BOADICEA

RISK MODELLING SOFTWARE ON THE WORLD WIDE WEB
Software and Data Processing Agreement

NOTICE TO USER: PLEASE READ THIS SOFTWARE AGREEMENT [‘THE AGREEMENT’] CAREFULLY. BY DOWNLOADING AND /OR USING ALL OR ANY PORTION OF THE SOFTWARE YOU INDICATE YOUR ACCEPTANCE OF THE FOLLOWING TERMS FROM ‘THE UNIVERSITY’. YOU AGREE TO BE BOUND BY ALL TERMS AND CONDITIONS OF THIS AGREEMENT. YOU AGREE THAT IT IS ENFORCEABLE AS IF IT WERE A WRITTEN NEGOTIATED AGREEMENT SIGNED BY YOU.

The Agreement is between
The Chancellor, Masters and Scholars of the University of Cambridge (the ‘University’) and you the Licensee (either an individual or a legal entity).

The Authors are employees of the University’s Department of Public Health and Primary Care who have written a Web based computer program known as BOADICEA (‘the Software’) which is available via the World Wide Web https://pluto.srl.cam.ac.uk/cgi-bin/bd4/v4/bd.cgi

1. Definitions
‘Authors’ means Dr Alex Cunningham, Dr Antonis Antoniou, Dr Andrew Lee and Dr Nasim Mavaddat
‘Data’ means Licensee’s anonymised patient Data,
‘Term’ means unlimited duration subject to clause 4,
‘Purpose’ means the use of the Software to store and process Data, and to calculate mutation carrier probabilities and cancer risks,
‘Use or Using’ means to access, use, run or otherwise benefit from using the Software during the Term.

2. The Licensee wishes to acquire a licence to Use the Software and the University has agreed to do so and hereby grants to Licensee a non exclusive, non transferable, non assignable right to Use the Software during the Term.

On (indicating) acceptance of the terms and conditions (below), the Licensee will be given a username and password (‘the Login’) to the Software. The purpose of acquiring the Login is to give the Licensee access to the Software for the Purpose’.

Terms and Conditions for Release of Software

3 Ownership and Use of Software

3.1 The University shall have sole and exclusive ownership of all right, title and interest in and to the Software, including all copyright and any other intellectual property rights therein. This Agreement grants a limited licence to Use the Software and shall not be construed to convey title to or ownership of the Software to Licensee. All rights in and to the Software not expressly granted to Licensee are reserved by the University. The Software is protected by copyright, trademark, patent and or other intellectual property rights and laws. Any unauthorised Use of the Software may violate such laws and these terms of Use.

3.2 Ownership of all clinical data and information stored and processed Using the Software shall remain with and vest in the Licensee. Licensee shall be responsible for all data and information collected, collated and processed using the Software and shall be responsible for compliance with all and any statutory obligations relating thereto.

3.3 The Licensee shall use the Software only for the Purpose. Licensee shall not modify, adapt, disassemble, reverse engineer, decompile, translate or otherwise attempt to discover the source code of the Software, or write or develop any derivative software or any other software program based on the Software or confidential information provided by the University or permit any of these things to happen except as allowed by applicable law.
3.4 The Licensee shall not distribute, sub-license, sell, lend, provide any commercial or fee paying services to third parties, provide access (including without limitation via a public-access internet site) to the whole or any part of the Software or use it to process the work of any third party.

3.5 The Licensee shall keep the Login secure. The Licensee shall not supply the Login to any other party. The Licensee shall refer to the University any request for the Software. The Licensee shall supervise the use of the Software, control access to it and keep it secure. The Licensee remains fully responsible at all times for all acts and omissions of anyone it allows to use the Software and for ensuring such person understands and observes this licence. This responsibility includes without limitation any employee, agent, students, consultant, independent contractor or visiting researcher.

4. Clinical Data Security

4.1 In order to Use the Software, Licensee will submit its clinical Data to the Software for processing.

4.2 The Software is Web server based and is run on the University's computer network. The University has provided this document ('the Boadicea Manual') detailing instructions for effective use of the Software. Licensee shall comply with all instructions and guidelines in the Boadicea Manual to ensure effective operation of the Software and appropriate results from data processed. The University shall not be liable for any faults, defects, errors or damage or loss to Licensee if the Licensee fails to comply with all instructions and guidelines in the Boadicea Manual.

4.3 The University has taken reasonable precautions to ensure that appropriate security measures are in place for hosting this service. The Software validates all incoming Data/information and all Data transmissions are encrypted.

4.4 Whilst steps have been taken by the University to ensure that the Web server and the Data held on it are secure, the University cannot guarantee that the Web server will not be subject to malicious attacks, and cannot therefore be held responsible or liable for the effects to Licensee in the event of any such attack occurring in the future.

5 Termination

The University may terminate this Agreement if Licensee fails to comply with the terms and conditions of this Agreement. Upon termination of this Agreement the Login will become invalid. The obligations of both parties in clauses 2 and 4 shall survive termination of this Agreement for whatever cause.

