children, and can display complex relations with segment intersections easily. However, it has had no functions for displaying some different genealogy layout styles. To cope with the difficulty, three new functions are added to the WHItEBasE method. First, even if there is a couple in a database, there is a requirement to display only a single parent. Genealogy with Direct Segments (DS) can be used for displaying connections that include a single parent and children directly. Second, if a lot of generations are displayed, the genealogical line becomes long and slender. They are often divided into plurality, and are written in parallel on paper media. Genealogy with Hooked Segments (HS) can be used for displaying genealogy in narrow area such as historical materials or publications. Third, there is a requirement to display both genealogy and its annotation data simultaneously in historical field. Annotation Data Always Displayed (ADAD) can be used for displaying annotation data around individuals. As a result, our improved software that can display DS, HS, and ADAD automatically and seamlessly by only mouse operation is presented.

Keywords: Family Trees, Pedigree, Remarriages, 2D Graphics

I. Introduction

A. Problem of Existing Genealogy Display Software

Nowadays, relations in family trees can automatically be displayed in almost all existing genealogy display software.

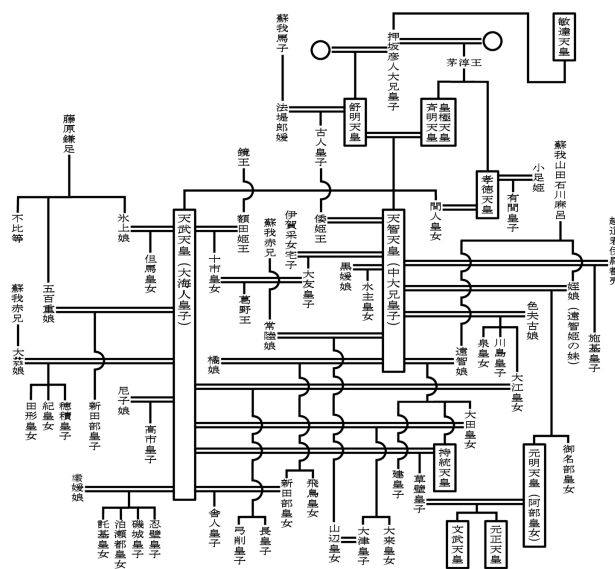


Figure 1: An example of genealogy with a lot of complex remarriages and segment intersections showing a family of old Japanese emperors by using KANJI and HIRAGANA that are Japanese characters (Modified from [1])

However, they cannot display complex relations perfectly such as shown in Fig. 1 [1] that includes a lot of remarriages and segment intersections on historical field. When complex relations are inputted in the existing software, one individual is often displayed in multiple places.

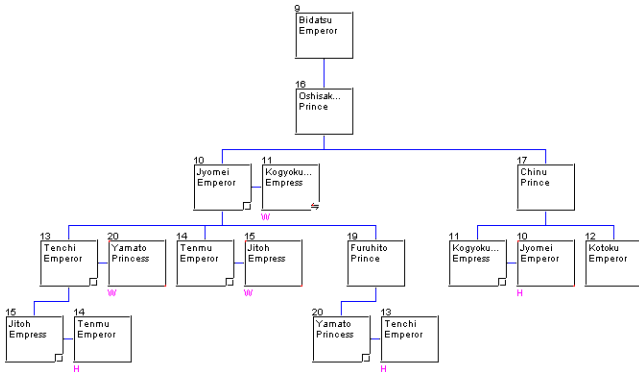


Figure 2: Alliance [2]

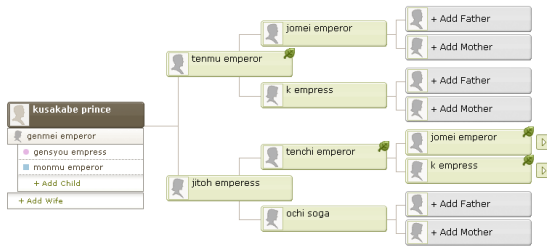


Figure 3: Ancestry [3]

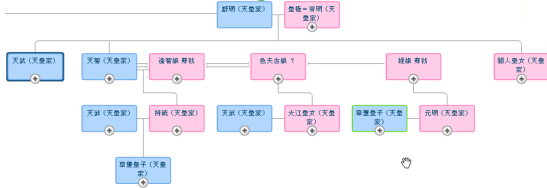


Figure 4: myHERITAGE [4]

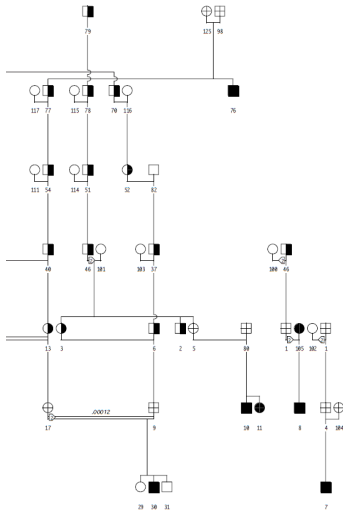


Figure 5: Pedree Draw [5]

For example, on Alliance [2] as shown in Fig. 2, the IDs: 10, 11, 13, 14, 15 and 20 are displayed twice respectively though each ID is the same individual. As a result, users must reconstruct the scattered individual placements into only one relation in their mind, though it is graphical display software. Similarly, a lot of existing genealogy display software [3]–[21] have the same problem as the following.

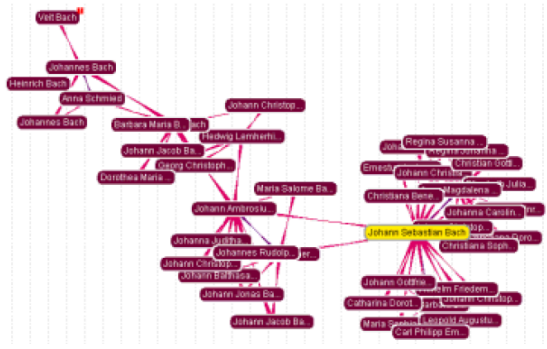


Figure 6: Topic Map [22]

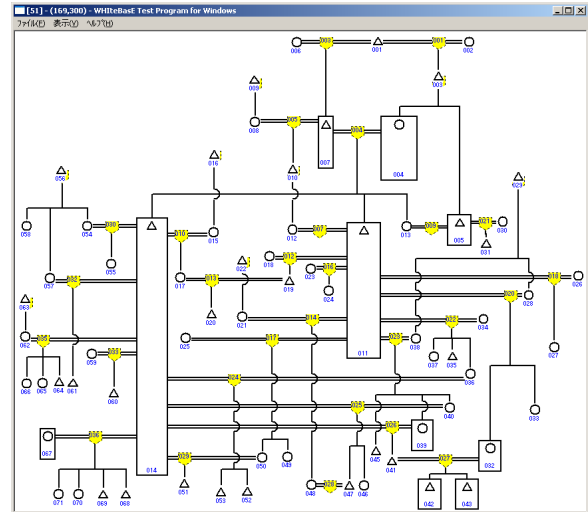


Figure 7: Our Previous Genealogy Display Software [24]

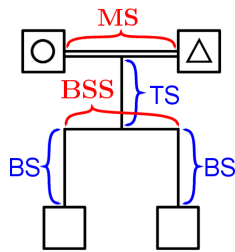


Figure 8: Segment Names in the regular layout style

Ancestry (Fig. 3 [3]) and myHERITAGE (Fig. 4 [4]), the well-known existing genealogy display software, have also no segment intersections and have the same problem too.

Pedree Draw (Fig. 5 [5],[6]) can display genealogy using segment intersections, and also there are some integrating programs for Pedree Draw[7],[8]. However, it has two problems. One is that the users cannot write generation in free positions because a generation grid is used. The other is that one individual cannot be located once because remarriages are displayed in two places.

On the other hand, 3D graphics, such as shown in Fig. 6, is rather more difficult to understand complex relations than 2D because many names and segments overlap [22].

GEDCOM [23], a de facto standard for recording genealogy data exchange format, is not enough to display complex relations because it considers no layout information. Details of others [9]–[21] have already been reported in [24].

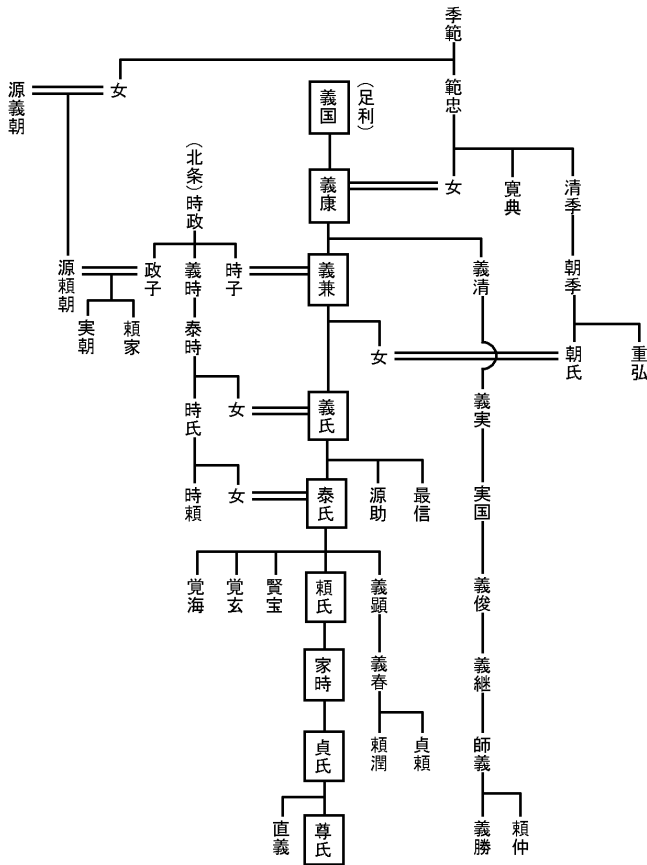


Figure 9: An Example of Genealogy with Direct Segments (DS) in the pamphlet of Kabasaki Hachimangu Shrine [25]

B. Our Previous Research

New kind of software has been constructed in our previous research so that it can display complex relations [24]. Our software uses an event oriented data management method, “WHIteBasE” (Widespread Hands to InTERconnect BASic Elements). It is a hidden node for integrating relations that include a married couple and their children. If WHIteBasE is used, the number of references becomes less than the existing methods and complex remarriages with segment intersections can be displayed perfectly (Fig. 7), where can realize an intuitive input and inspection such as map image display systems on the Internet.