6 Disclaimer and Limitation of Liability

6.1 The Software is provided on an 'As Is' basis, without warranty of any kind. The University makes no representations and extends no warranties of any kind, either expressed or implied as to the accuracy, efficacy, completeness, capabilities or safety of the Software or of any information supplied therewith. The University gives no express or implied warranties of merchantability or fitness for a particular purpose, or that the use of the material will not infringe any patent, copyright, trademark, or other proprietary rights.

6.2 Limitation of Liability

Errors can occur in the use of the Software and the University offers no assurance that they will be corrected. No liability will be accepted in respect of software defects, service interruptions, nor in the event of any viruses, worms Trojan horse and or other harmful components being present in or transmitted by our systems and networks.

6.3 In no event shall the University be liable for any use by the Licensee (or its employees or agents) of the Software licensed under this Agreement for any of the following losses or damages (whether such losses be foreseen, foreseeable, known or otherwise): loss of data, revenue, anticipated profits, business, opportunity, goodwill or injury to reputation, loss suffered by third parties, any direct, indirect, special, incidental or consequential loss or damages arising out of the use of the Software. Licensee agrees to indemnify and hold harmless the University for any loss, claim, damage or liability, of whatsoever kind or nature, due to or arising from the use of the Software by the Licensee, except when caused by the gross negligence or wilful misconduct of the University.
6.4 Save as stated in clause 4, all provisions relating to ownership, exclusion of warranty and limitation of liability shall survive the termination or early expiry of this Agreement.

7 Privacy Policy

Registration follows acceptance of these terms and conditions. When you register, your personal details will be collected and held securely in accordance with the Data Protection Act 1998. The information we collect will be used to enable the University to grant the Licensee access to the Software during the period agreed under this licence and not for any other purposes. The University will not pass on your details to any third party.

8. General

8.1 Dispute Resolution: If the parties are unable to settle any dispute by negotiation within twenty-eight (28) days the parties will attempt to settle it by mediation in accordance with the Centre for Effective Dispute Resolution (CEDR) Model Mediation Procedure.

8.2 The Licensee may not assign this agreement.

8.3 This Agreement constitutes the entire agreement and understanding of the parties and supersedes all negotiations, understandings or previous agreement between the parties relating to the subject matter of this Agreement.

8.4 English law shall apply to this Agreement, and the English courts shall have exclusive jurisdiction in all matter of construction and interpretation of this Agreement.
BOADICEA PUBLICATIONS

This user guide describes BOADICEA Web Application version 4.0 (BWA 4.0).

BWA 4.0 is described in this paper:


We request that users please cite this paper when describing BWA 4.0 results.

Available online [here](#)

BWA 4.0 uses technology described in this paper:


Available online [here](#)

BWA 4.0 incorporates data described in this paper:


Available online [here](#)

This paper describes how we developed the BWA:


Available online [here](#)
A validation study describing the performance of BOADICEA for breast cancer risk prediction is described in this paper:


Available online [here](#).

A validation study describing the performance of BOADICEA and other risk models is described in this paper:


Available online via PubMed [here](#).

BWA 3.0 (previous version) is described in this paper:


Available online [here](#).

BWA 2.0 (previous version) is described in this paper:


Available online via PubMed [here](#).
An earlier version of the BOADICEA model is described in the following papers:


Available online [here](#)


Available online via PubMed [here](#)


Available online [here](#)


Available online [here](#)
# Table of Contents

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. <strong>INTRODUCTION</strong></td>
<td>1</td>
</tr>
<tr>
<td>1.1 Computer requirements</td>
<td>1</td>
</tr>
<tr>
<td>1.2 Web page submission</td>
<td>2</td>
</tr>
<tr>
<td>1.3 BWA workflows</td>
<td>2</td>
</tr>
<tr>
<td>Online processing workflow</td>
<td>3</td>
</tr>
<tr>
<td>Batch processing workflow</td>
<td>3</td>
</tr>
<tr>
<td>Selecting your workflow</td>
<td>3</td>
</tr>
<tr>
<td>2. <strong>BUILDING A PEDIGREE ONLINE</strong></td>
<td>4</td>
</tr>
<tr>
<td>2.1 Building the core family</td>
<td>5</td>
</tr>
<tr>
<td>Clinical history</td>
<td>6</td>
</tr>
<tr>
<td>Breast cancer pathology</td>
<td>7</td>
</tr>
<tr>
<td>Genetic testing</td>
<td>7</td>
</tr>
<tr>
<td>Specifying parameters for the consultand</td>
<td>8</td>
</tr>
<tr>
<td>Specifying parameters for family members with cancer</td>
<td>8</td>
</tr>
<tr>
<td>Specifying parameters for family members without cancer</td>
<td>8</td>
</tr>
<tr>
<td>Adding family members where no information exists</td>
<td>8</td>
</tr>
<tr>
<td>2.2 Adding siblings and extended family members</td>
<td>9</td>
</tr>
<tr>
<td>Scrolling the pedigree table</td>
<td>9</td>
</tr>
<tr>
<td>Editing family member details</td>
<td>10</td>
</tr>
<tr>
<td>Adding family members</td>
<td>10</td>
</tr>
<tr>
<td>Deleting family members</td>
<td>12</td>
</tr>
<tr>
<td>2.3 Identifying monozygotic twins</td>
<td>13</td>
</tr>
<tr>
<td>2.4 Ashkenazi Jewish pedigrees</td>
<td>14</td>
</tr>
<tr>
<td>Specifying Ashkenazi Jewish status when you build pedigrees online</td>
<td>14</td>
</tr>
<tr>
<td>Updating Ashkenazi Jewish status when you edit pedigrees online</td>
<td>14</td>
</tr>
</tbody>
</table>
3. **REVIEWING YOUR PEDIGREE**