In our previous genealogy display software, the regular Japanese layout style has been used (Fig. 8). It includes a double horizontal segment MS (Marriage Segment), a vertical segment TS (Trunk Segment), a horizontal segment BSS (Brothers and Sisters Segment), and a vertical segment BS (Branch Segment). The triangle ‘△’ denotes a male and the circle ‘○’ denotes a female that are a couple connected by using MS. Children are connected from the intermediate of MS by using TS, BSS and BS.

C. Displaying Genealogy with Various Layouts

There are mainly three more different but major layout styles on paper media as the following.

One is that only a single parent connects with children directly (Fig. 9). Using this style, the stream of main persons can be understood easily. It is called “Genealogy with Direct

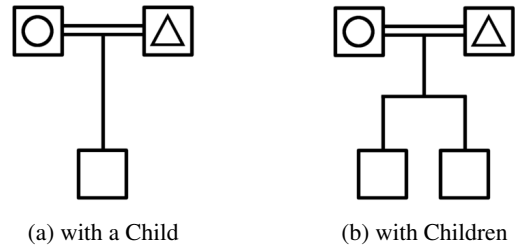


Figure 10: Regular Layout

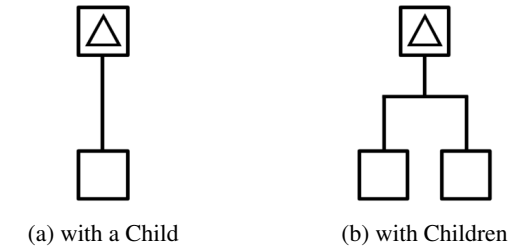


Figure 11: DS from a Single Parent

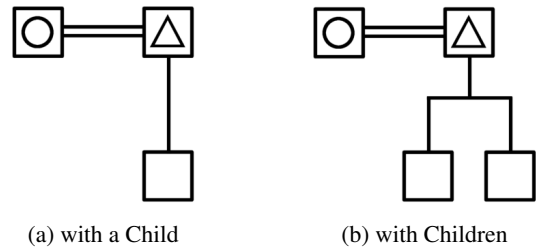


Figure 12: DS from parents

Segments (DS)” in this research. Connections from parents to children have three types as the following:

- (A) **Regular Layout:** One married couple connects with a child/children using TS generated from the intermediate of MS (Figs. 10(a),(b)).
- (B) **DS from a Single Parent:** Only a single parent connects with a child/children using TS directly without using MS (Figs. 11(a),(b)).
- (C) **DS from Parents:** Only a single parent that has connected with the other parent using MS connects with a child/children using TS directly (Figs. 12(a),(b)).

Another is that parents and their children are connected in parallel layout using hooked segments as shown in Fig. 13. Figs. 14(a)–(c) show the shapes of segments. Using hooked segment style, the long and slender layout can be displayed in narrow area easily. It is called “Genealogy with Hooked Segments (HS)” in this research. Connections from parents to children using HS have three types as the following:

- (a) **HS from MS:** One married couple connects with a child/children using TS generated from the intermediate of MS (Figs. 15(a),(b)).
- (b) **HS from a Single Parent:** Only a single parent connects with a child/children using TS directly without using MS (Figs. 16(a),(b)).
- (c) **HS from Parents:** Only a single parent that has connected with the other parent using MS connects with a child/children using TS directly (Figs. 17(a),(b)).

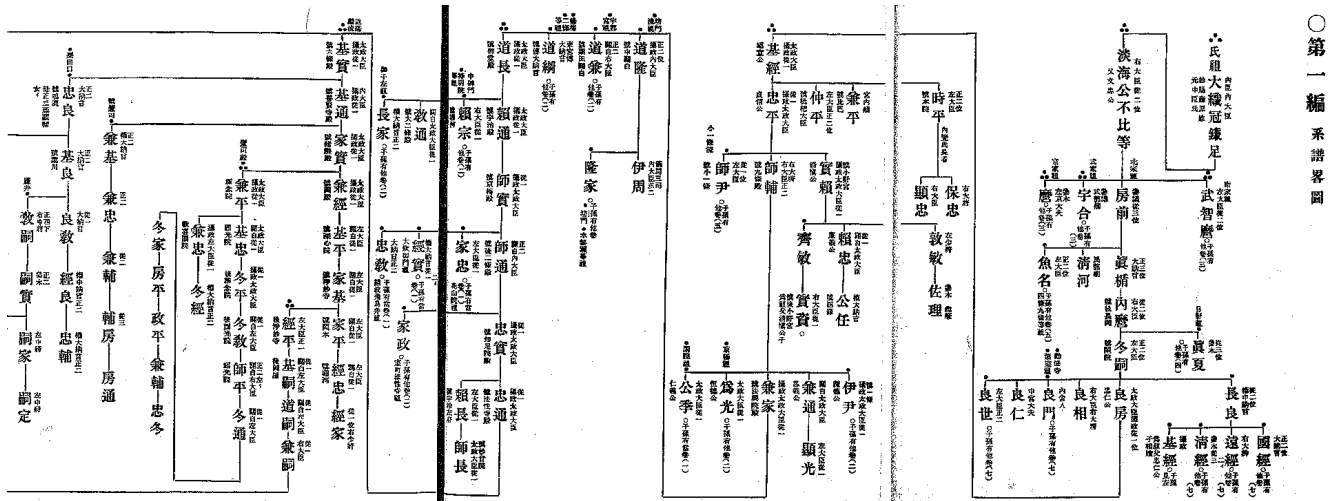


Figure 13: Genealogy with Hooked Segments (HS) [26]

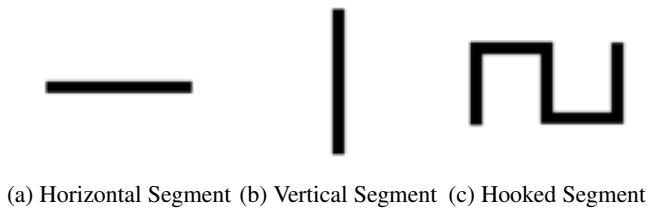


Figure 14: Shapes of Segments

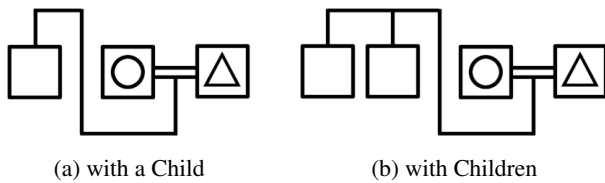


Figure 15: HS from MS

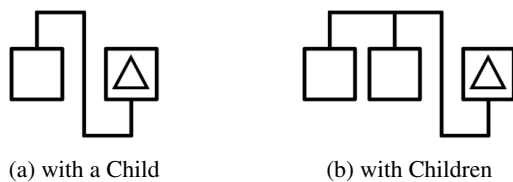


Figure 16: HS from a Single Parent

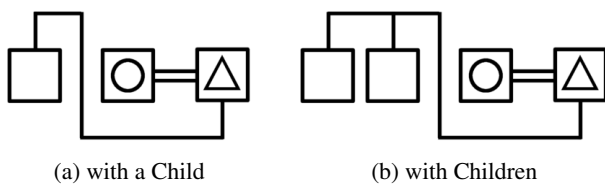


Figure 17: HS from Parents

The other is that there is a requirement to display both genealogy and its annotation data simultaneously in historical field. Various kinds of information is very important for understanding personalities. Fig. 18 shows that two individuals' names written by using the largest characters' font-size and their annotation data around their names are displayed simultaneously [26]. In general, annotation data is classified as the following:

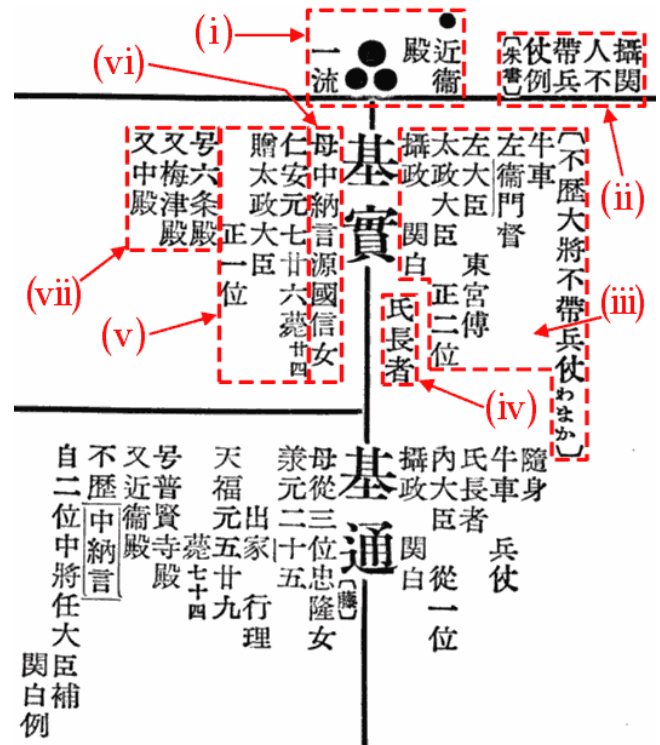


Figure 18: Annotation Data Always Displayed [26]

- (i) **Lineage:** Family Line Name, Identification Mark, etc. ((i) in Fig. 18)
- (ii) **Career:** Official Rank, Status, One's Age at Death, Brief Personal Record, etc. ((ii)–(v) in Fig. 18)
- (iii) **Family:** Mother's background, etc. ((vi) in Fig. 18)
- (iv) **Name:** Ordinary name, Alias, etc. ((vii) in Fig. 18)

In addition, Fig. 19 shows the annotation data using long text [27]. In this case, the main information contains not only person's name but also one's career text. It is very important to display them simultaneously. It is called "Annotation Data Always Displayed (ADAD)" in this research.

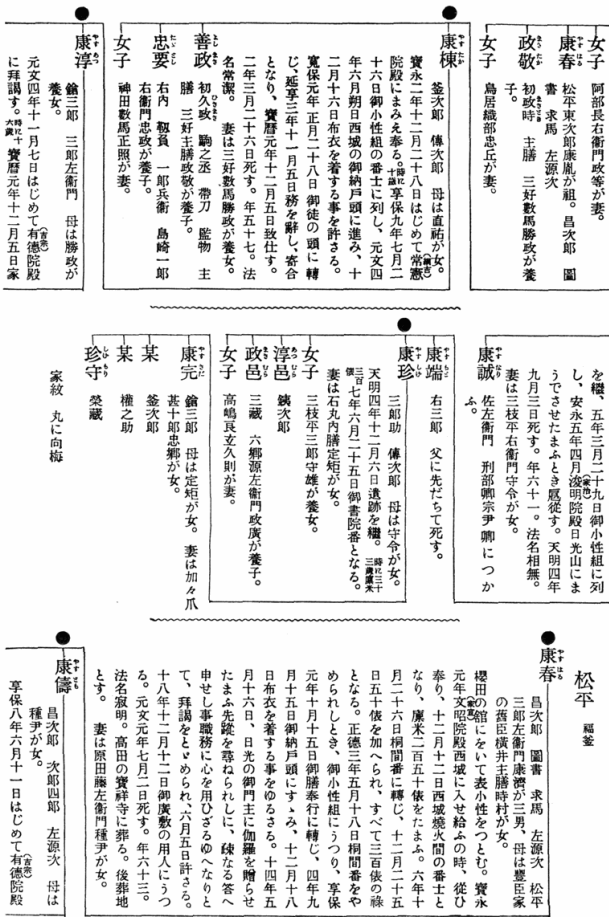
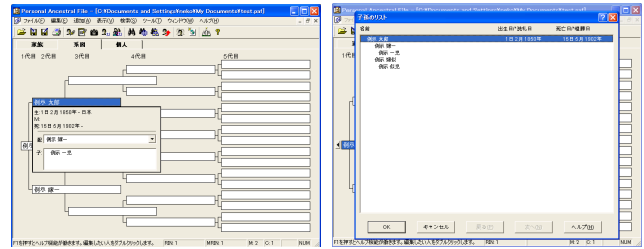
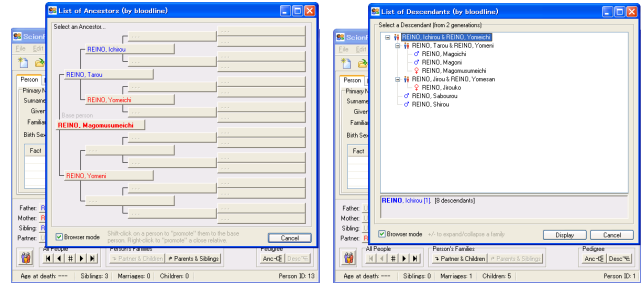


Figure 19: Annotation Data Always Displayed by using Long Texts [27]



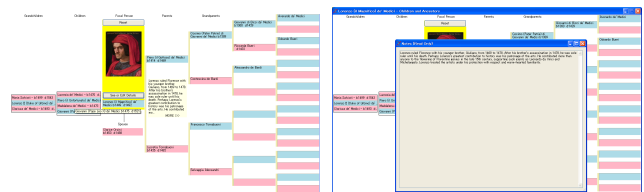
(a) Ascendants (b) Descendants

Figure 21: PAF (Personal Ancestral File)[17]



(a) Ascendants (b) Descendants

Figure 22: ScionPC (ScionPC Genealogical Management System)[18]



(a) Genealogy Display (b) Annotation Data

Figure 23: XY Family Tree[19]

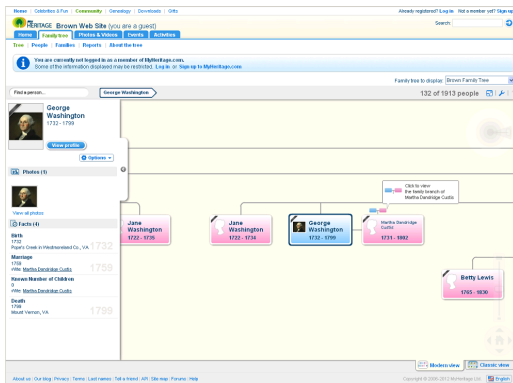


Figure 20: MyHeritage[4]

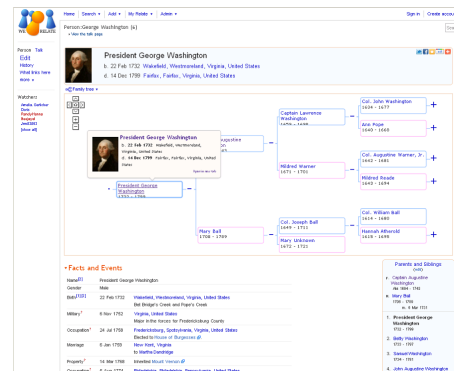


Figure 24: WeRelate[20]

These three kinds of layout styles, DS, HS and ADAD, cannot be displayed in the existing software, because almost all of them only display relations in rigid positions and use multi frames or windows for displaying annotation data separately. For example, MyHeritage (Fig. 20 [4]) cannot display generation in narrow area and has no annotation data display. PAF (Personal Ancestral File, Fig. 21 [17]) and ScionPC (ScionPC Genealogical Management System, Fig. 22 [18]) cannot display ascendants, descendants and all of annotation data simultaneously. XY Family Tree (Fig. 23 [19]) can only display limited generations and annotation data window hides the genealogy. WeRelate (Fig. 24 [20]) can only display

ascendants and annotation data window hides the genealogy. Others [5]–[16] has the similar problem. Therefore, it is necessary to construct new software.

D. The Purpose of Our Research

In this research, an upgrade, adding three kinds of layouts that consist of DS, HS and ADAD to our previous genealogy display software by using the WHiteBasE method, is proposed. Our improved software that can also display DS, HS and ADAD automatically and seamlessly by only mouse operation is presented.