3.1 Pedigree table view

3.2 Pedigree drawing

3.3 Selecting the target

4. **ADJUSTING MODEL PARAMETERS**

4.1 Mutation frequencies

4.2 Mutation search sensitivities

4.3 Cancer incidence rates

4.4 Output data display format

5. **COMPUTING RISKS**

5.1 Pedigree validation

5.2 Graphing breast cancer risks

5.3 Graphing ovarian cancer risks

6. **INTERPRETING RESULTS**

6.1 Mutation carrier probabilities

6.2 Breast and ovarian cancer risks

7. **SAVING RESULTS**

7.1 Processing report PDF

7.2 Mutation carrier probabilities

7.3 Breast and ovarian cancer risks

7.4 Input pedigree
8. **UPLOADING PEDIGREE FILES FROM YOUR COMPUTER**
   - Uploading a single pedigree
   - Uploading multiple pedigrees

9. **BATCH PROCESSING**
   9.1 Pedigree validation
   - Checking pedigree validation results
   9.2 Adjusting model parameters
   9.3 Computing risks
   9.4 Saving results
   - Input pedigrees
   - Mutation carrier probabilities
   - Breast and ovarian cancer risks

10. **LOGGING OUT**
1. INTRODUCTION

The BOADICEA Web Application (BWA) is a computer program that is used to estimate mutation carrier probabilities and breast/ovarian cancer risks on the basis of family history. This guide provides a brief introduction to its use. We strongly recommend that new users read this document before attempting to use this software. Additional information is available in the Frequently Asked Questions section of the BOADICEA Web site. This document accompanies BWA version 4.0 (BWA 4.0).

In this guide, we define the following terms:

A pedigree is an input pedigree data set that describes a single family;

The core family is a nuclear family that consists of the consultand and her parents;

The target is the index or the subject of the BOADICEA risk calculation;

We refer to the mutation carrier probabilities and breast/ovarian cancer risks predicted by the program as the BOADICEA risks;

A BOADICEA pedigree data file is a digital data file in the BOADICEA pedigree data file format (described in Appendix A) that contains up to 500 separate pedigrees.

In the sections that follow, key points are marked with an arrowhead ►, and Web page names are identified with UPPERCASE BOLD text.

1.1 Computer requirements

The program has been designed for use with modern Web browsers such as Chrome, Safari and Firefox. However, you may need to adjust your browser settings to enable the program to work properly.

► Your browser must have ‘active scripting’ enabled so that the program can validate input data.

► The program displays pedigree drawings in popup windows. Some browsers will prompt you to ‘Allow popup windows from this site?’ If you OK this, then the pedigree drawing module should work properly.
1.2 Web page submission

There are some restrictions on how you submit Web pages for processing.

► Always use the function buttons to submit each Web page for processing (do not press the ‘Return’ key). Also, try to avoid pressing the a button several times if the program fails to respond right away.

► Do not use the ‘forward’ or ‘back’ arrows in the top left-hand corner of your browser to navigate between cached Web pages, as the program processes Web pages in a pre-determined order.

► If you press either a ‘Reset’ and ‘Next Pedigree’ function button on a Web page, the program will reset your session (as it appears when you first login). If you press a ‘Logout’ button, the program will terminate the session and delete all accompanying data files from the BWA server.

1.3 BWA workflows

You can either: (1) build a new pedigree online, and to compute BOADICEA risks and save your results (online processing workflow, Figure 1); or (2) upload a BOADICEA pedigree data file with up to 500 pedigrees, and to compute BOADICEA risks for all the pedigrees in a single processing run (batch processing workflow, Figure 1).

![BWA Workflows Diagram](image)

**Figure 1. BWA workflows.** The online processing workflow (shaded green) enables you to build a new pedigree online, and to compute BOADICEA risks and save your results. The batch processing workflow (initial steps shaded blue) enables you to upload a BOADICEA pedigree data file with up to 500 pedigrees, and to compute BOADICEA risks for all the pedigrees in a single processing run.
Online processing workflow

The BWA online processing workflow consists of the following main activities:

- Create the pedigree data set
- Validate the pedigree data set
- Review the pedigree data set
- Adjust model parameters
- Compute risks
- Interpret results
- Save results

These activities are described in sections 2 to 8 of this guide.