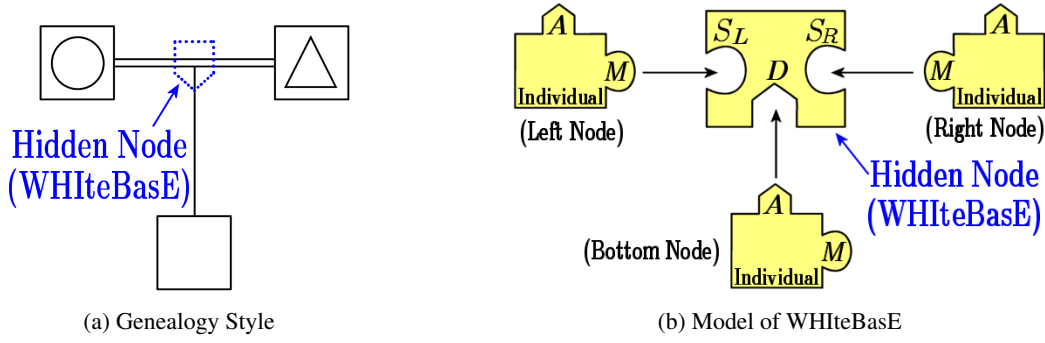


Figure 25: Connection model for a married couple and their child

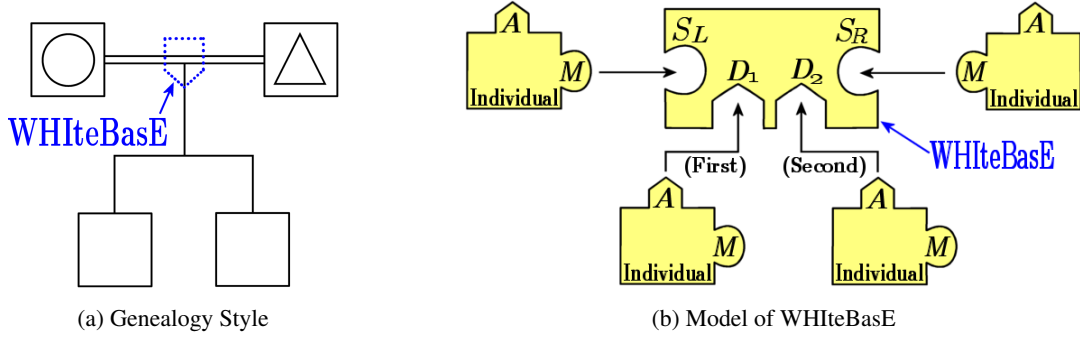


Figure 26: Connection model for a married couple and their children

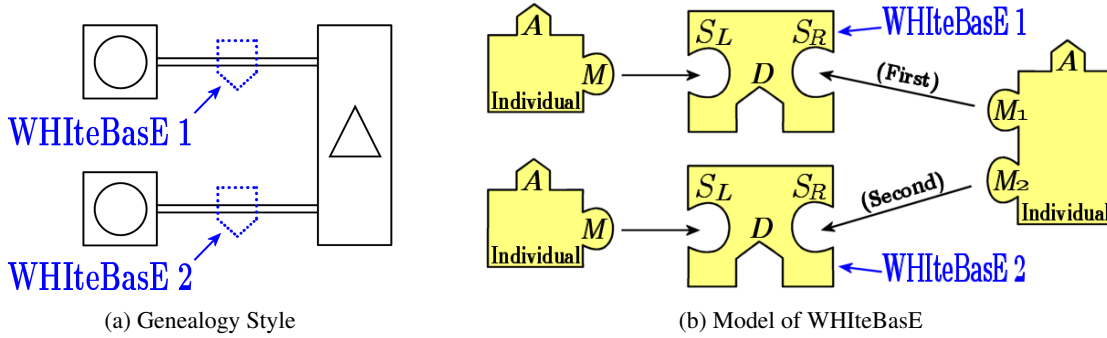


Figure 27: Connection model for remarriages

II. WHiteBasE

A. Model of WHiteBasE

In this section, the WHiteBasE model that is our previous proposal [24] is briefly introduced.

This is a kind of new data management method. A relation between a married couple and their child is managed as an event by using a Hidden Node, “WHiteBasE” as shown in Fig. 25(a). This connection model using the WHiteBasE is shown in Fig. 25(b). The WHiteBasE has three keyholes, S_L, S_R (Substance) and D (Descendant). Individuals have two keys, A (Ascendant) and M (Marriage). A can connect with D , and M can connect with S_L or S_R , where denote one family.

B. For Children and Remarriages

For children as shown in Fig. 26(a), D is extended in multiple keyholes D_j as shown in Fig. 26(b). For remarriages as shown in Fig. 27(a), M is extended in multiple keys M_k (Fig. 27(b)) and plural WHiteBasEs are used. That can define all of biological relations perfectly.

C. Definition of WHiteBasE

A set of W_i that defines WHiteBasEs and a set of I_j that defines Individual Nodes are represented by

$$W_i = \{S_L, S_R, D_j, \mathbf{Q}\} \quad \begin{cases} i = 0, 1, \dots, i_{max} \\ j = 0, 1, \dots, j_{max} \\ k = 0, 1, \dots, k_{max} \end{cases} \quad (1)$$

where i, j, k denote IDs on the data table respectively, $i_{max}, j_{max}, k_{max}$ are the maximum values, WHiteBasEs (W_i) are managed by data table separated from Individuals (I_j). \mathbf{Q} denotes a set of coordinate values of each position managed by a WHiteBasE (Fig. 28) and is represented by

$$\mathbf{Q} = \{q_b, q_L, q_R, q_d, q_{a_j}, q_{c_j}, q_{tl}, q_{rb}\} \quad (2)$$

where q_b denotes a WHiteBasE’s position, q_L, q_R denote the parents’ positions, q_d denotes a junction’s position between MS and TS, q_{c_j} denotes children’s positions, q_{a_j} denotes junctions’ positions between BSS and BS, q_{tl}, q_{rb} denote positions of top-left and bottom-right of all area managed by a WHiteBasE. \mathbf{Q} are written on the coordinate system Σ_{world} measured from the origin of the displaying area.

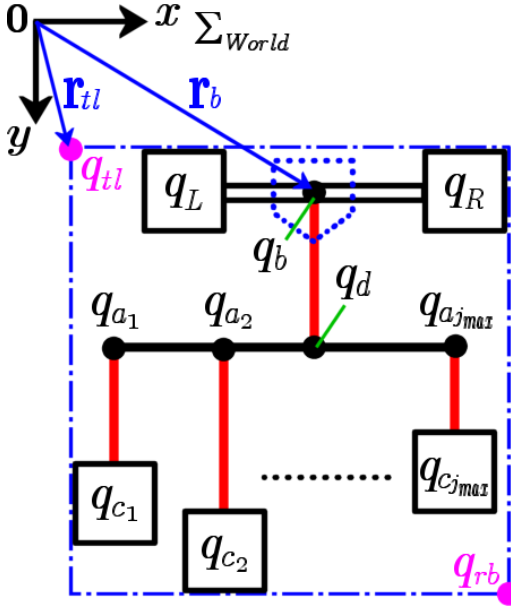


Figure 28: Coordinate System

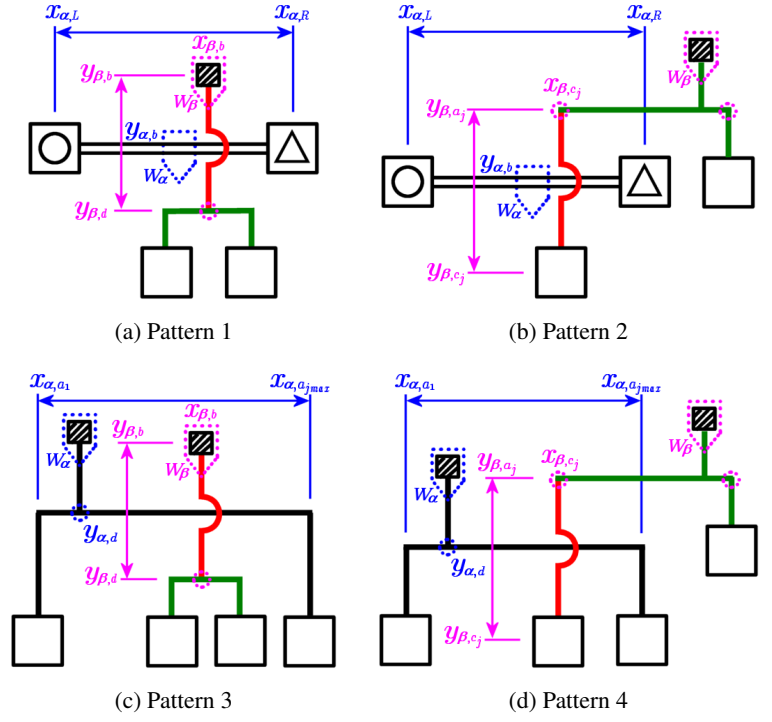


Figure 29: Search Algorithm of segment intersections

D. Search algorithm of Segment Intersections

Using segment intersections is necessary for displaying complex relations. If only one WHItEBasE is used, there is no segment intersections. On the other hand, if plural WHItEBasEs are used and horizontal segments (MS, BSS) and vertical segments (TS, BS) are displayed, the positions of segment intersections can be calculated by using only four patterns of line crossing on WHItEBasEs α and β as the following:

- MS of W_α and TS of W_β are crossing (Fig. 29(a))
If $x_{\alpha,L} < x_{\beta,b} < x_{\alpha,R}$ & $y_{\beta,b} < y_{\alpha,b} < y_{\beta,d}$,
the segment intersection is $(x_{\beta,b}, y_{\alpha,b})$.
- MS of W_α and BS of W_β are crossing (Fig. 29(b))
If $x_{\alpha,L} < x_{\beta,c_j} < x_{\alpha,R}$ & $y_{\beta,a_j} < y_{\alpha,b} < y_{\beta,c_j}$,
the segment intersection is $(x_{\beta,c_j}, y_{\alpha,b})$.
- BSS of W_α and TS of W_β are crossing (Fig. 29(c))
If $x_{\alpha,a_1} < x_{\beta,b} < x_{\alpha,a_{jmax}}$ & $y_{\beta,b} < y_{\alpha,d} < y_{\beta,d}$,
the segment intersection is $(x_{\beta,b}, y_{\alpha,d})$.
- BSS of W_α and BS of W_β are crossing (Fig. 29(d))
If $x_{\alpha,a_1} < x_{\beta,c_j} < x_{\alpha,a_{jmax}}$ & $y_{\beta,a_j} < y_{\alpha,d} < y_{\beta,c_j}$,
the segment intersection is $(x_{\beta,c_j}, y_{\alpha,d})$.

These four patterns are only calculated while only two management rectangle q_{tl}, q_{rb} of WHItEBasEs α and β are overlapped. Therefore, this algorithm is faster than the whole search algorithm for all horizontal and vertical segments.

E. Advantages of WHItEBasE

One of advantages using WHItEBasE is the decreased reference volume. Using the existing software, all of individuals connect with other individuals (Fig. 30(a)).

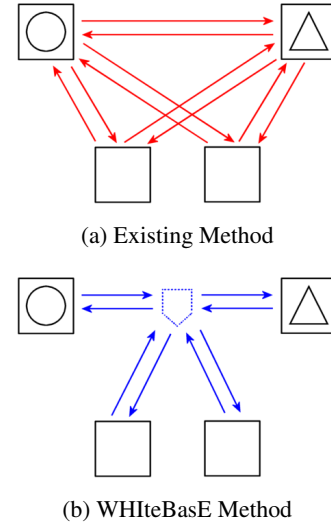


Figure 30: Number of references

On the other hand, using the WHItEBasE method, two reference links per a child decrease (Fig. 30(b)). Moreover, the user can understand the complex relations intuitively and can input and inspect them easily (Fig. 7).

III. Genealogy with Direct Segments

A. Direct Segments

Using Direct Segments (DS) is necessary for connecting parent(s) and their child/children directly as shown in Fig. 11 and Fig. 12. Fig. 31 shows the segment names for using DS. In this case, one parent connects with child/children directly using only TS instead of both MS and TS. If there is only a single parent, MS is omitted.

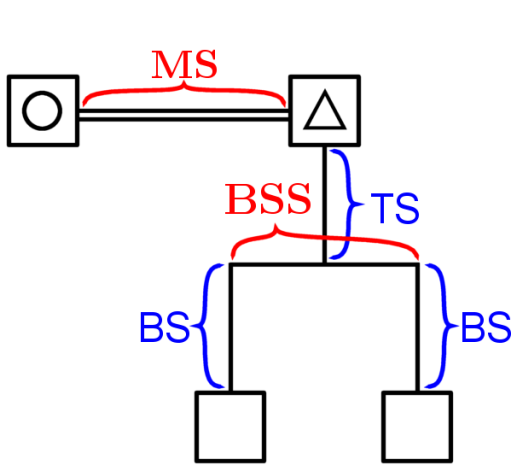


Figure 31: Segment Names for DS

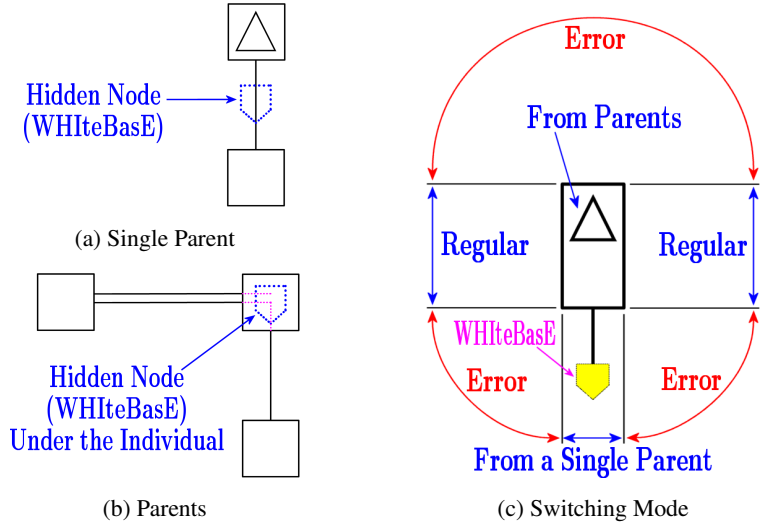


Figure 32: Genealogy with Direct Segments

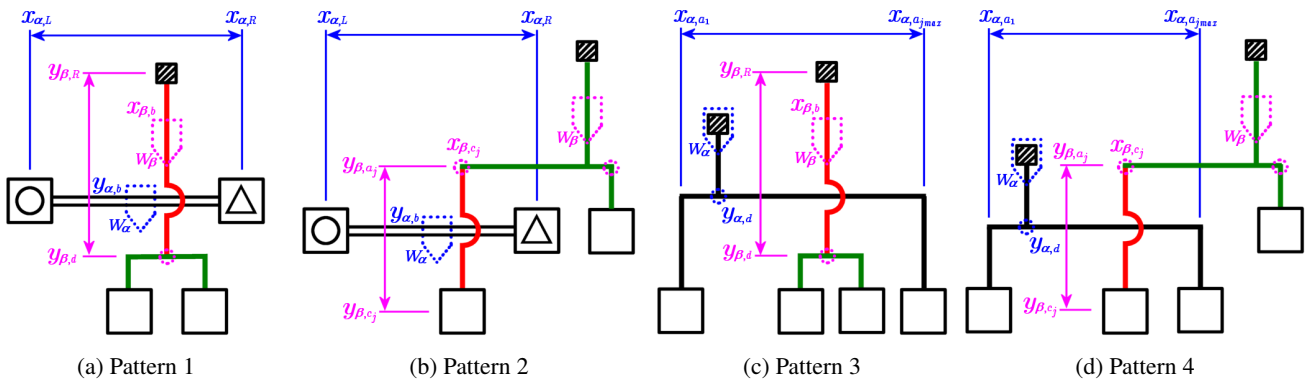


Figure 33: Search Algorithm for Segment Intersections Using DS

B. Automatic Switching Method

Switching method for genealogy with Direct Segments from regular layouts is introduced. The difference of Fig. 10, Fig. 11 and Fig. 12 is only layout styles. The relations between parents and children are the same. In Fig. 11, there must be a couple too because there are children. It is only omitting to display the '○'. On the other hand, positions of individuals and WHiteBasEs can be set freely by only mouse operations in our software. Therefore, the styles are automatically switched according to the positions without changing the connection model as the following:

- (A) **Regular Layout** is used while WHiteBasE lies at the junction between MS and TS (Fig. 25(a)).
- (B) **DS from a Single Parent** is used while WHiteBasE lies under a parent (Fig. 32(a)).
- (C) **DS from Parents** is used while WHiteBasE overlapped one of parents (Fig. 32(b)).

Fig. 32(c) shows each area of these styles (A)–(C).

C. Search algorithm of Segment Intersections using DS

The search method of segment intersections by using DS is almost the same as that of regular layout as shown in Fig. 29. The difference is only $y_{\beta,b}$ and $y_{\beta,R}$ in patterns 1 and 3 as the following:

- (a) MS of W_α and TS of W_β are crossing (Fig. 33(a))
If $x_{\alpha,L} < x_{\beta,b} < x_{\alpha,R}$ & $y_{\beta,R} < y_{\alpha,b} < y_{\beta,d}$,
the intersection is $(x_{\beta,b}, y_{\alpha,b})$.
- (b) MS of W_α and BS of W_β are crossing (Fig. 33(b))
If $x_{\alpha,L} < x_{\beta,c_j} < x_{\alpha,R}$ & $y_{\beta,a_j} < y_{\alpha,b} < y_{\beta,c_j}$,
the intersection is $(x_{\beta,c_j}, y_{\alpha,b})$.
- (c) BSS of W_α and TS of W_β are crossing (Fig. 33(c))
If $x_{\alpha,a_1} < x_{\beta,b} < x_{\alpha,a_{j_{max}}}$ & $y_{\beta,R} < y_{\alpha,d} < y_{\beta,d}$,
the intersection is $(x_{\beta,b}, y_{\alpha,d})$.
- (d) BSS of W_α and BS of W_β are crossing (Fig. 33(d))
If $x_{\alpha,a_1} < x_{\beta,c_j} < x_{\alpha,a_{j_{max}}}$ & $y_{\beta,a_j} < y_{\alpha,d} < y_{\beta,c_j}$,
the intersection is $(x_{\beta,c_j}, y_{\alpha,d})$.

Note that this new search algorithm can be used not only for the DS but also for the regular layout.

IV. Genealogy with Hooked Segments

A. Hooked Segments

Using Hooked segment (HS) is necessary for connecting parents and children in parallel layouts as shown in Figs. 15–17. Each style has the same HS shape (Fig. 14(c)). Therefore, only BSS is divided into BSS_l , BSS_v and BSS_h^* and the

*The subscripts of BSS_l , BSS_v and BSS_h mean Low, Vertical and High respectively since facing down of Y axis is positive.