Batch processing workflow

The BWA batch processing workflow consists of the following main activities:

- Upload a BOADICEA pedigree data file with up to 500 pedigrees
- Validate the pedigree data sets
- Compute risks
- Save results

These activities are described in section 9 of this guide.

Selecting your workflow

Once you have logged in, the program generates a SESSION OPTION Web page (Figure 2). This Web page provides two options: 'Build a simple pedigree online', or 'Upload a pedigree file from your computer'.

If you select the first option 'Build a simple pedigree online', the program will then generate a series of Web pages to enable you to do that (see section 2 below).

Figure 2. The SESSION OPTION Web page. This Web page provides two options: build a simple pedigree online, or upload a pedigree file from your computer. The line of text extending along the bottom of the Web page 'Model: UK mutation frequencies…' shows the default model parameter settings.
Alternatively, if you choose the option 'Upload a pedigree file from your computer', you can upload either: (1) a single BOADICEA pedigree that you have built previously and saved on your computer, or (2) a BOADICEA pedigree data file that contains up to 500 pedigrees for batch processing (see section 8 'Uploading pedigree files from your computer' for more details). The SESSION OPTION Web page (Figure 2) also displays the default model parameter settings in a line of text along the bottom of the Web page (model parameters are described in section 4 of this guide).

2. BUILDING A PEDIGREE ONLINE

The program enables you to build and edit simple pedigrees online (Figure 3).

Figure 3. Sample pedigree built online with the program. The pedigree is annotated in the conventional manner: the target '301' is marked with an arrow, and individuals who have developed cancer are shaded.

If you select the first option 'Build a simple pedigree online' on the SESSION OPTION Web page (Figure 2), the program will then generate a PEDIGREE NUMBER Web page (Figure 4). The PEDIGREE NUMBER Web page enables you to specify an identifier for your pedigree for archival purposes.

► Pedigrees built online must have simple structures e.g. they cannot include loops. Section 8 below describes how you can upload and process pedigrees with more complex structures.
Online pedigree building is a two stage process:

1. Build the ‘core’ family (consisting of the target and her parents)
2. Add additional family members (including grandparents, aunts, cousins etc)

These activities are described below.

### 2.1 Building the core family

When you build a pedigree online, you must first build the core family (consisting of the target and her parents). The program generates CONSULTAND (Figure 5), MOTHER OF CONSULTAND and FATHER OF CONSULTAND Web pages for this purpose.

At first sight, the CONSULTAND Web page (Figure 5) appears quite complicated. However, it been designed to enable you to input data quickly and easily.

CONSULTAND Web pages have three tabbed sections labelled 'Clinical history' (Figure 5a), 'Breast cancer pathology' (Figure 5b), and 'Genetic testing (Figure 5c)'. You can access each section by clicking on the corresponding tab.

► The program assumes that the consultand is the target by default.
Clinical history

You can use the 'Clinical history' section (Figure 5a) to specify sex, vital status, age or age at death (age at last follow up), cancer history and genetic status. In particular, you can specify an age at cancer diagnosis here for breast cancer, contralateral breast cancer, ovarian cancer, prostate cancer and pancreatic cancer.

The text fields labelled 'Exact' enable you to specify an exact age (or age at cancer diagnosis) in years. If you do not know the exact age, you can still specify an approximate age using the 'Approx' selection list instead, which enables you to specify the age within a 10-year interval. If you do this, then the program will assume that the age is at the centre of that 10-year
interval (e.g. if you select an approximate age of '30-40', then the program will set the age to be 35 years).

Setting the current age from year of birth

If the family member is alive, you can set her current age from her year of birth (or vice versa). To do this, type a year into the ‘Year of birth’ text field, and click the ‘Age or age at death’ radio button. The current age will then be set automatically in the ‘Year of birth’ text field.

Breast cancer pathology

You can use the 'Breast cancer pathology' section (Figure 5b) to enter breast cancer pathology results.

► The program assumes that the breast cancer pathology samples were taken from the individual's first breast cancer. Therefore, in order to specify these breast cancer pathology parameters, you must ensure that the corresponding age at breast cancer diagnosis has been specified in the 'Clinical history' section.

The 'Breast cancer pathology' section prompts for the following parameters:

- Estrogen Receptor (ER)
- Progesterone Receptor (PR)
- Human Epidermal Growth Factor Receptor Two (HER2)
- Cytokeratin Fourteen (CK14)
- Cytokeratin Five/Six (CK5/6)

For modelling purposes, only certain combinations of pathology parameters are permitted. As a result, the program will enforce the following rules:

- ER status must be specified as 'positive' or 'negative'
- PR and HER status can only be specified for ER 'negative' family members
- CK14 and CK5/6 status can only be specified for triple negative* family members

*Triple negative family members are ER negative, PR negative and HER2 negative.

Genetic testing

You can use the 'Genetic testing' section (Figure 5c) to enter genetic test results for the following genes:

- BRCA1
- BRCA2
- PALB2
- ATM
- CHEK2
Once you have specified this information for the consultand, press ‘Continue’ to submit the CONSULTAND Web page for processing. The program will then generate additional MOTHER OF CONSULTAND and FATHER OF CONSULTAND Web pages to enable you to specify the same information for the consultand's parents.