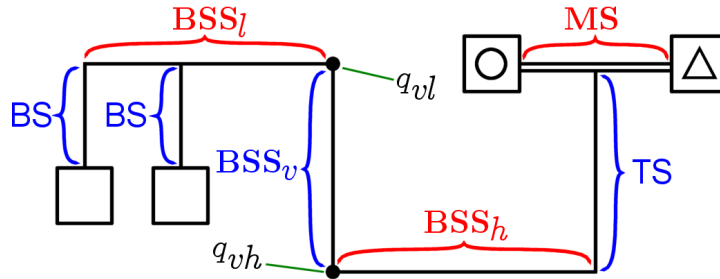


Figure. 34: Segment Name for Hooked Segments

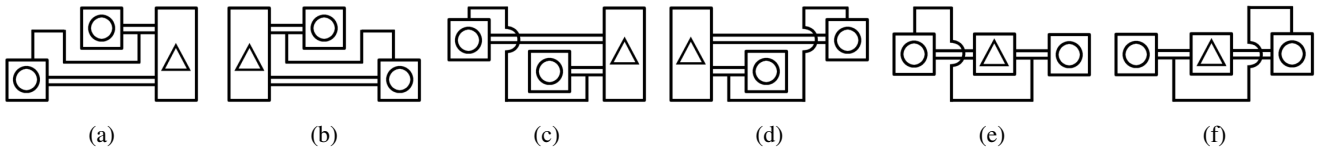


Figure. 35: Remarriage with two wives; one is a child of the other

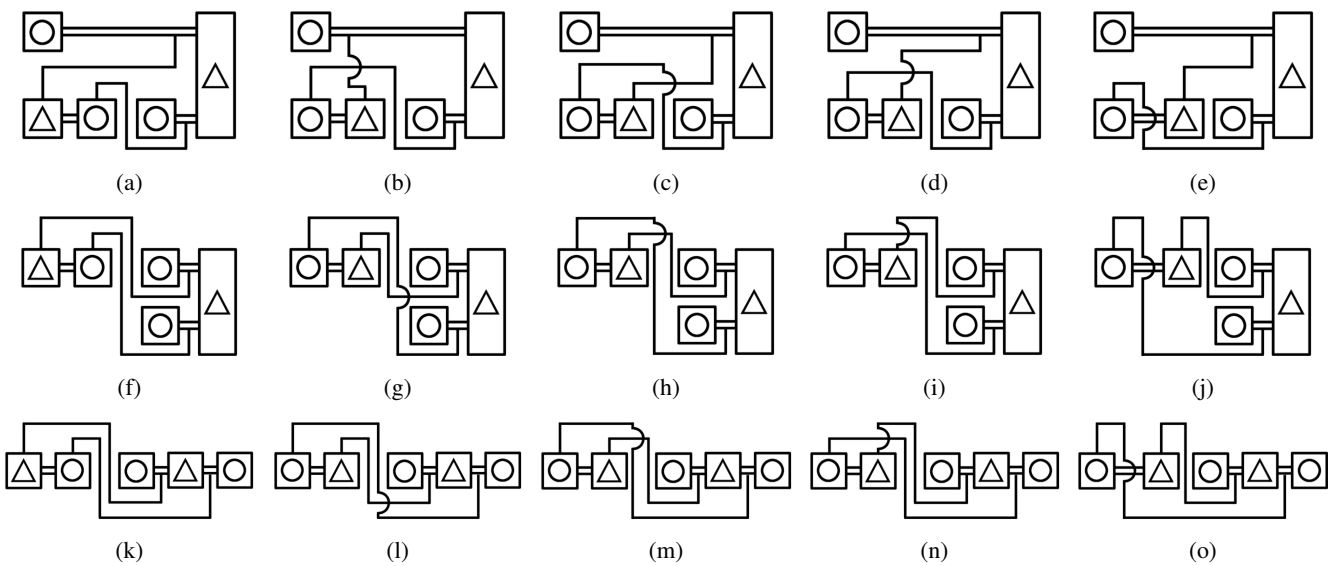


Figure. 36: Remarriage with two wives who are niece sisters

position q_{vl}, q_{vh} are added in Eq. (2) as shown in Fig. 34 represented by

$$Q = \{q_b, q_L, q_R, q_d, q_{a_j}, q_{c_j}, q_{vl}, q_{vh}, q_{tl}, q_{rb}\}. \quad (3)$$

The displaying rules of HS are defined in this research as the following:

- The HS shape is four times broken segment (Fig. 14(c)).
- One HS is only used for one family.
- The start of HS connects with MS in Regular layout or parents using DS.
- The end of HS connects with a child/children.
- Symmetric HS is provided (Only either can be used).
- HS is not used if there is no necessity layout.

B. Minimum Unit of Segment Intersections using HS

Where segment intersections using HS occur has been investigated in this research as the following:

A set of family

This is a kind of tree structure as shown in Figs. 15–17. In this case, there is no segment intersection even if HS is used.

Remarriage with two wives; one is a child of the other

Figs. 35(a)–(f) show this situation. It is a rare case, however, it has to enable to display biologically. (a) and (b) denote the samples by using HS for narrow display area. In these cases, there is no segment intersection. On the other hand, (c)–(f) denote the samples by using HS for parent-and-child layout is upside down. In these cases, there is one segment intersection respectively.

Remarriage with two wives who are niece sisters

Figs. 36(a)–(o) show this situation that all samples (a)–(o) are the same relation. (a)–(e) denote the samples using one HS. (f)–(j) denote the samples using two HSs. (k)–(o) denote the samples using two HSs that all individuals are located horizontally. In (a),(f),(k), there is no segment intersection. The other has one segment intersection respectively.

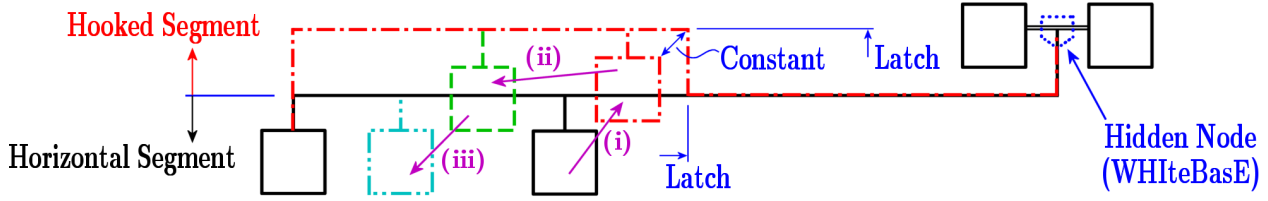


Figure 37: Switching method for regular layout and HS layout

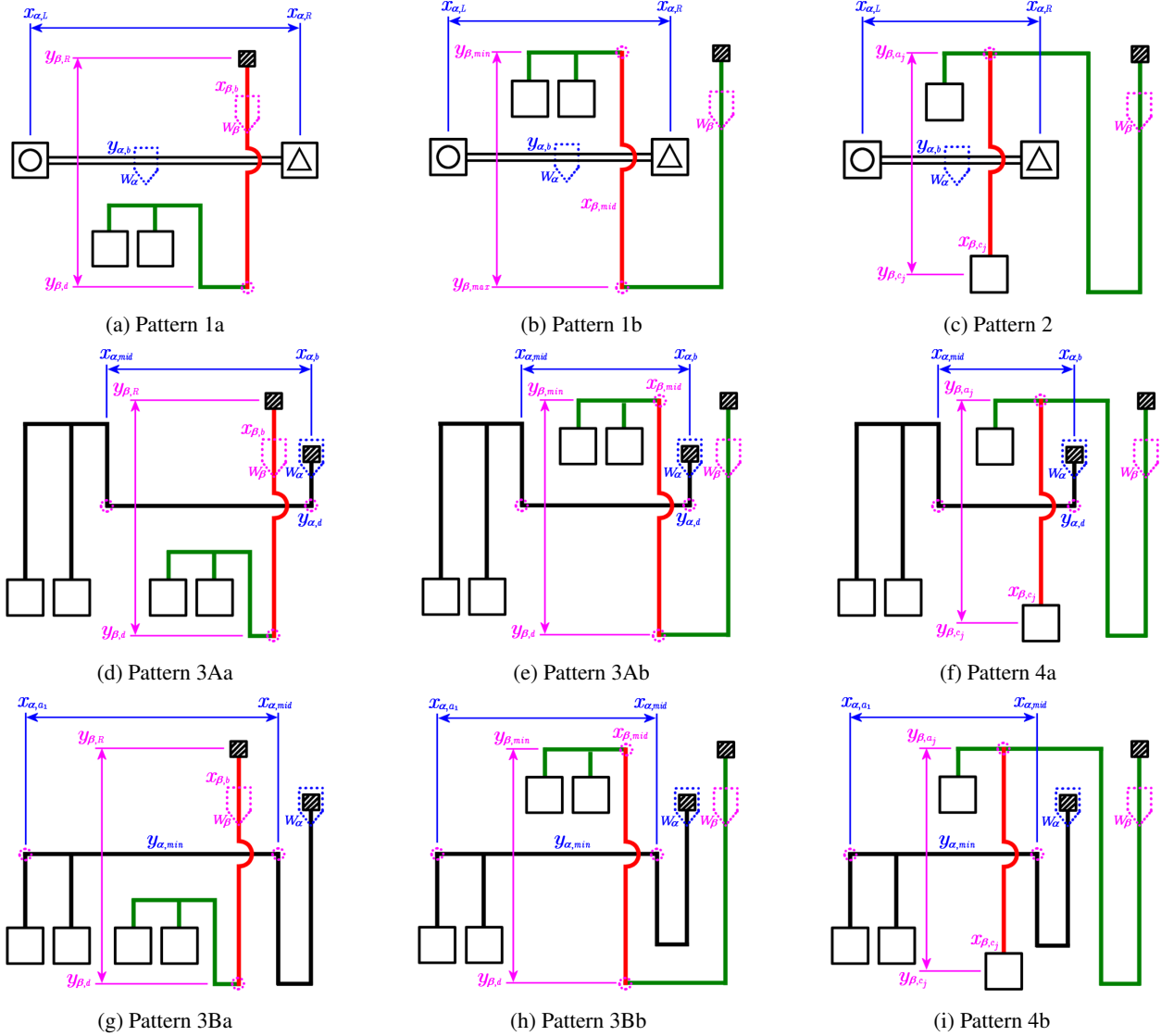


Figure 38: Search algorithm for Hooked Segments

These cases are called “Minimum Unit of Segment Intersections using HS” in this research. Existing the minimum unit shows the necessity of search method for segment intersections using HS. Extending Figs. 33(a)–(d) makes it.

C. Automatic Switching Method

The switching method between regular layout and HS is described. HS is only displayed while children are above the horizontal segment[†] BSS as shown in Fig. 37. Therefore, HS is automatically occurred when a child is moved to above BSS by mouse operation as shown in the arrow (i) in Fig. 37.

[†]To display relations between parents and children vertically is assumed.

The distance between q_{vl} and a child is kept constantly in the direction to the WHiteBasE and it is latched in the direction of the upper right. That is, q_{vl} does not move even if a child is moved in the direction of the lower left as shown in the arrow (ii) in Fig. 37. HS disappears and the regular layout is appeared automatically when a child is moved to lower BSS as shown in the arrow (iii) in Fig. 37. If children are above BSS, the Lowest position of children is used for q_{vl} .