Specifying parameters for the consultand

The following parameters must be specified on the CONSULTAND Web page (Figure 5):

- First name/ID
- Age or age at death
- Year of birth

When a CONSULTAND Web page is generated for the first time, the ‘First name/ID’ text field is initialised with ‘Anon’ for ‘anonymous’. To update the ‘First name/ID’, left click the text box to clear it, and enter your own identifier.

Specifying parameters for family members with cancer

The following parameters must be specified for family members with cancer to avoid underestimating risks:

- Age or age at death
- Year of birth
- Age at cancer diagnosis

► If you specify an age at cancer diagnosis as ‘Unknown’, the program will set it equal to the ‘Age or age at death’.

► If you specify an ‘unknown' age at cancer diagnosis with the ‘AU' code in a BOADICEA pedigree data file (see Appendix A for format description), the program will set it equal to the ‘Age or age at death.

Specifying parameters for family members without cancer

Family members without cancer must have the following parameters specified in order to be taken into account in the BOADICEA risk calculation:

- Age or age at death
- Year of birth

Family members who lack this information are ignored in BOADICEA risk calculations.

Adding family members where no information exists

Sometimes, you may need to add a family member where no information exists. Under these circumstances, press the 'Skip' submit button at the bottom right-hand corner of the Web
When you do this, the program will set the 'First name/ID' to ‘Anon’, the ‘Age or age at death’ to ‘Unknown’ and the ‘Year of birth’ to ‘Unknown’, and clear all other data on the Web page.

► The 'Skip' button is disabled on the CONSULTAND Web page as the consultand must have a valid the ‘Age or age at death’ and 'Year of birth'.

### 2.2 Adding siblings and extended family members

Once you have built the core family, the program will generate a PEDIGREE TABLE VIEW Web page (Figure 6) which will display the current input pedigree as a tabulated data set. Each table row describes a single family member (the tabulated data parameters are described in section 3 of this guide). The PEDIGREE TABLE VIEW Web page (Figure 6) also displays the current model parameter settings in a line of text extending across the bottom left-hand corner of the Web page (model parameters are described in section 4 of this guide).

![Figure 6. The PEDIGREE TABLE VIEW Web page. This Web page displays the input pedigree as a tabulated data set. It includes two sets of function buttons along the bottom of the Web page: the top row of buttons (grey background) are used to navigate and edit the pedigree; the bottom row of buttons (blue background) include functions to manage the login session, update BOADICEA model parameters, draw the pedigree, switch the target and compute BOADICEA risks. The line of text extending across the bottom left-hand corner of the Web page 'Model: UK mutation frequencies...' shows the current model parameter settings.](image)

The PEDIGREE TABLE VIEW Web page provides editing functions (grey table row, Figure 6) that are used to navigate the pedigree and to add additional family members. These functions are described below.

**Scrolling the pedigree table**

The PEDIGREE TABLE VIEW Web page (Figure 6) displays up to ten table rows at a time. Press the ‘Page Up’ function button (bottom left-hand corner, Figure 6) to scroll up through the pedigree table, or the corresponding 'Page Down' function button to scroll down it.
Editing family member details

You can edit details of any family member using the ‘Edit’ function. To do this, first select the individual in the table whose details you want to edit by left clicking the appropriate table row. When you do this, the table row will then be highlighted in white. Then press the ‘Edit’ function button (grey table row, Figure 6) to retrieve the data for that individual. The program will then generate an EDIT DETAILS Web page with that person's details (the EDIT DETAILS Web page has the same format as the CONSULTANT Web page, Figure 5). Once you have updated the data and resubmitted the EDIT DETAILS Web page, the PEDIGREE TABLE VIEW Web page will be displayed again with the updated pedigree.

Adding family members

You can add siblings and extended family members using the ‘Add’ function. The 'Add' function enables you to select an existing family member and then add her: (1) parents, (2) partner and offspring or (3) sibling(s).

To do this, you must first select the relevant family member by left clicking the corresponding table row in the PEDIGREE TABLE VIEW Web page (Figure 6). When you do this, the table row will be highlighted in white. Then press the ‘Add’ function button (grey table row, Figure 6) to generate an ADD NEW FAMILY MEMBER Web page (Figure 7).

The ADD NEW FAMILY MEMBER Web page offers four options:

- Add parents
- Add a partner and offspring
- Add sibling(s)
- Return to PEDIGREE TABLE VIEW

Figure 7. The ADD NEW FAMILY MEMBER Web page.
The individual that you have just selected may or may not have parents included in the pedigree.

If the selected individual's parents are already included in the pedigree, the 'Add parents' option on the ADD NEW FAMILY MEMBER Web page will be disabled because each family member can only have one set of parents.

Alternatively, if the selected individual's parents are not included in the pedigree, the ‘Add a new sibling’ option on the ADD NEW FAMILY MEMBER Web page will be disabled because you cannot add siblings under these circumstances (you must add the parents first).

Select your preferred option on the ADD NEW FAMILY MEMBER Web page and press ‘Continue’ to submit your request for processing.

Adding parents

If you select the ‘Add parents’ option, the program will generate ADD FATHER and ADD MOTHER Web pages to enable you to add these new family members.

Adding a partner and offspring

If you select the ‘Add a partner and offspring’ option, the program will generate ADD NEW PARTNER and ADD OFFSPRING Web pages to enable you to add these new family members.

Adding siblings

To add one or more siblings, select the ‘Add a new sibling’ option on the ADD NEW FAMILY MEMBER Web page (Figure 7), and then use the 'No.' selection list to specify the number of siblings you wish to add (you can add up to five new siblings at a time). The program will then generate the corresponding number of ADD SIBLING Web pages to enable you to add these new family members.

The Web pages used to add extended family members have the same format as the CONSULTAND Web page (Figure 5). Once you have input details of the new family member(s), the program will return an updated PEDIGREE TABLE VIEW Web page.

► New family members are added to the end of the pedigree so you may have to scroll down the table in the PEDIGREE TABLE VIEW Web page to see them.

Adding aunts, uncles and cousins

Once you have built the core family, you may wish to add aunts, uncles and cousins. This is straightforward. However, in order to add (for example) a maternal aunt, you must first add maternal grandparents. This is necessary because the maternal grandparents provide the physical link in the pedigree between the target's mother and maternal aunt.
To add a maternal aunt, first add maternal grandparents by selecting the target's mother (left click the relevant table row in the PEDIGREE TABLE VIEW Web page, Figure 6), and then press the 'Add' button to access the ADD NEW FAMILY MEMBER Web page (Figure 7).

You can then use the 'Add parents' option to add the target's maternal grandparents.

► If you have no information at all on the maternal grandparents, you can use the 'Skip' button to skip past the ADD MOTHER and ADD FATHER Web pages so that these individuals will be included in the pedigree, but they will make no contribution to the calculated BOADICEA risks.

Once you have added the maternal grandparents, select the target's mother again on the PEDIGREE TABLE VIEW Web page, and press the 'Add' function button (Figure 6) to access the ADD NEW FAMILY MEMBER Web page (Figure 7), and then use the 'Add a new sibling' option to add the mother's sister (i.e. the target's maternal aunt).

Once you have added the target's maternal aunt, you can then add a maternal cousin. To do this, select the target's maternal aunt on the PEDIGREE TABLE VIEW Web page (Figure 6), and press the 'Add' button to access the ADD NEW FAMILY MEMBER Web page (Figure 7), and then use the 'Add a partner and offspring' option to add a new maternal uncle and offspring (i.e. the target's maternal cousin). If you have no information at all on the maternal uncle, you can use the 'Skip' function button to skip past the initial ADD PARTNER Web page.

Deleting family members

You can delete family members using the ‘Delete’ function button. To do this, select the individual that you want to delete (left click the relevant table row in the PEDIGREE TABLE VIEW Web page, Figure 6), and press the ‘Delete’ button (grey row, Figure 6) to submit your request. The program will then check the structure of the pedigree to ensure that the individual can be safely deleted.

► The program will not allow a deletion that will break the pedigree into separate trees. As a result, you can only delete founders and individuals without partners.

► If you delete the last remaining child in a nuclear family where one parent is a 'marry-in' (an individual with no other first-degree relatives), then both the marry-in and the child will be deleted.

► Pedigrees must have a minimum of three family members. As a result, you cannot delete family members when just the core family remains.

If the requested deletion operation will break the pedigree into separate trees, the program will return an ERROR Web page (Figure 8) describing the problem. Otherwise, the selected individual will be deleted and the program will return an updated PEDIGREE TABLE VIEW Web page (Figure 6).
2.3 Identifying monozygotic twins

You can also use the program pedigree functions to identify monozygotic (MZ) twins in your pedigree.

► MZ twins must have the same year of birth, sex, age (if both living) and genetic test results.

► You can twin siblings where one individual has had a genetic test. If both siblings have had a genetic test (rare in practice), the genetic test results must be compatible.

► The program only allows you to set MZ twins. MZ triplets and quadruplets are not allowed (rare in practice).

To identify MZ twins in your pedigree, press the ‘MZ Twin’ button on the PEDIGREE TABLE VIEW Web page (grey row, Figure 6). The program will then search your pedigree for:

- Existing MZ twins
- Siblings that have not been identified as MZ twins but could be

► Searching large pedigrees for MZ twins can be time consuming.

When the search is complete, the program will return a TWIN FAMILY MEMBERS Web page (Figure 9) which enables you to select or deselect MZ twins.

The ‘Select MZ twins’ pull-down menu (Figure 9) lists all pairs of siblings in the pedigree with the same year of birth, sex, age (if both living) and genetic test results. These siblings could potentially be MZ twins, but have not been identified as such. To identify MZ twins, select the relevant pair of siblings from this list and press the ‘Continue’ button. The program will then update your pedigree and return a PEDIGREE TABLE VIEW Web page (Figure 6).
new MZ twins will be identified in the pedigree table with unique identifiers in the ‘MZtwin’ data column (Figure 6).