D. Search Algorithm of Segment Intersections Using HS

In this case, there are both three kinds of horizontal segments and three kinds of vertical segments. Therefore, the algorithm is classified by using nine patterns as the following:

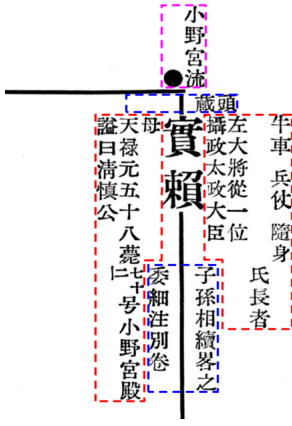


Figure 39: Sample of ADAD [26]

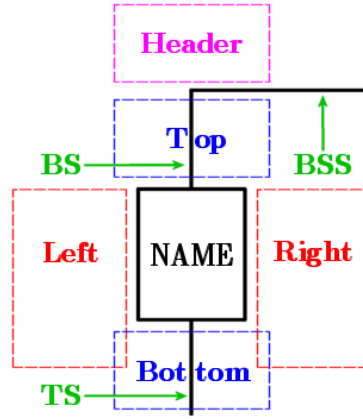


Figure 40: ADAD text Areas

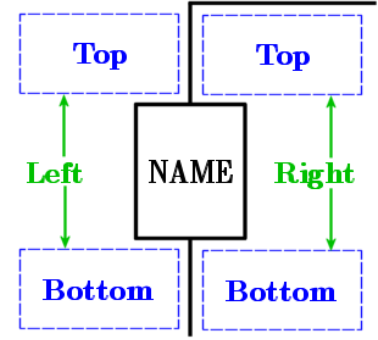


Figure 41: Left or Right Side Layouts

- MS of W_α and TS of W_β are crossing (Fig. 38(a))
If $x_{\alpha,L} < x_{\beta,b} < x_{\alpha,R}$ & $y_{\beta,R} < y_{\alpha,b} < y_{\beta,d}$,
the intersection is $(x_{\beta,b}, y_{\alpha,b})$.
- MS of W_α and BSS_v of W_β are crossing (Fig. 38(b))
If $x_{\alpha,L} < x_{\beta,mid} < x_{\alpha,R}$ & $y_{\beta,min} < y_{\alpha,b} < y_{\beta,max}$,
the intersection is $(x_{\beta,mid}, y_{\alpha,b})$.
- MS of W_α and BS of W_β are crossing (Fig. 38(c))
If $x_{\alpha,L} < x_{\beta,c_j} < x_{\alpha,R}$ & $y_{\beta,a_j} < y_{\alpha,b} < y_{\beta,c_j}$,
the intersection is $(x_{\beta,c_j}, y_{\alpha,b})$.
- BSS_h of W_α and TS of W_β are crossing (Fig. 38(d))
If $x_{\alpha,mid} < x_{\beta,b} < x_{\alpha,b}$ & $y_{\beta,R} < y_{\alpha,d} < y_{\beta,d}$,
the intersection is $(x_{\beta,b}, y_{\alpha,d})$.
- BSS_h of W_α and BSS_v of W_β are crossing (Fig. 38(e))
If $x_{\alpha,mid} < x_{\beta,mid} < x_{\alpha,b}$ & $y_{\beta,min} < y_{\alpha,d} < y_{\beta,max}$,
the intersection is $(x_{\beta,mid}, y_{\alpha,d})$.
- BSS_h of W_α and BS of W_β are crossing (Fig. 38(f))
If $x_{\alpha,mid} < x_{\beta,c_j} < x_{\alpha,b}$ & $y_{\beta,a_j} < y_{\alpha,d} < y_{\beta,c_j}$,
the intersection is $(x_{\beta,c_j}, y_{\alpha,d})$.
- BSS_l of W_α and TS of W_β are crossing (Fig. 38(g))
If $x_{\alpha,a_1} < x_{\beta,b} < x_{\alpha,mid}$ & $y_{\beta,R} < y_{\alpha,min} < y_{\beta,d}$,
the intersection is $(x_{\beta,b}, y_{\alpha,min})$.
- BSS_l of W_α and BSS_v of W_β are crossing (Fig. 38(h))
If $x_{\alpha,a_1} < x_{\beta,mid} < x_{\alpha,mid}$ & $y_{\beta,min} < y_{\alpha,min} < y_{\beta,d}$,
the intersection is $(x_{\beta,mid}, y_{\alpha,min})$.
- BSS_l of W_α and BS of W_β are crossing (Fig. 38(i))
If $x_{\alpha,a_1} < x_{\beta,c_j} < x_{\alpha,mid}$ & $y_{\beta,a_j} < y_{\alpha,min} < y_{\beta,c_j}$,
the intersection is $(x_{\beta,c_j}, y_{\alpha,min})$.

In addition, these patterns follow the pattern names as shown in Figs. 33(a)–(d). Note that this new search algorithm can be used not only for the HS but also for the regular layout and DS. Only this algorithm is used in this research.

V. Annotation Data Always Displayed

A. Annotation Data

Typical annotation data is found around individual's name as shown in Fig. 39. It is clear that quarter size characters of name characters are used for showing annotation data in historical materials. The annotation texts do not overlap with segments. Note that the name and annotation data are shown simultaneously.

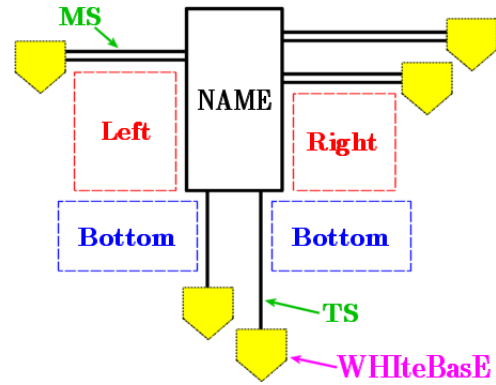


Figure 42: Avoiding Segments

B. Text Areas Setting

Considering the samples as shown in Figs. 18–19 and Fig. 39, the ADAD text areas as shown in Fig. 40 are classified as the following:

- Header:** It is located at upper side of the BSS along the center bottom margin.
- Left:** It is located at left side of the individual's name along the right top margin.
- Right:** It is located at right side of the individual's name along the left top margin.
- Top:** It is located at upper side of the individual's name along the bottom margin.
- Bottom:** It is located at under side of the individual's name along the top margin.

In Top and Bottom, the segments go through the text. Therefore, there have to be two more layouts; left side and right side of the BS or TS as shown in Fig. 41. On the other hand, if the individual has a lot of relations of remarriages, a lot of MS and TS connect with the individual. Therefore, the left and right texts are avoided a lot of MS and TS.

These five areas are provided for writing text input in this research. All of ADAD texts are kept in the individual data. When the position of individual are moved, the ADAD texts are moved together automatically.

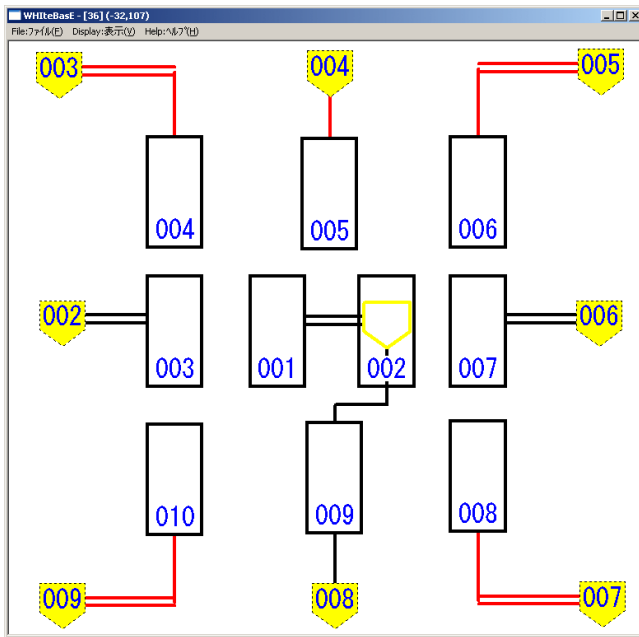


Figure 43: Sample of DS

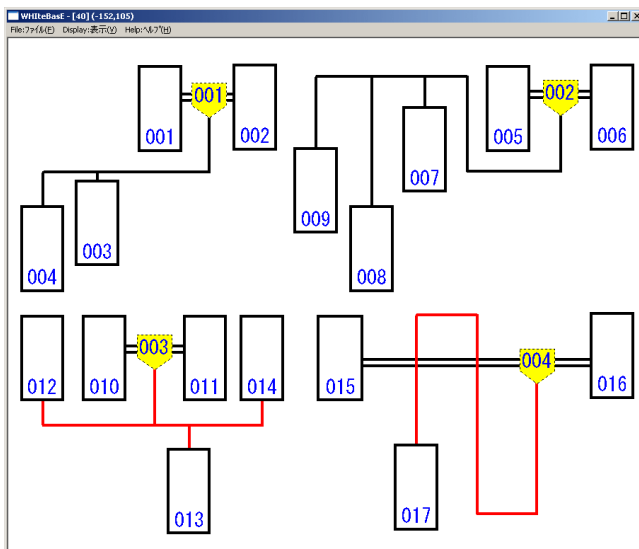


Figure 44: Sample of HS

VI. Demonstration of Our New Software

A. Displaying DS

Fig. 43 shows the sample of DS display in our software. In this case, there are 10 individuals and 9 WHItEBasEs.

WHItEBasEs 002 and 006 connect with individuals 003 and 007 respectively as marriages using the regular layout. WHItEBasE 008 connects with individual 009 as a marriage using DS from a single parent. WHItEBasE 001, that is under the individual 002, connects with individual 001 as a marriage using MS of DS from parents, and also connects with individual 009 as a child.

The others with red segments denote the error connections that are not defined in the given layout styles. These layouts are automatically and seamlessly changed according to the positions of both individuals and WHItEBasEs by only mouse operations.