The ‘Deselect MZ twins’ pull-down menu (Figure 9) lists the existing MZ twins in the pedigree. To deselect existing MZ twins, select the relevant pair of MZ twins from this list and press the ‘Continue’ button. The program will then update your pedigree (i.e. remove MZ twin status from these individuals) and return a PEDIGREE TABLE VIEW Web page (Figure 6).

### 2.4 Ashkenazi Jewish pedigrees

The program can also be used to compute risks for individuals with Ashkenazi Jewish ancestry. If you identify an input pedigree as an Ashkenazi Jewish pedigree, the program will adjust the model parameters (described in section 4 of this guide) so that Ashkenazi Jewish mutation frequencies are set before you run your BOADICEA risk calculation. Additional information on processing Ashkenazi Jewish pedigrees is available in the Frequently Asked Questions section of the BOADICEA Web site.

**Specifying Ashkenazi Jewish status when you build pedigrees online**

When you build a pedigree online, you can identify an Ashkenazi Jewish pedigree by selecting the ‘Ashkenazi origin’ checkbox on the CONSULTAND Web page (Figure 5). Then, once you have built the core family and the program has returned a PEDIGREE TABLE VIEW Web page (Figure 6), the model parameter settings (specified in a line of text in the bottom left-hand corner of the Web page) will indicate that ‘Ashkenazi Mutation Frequencies’ have been set. Similarly, the target will be identified as having Ashkenazi Jewish ancestry with the acronym 'AJ' in the ‘Ashkn’ column.

► When you build pedigrees online, the ‘Ashkenazi origin’ checkbox is only enabled on the CONSULTAND Web page as the program only requires you to supply this information once.

**Updating Ashkenazi Jewish status when you edit pedigrees online**

Once your pedigree is displayed in the PEDIGREE TABLE VIEW Web page (Figure 6), the only way to select (or deselect) Ashkenazi Jewish mutation frequencies is to use the ‘Model Parameters’ module (see section 4 of this guide for more details).
3. REVIEWING YOUR PEDIGREE

3.1 Pedigree table view

Once you have built your pedigree, you can review it in the PEDIGREE TABLE VIEW Web page (Figure 6) before you run a BOADICEA risk calculation. Each table row describes a single family member. The corresponding column headings are described in Table 1 below.

<table>
<thead>
<tr>
<th>Column Heading</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Name</td>
<td>First name/ID of the family member</td>
</tr>
<tr>
<td>Tgt</td>
<td>The target (index or subject of the risk calculation)</td>
</tr>
<tr>
<td>IndivID</td>
<td>The unique ID of the family member</td>
</tr>
<tr>
<td>FathID</td>
<td>The unique ID of the family member's father</td>
</tr>
<tr>
<td>MothID</td>
<td>The unique ID of the family member's mother</td>
</tr>
<tr>
<td>Sex</td>
<td>Male or female</td>
</tr>
<tr>
<td>MZtwin</td>
<td>Single characters used to identify identical twins</td>
</tr>
<tr>
<td>Status</td>
<td>Dead or alive</td>
</tr>
<tr>
<td>Age</td>
<td>Age or age at death (age at last follow up)</td>
</tr>
<tr>
<td>Yob</td>
<td>Year of birth</td>
</tr>
<tr>
<td>1BrCa</td>
<td>Age at first breast cancer diagnosis</td>
</tr>
<tr>
<td>2BrCa</td>
<td>Age at contralateral breast cancer diagnosis</td>
</tr>
<tr>
<td>OvCa</td>
<td>Age at ovarian cancer diagnosis</td>
</tr>
<tr>
<td>ProCa</td>
<td>Age at prostate cancer diagnosis</td>
</tr>
<tr>
<td>PanCa</td>
<td>Age at pancreatic cancer diagnosis</td>
</tr>
<tr>
<td>Ashkn</td>
<td>Ashkenazi origin</td>
</tr>
<tr>
<td>Genetic Tests</td>
<td>Genetic test results e.g. BRCA1 +ve</td>
</tr>
<tr>
<td>Pathology</td>
<td>Pathology test results e.g. ER -ve</td>
</tr>
</tbody>
</table>

Table 1. PEDIGREE TABLE VIEW Web page column headings.
3.2 Pedigree drawing

You can also use the PEDIGREE TABLE VIEW Web page 'Draw' function to draw your pedigree. If you press the 'Draw' function button, a pedigree drawing should appear in a popup window in a few seconds (Figure 10).

Figure 10. Sample pedigree drawing. Pedigree drawings are annotated in the conventional manner: the target '301' is identified with an arrow, and family members who have developed cancer are shaded. The text beneath each family member includes: a unique identifier, first name/ID and age at last follow up, year of birth, cancer history, genetic status and pathology status.

► In some cases, Kinship may fail to generate a pedigree drawing. If this happens, the pedigree drawing window will display an error message or will appear blank. However, this will not affect subsequent risk calculations.