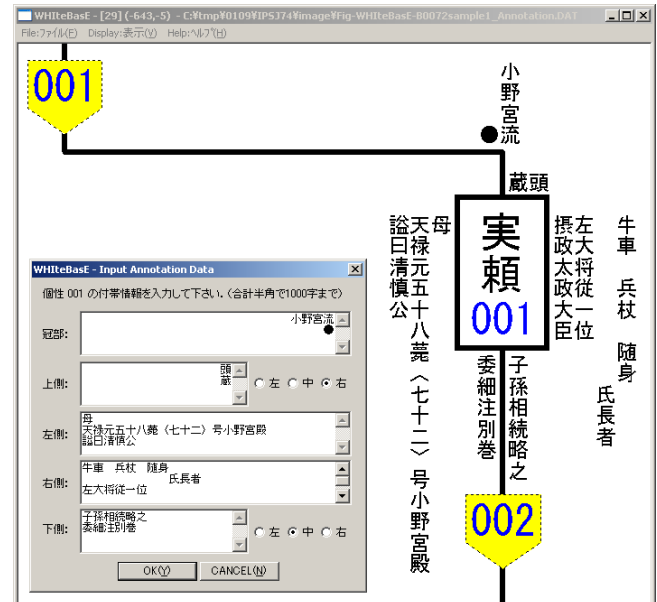


Figure 45: Sample of ADAD

B. Displaying HS

Fig. 44 shows the sample of HS display in our software. In this case, there are 17 individuals and 4 WHItEBasEs.

A family of WHItEBasE 001 that consists of individuals 001–004 is the regular layout, because all children are located under the BSS.

On the other hand, a family of WHItEBasE 002 that consists of individuals 005–009 is the HS layout, because one of individuals, 007, is located upper the BSS. Switching from the regular layout to the HS layout is occurred by only positions of children whether upper or under of the BSS. If all children 007–009 move to the position under the BSS, WHItEBasE 002 does not have the HS.

A family of WHItEBasE 003 that consists of individuals 010–014 is the error layout of HS, because that are not defined. In this research, symmetric HS is provided but only ether can be used. Therefore, if children are located in the left and right of the WHItEBasE separately, the HS becomes red segments. In addition, a family of WHItEBasE 004 that consists of individuals 015–017 is also the error layout of HS. Using HS can draw the BSS upper MS. Therefore, the HS becomes red segments too.

C. Displaying ADAD and its dialog

Fig. 45 shows the sample of ADAD in our software. In this case, there are one individual and two WHItEBasEs with the input dialog for ADAD.

The ascendant of individual 001 is WHItEBasE 001. The descendant of individual 001 is WHItEBasE 002. Individual 001 has a lot of annotation data that includes Head, Top, Left, Right, and Bottom. Annotation texts can be inputted by using the input dialog of each individual.

In this case, the position of Top is set to the right, and the position of Bottom is set to the center. Therefore, the Top and bottom texts are located at the left-top and right-bottom of the individual respectively. Note that the TS of WHItEBasE 002 goes through the center of Bottom text.

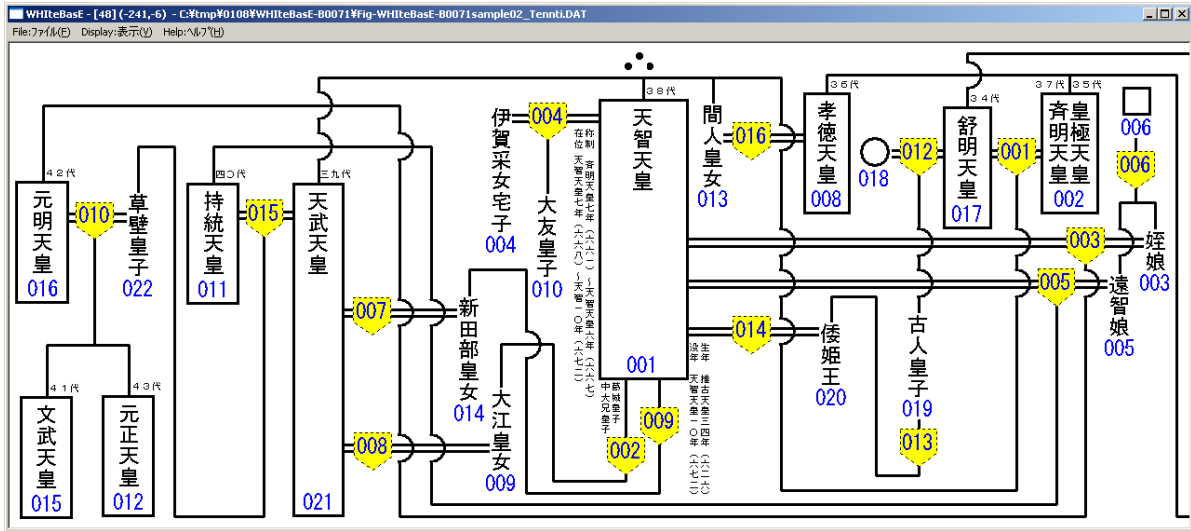


Figure. 46: Sample of genealogy in Japanese Using Our New Genealogy Display Software

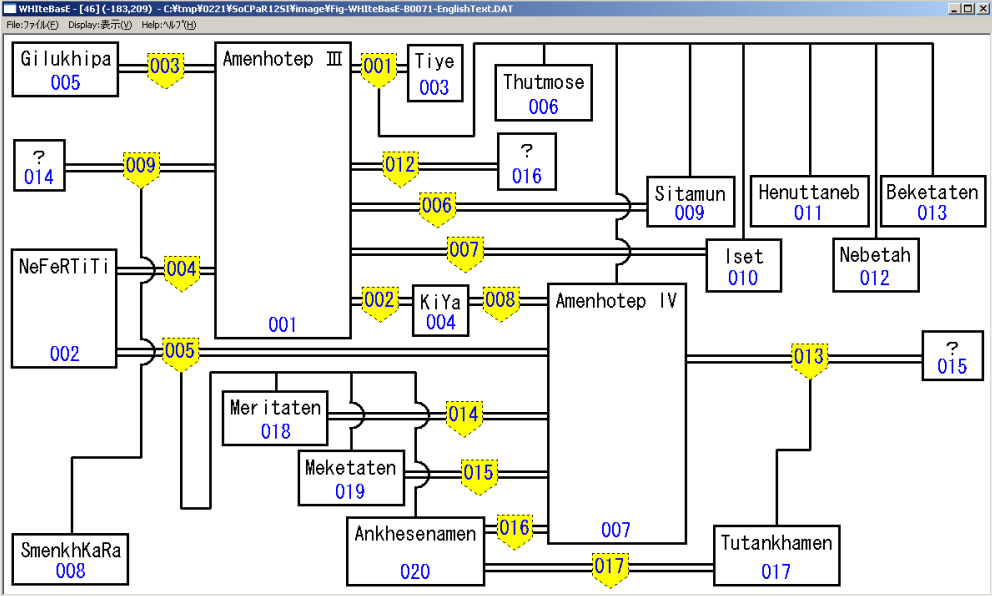


Figure. 47: Sample of genealogy in English Using Our New Genealogy Display Software

If the dialog is closed, the annotation data is always displayed around the individual’s text box. Therefore, if the individual 001 is moved, its annotation data is automatically moved together. As a result, all annotation data can be read continuously.

D. Sample Display

Fig. 46 shows the sample of genealogy in Japanese using our new genealogy display software that can display DS, HS with segment intersections and ADAD.

The individual 001 who is the main person in this example connects with the WHiteBasE 001 as his ascendant, and six WHiteBasEs; 003, 005, 014, 009, 002, and 004 as remarriages. It means that the individual 001 has six wives. Even if some are relatives of him, the complex relations can be understood easily. The numbers of Top annotation data can indicate what generation. Header, Left, Right and Bottom of the individual 001’s annotation data can indicate his person-

ality. As a result, using DS, HS and ADAD, genealogy in narrow area can be displayed.

In addition, Fig. 47 shows the sample of genealogy in English. Note that Horizontal texts can be inputted.

VII. Conclusion

In this research, Genealogy with DS, HS and ADAD could be constructed by using the WHiteBasE method. Even if DS and HS are used, segment intersections could be displayed automatically and seamlessly by only mouse operation. As a result, a lot of individuals with complex relations could be displayed in narrow area using one window. Even if the client area is filled, scrolling mouse wheel, the zoom rate can be changed and displaying area beyond the window size can be used. Using our method, genealogy required in a favorite rectangle size can be displayed easily.

Our future research will be to construct adopted children, automated layouts, generation search, etc.

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Authors Biographies

Seiji Sugiyama has been an assistant professor at the College of Information Science and Engineering, Ritsumeikan University, Japan, since 2009. He received his B. Eng., his M. Eng. and his Ph.D. Eng. from Ritsumeikan University, in 1992, 1997 and 2000, respectively. He was a part-time lecturer at both Ritsumeikan University, during 2001–2004 and 2007, and Otani University, Japan, in 2001 and 2002, respectively. He was a lecturer at Otani University, during 2003–2006. And he was a research associate at Ritsumeikan University, in 2008. He was awarded a research prize “Yamashita-kinen” for a paper of the MaSSText from the Information Processing Society of Japan, in 2009. His research interests include interface designing and robotics.

Atsushi Ikuta is currently a part-time lecturer at Otani University and Ryukoku University, Japan. He received his B.A. and M.A. degrees at Kyoto Prefectural University, Japan, in 1997 and 1999, respectively. His research interests include historical science and interface designing.

Daisuke Yokozawa is currently a part-time lecturer at Otani University and Ryukoku University, Japan. He received his B.A. and M.A. degrees at Ryukoku University, Japan, in 1997 and 2000, respectively. His research interests include historical science and interface designing.

Miyuki Shibata is currently an associate professor at the Department of Humane Informatics, Faculty of Letters, Otani University, Japan. She received her B.A. at Kyoto Notre Dame University, Japan, in 1987. Her research interests include interface designing and intellectual property law.

Tohru Matsuura is currently a clinical professor and deputy director at Hokkaido University Hospital, Japan. He received M.D. from Hokkaido University School of Medicine, Japan, in 1979. His major has been clinical neurology, electrophysiology and medical informatics.