Additional information on pedigree drawing is available in the Frequently Asked Questions section of the BOADICEA Web site.
3.3 Selecting the target

In the PEDIGREE TABLE VIEW Web page (Figure 6), the target is identified in the table with an arrow '<' in the 'Tgt' column and a grey table row.

If you wish, you can select a different family member as the target before you run your risk calculation. To select the new target, left click the corresponding table row, and press the ‘Switch’ function button. If the selected individual has a valid year of birth and age at last follow up, the program will return an updated PEDIGREE TABLE VIEW Web page with the new target highlighted as above. In this way, you can compute risks for different family members.

► The target must have a valid year of birth and age at last follow up. As a result, the program will generate an error message if you try to select an individual without this information as the new target.

4. ADJUSTING MODEL PARAMETERS

BOADICEA risks are also dependent on the model parameters (e.g. mutation frequencies and mutation search sensitivities) specified in the risk calculation. As a result, the program includes a ‘Model Parameters’ module that enables you to adjust these parameters before you run a risk calculation.

The default model parameter settings are displayed on the SESSION OPTION Web page (Figure 2) when you first login. Similarly, the current model parameter settings are displayed in the PEDIGREE TABLE VIEW Web page (Figure 6) once you have built the core family.

To change the current model parameter settings (e.g. for different populations), press the ‘Model’ function button on the PEDIGREE TABLE VIEW Web page (Figure 6). The program will then return a MODEL PARAMETERS Web page (Figure 11).

![Model Parameters Web page](image)

Figure 11. The MODEL PARAMETERS Web page.
The **MODEL PARAMETERS** Web page (Figure 11) enables you to adjust the following parameters:

- BRCA1, BRCA2, PALB2, ATM, CHEK2 mutation frequencies
- BRCA1, BRCA2, PALB2, ATM, CHEK2 mutation search sensitivities
- Cancer incidence rates
- Output data display format

You can change any of these parameters before you run a risk calculation.

 ► **WARNING** BOADICEA risks are critically dependent on the model parameter settings. If you are in any doubt about your model parameter settings, please contact us for further clarification (see the Contacts section of the BOADICEA Web site for more details).

 ► When you login, the program sets the following default model parameters: ‘UK’ mutation frequencies, ‘Default’ mutation search sensitivities, UK cancer incidence rates and ‘Percent’ output data format.

 ► If you reset the current session by pressing either a ‘Reset’ or ‘Next Pedigree’ function button, the program will restore the default model parameter settings.

### 4.1 Mutation frequencies

The first section of the **MODEL PARAMETERS** Web page (Figure 11) shows the current BRCA1, BRCA2, PALB2, ATM and CHEK2 mutation frequencies.

The mutation frequency is defined as the proportion of all alleles in the population that is made of pathogenic mutations. It should not be confused with mutation carrier frequency which is a different quantity. For example, if \( p \) represents the mutation frequency in the population, the mutation carrier frequency is \( p^2 + 2p(1-p) \). In this example, the BOADICA input should be "\( p \)".

 ► If you are uncertain how to specify mutation frequencies, please contact us for further clarification.

To change these parameters, you can select one of the following options on the ‘Set mutation frequencies’ selection list:

- UK
- Ashkenazi
- Iceland
- Custom

If you select either the ‘UK’, ‘Ashkenazi’ or ‘Iceland’ option, appropriate preset mutation frequencies will appear in the adjacent text boxes. If you select the ‘Custom’ option, the program will clear and sensitise the adjacent text boxes, to enable you to input your own settings.
4.2 Mutation search sensitivities

The second section of the MODEL PARAMETERS Web page (Figure 11) shows the current BRCA1, BRCA2, PALB2, ATM and CHEK2 mutation search sensitivities.

Mutation search sensitivities define the proportion of mutations that a mutation search is known to detect. They are expressed as decimal numbers in the range 0 to 1. For example, if you know that your mutation search detects 90% of BRCA1 mutations, you should input 0.9 in the BRCA1 text box on the MODEL PARAMETERS Web page.

To change these parameters, select one of the two options on the ‘Set mutation search sensitivities’ selection list: ‘Default’ or ‘Custom’. If you select the ‘Default’ option, default mutation search sensitivities will appear in the adjacent text boxes. If you select the ‘Custom’ option, the program will clear and sensitise the adjacent text boxes, to enable you to input your own settings.

► If you are uncertain how to specify mutation search sensitivities, please contact us for further clarification.

4.3 Cancer incidence rates

The third section of the MODEL PARAMETERS Web page (Figure 11) shows the cancer incidence rates. You can select the cancer incidence rates to use in your risk calculation from the following options:

- UK
- UK-version-1
- Australia
- Canada
- USA-white
- Denmark
- Finland
- Iceland
- New Zealand
- Norway
- Sweden

The 'UK' option specifies the most up-to-date UK cancer incidence rates. The 'UK-version-1' option specifies the UK cancer incidence rates used in previous versions of the program.
4.4 Output data display format

The fourth section of the MODEL PARAMETERS Web page (Figure 11) shows the current output data display format. This parameter determines how BOADICEA risks will be formatted in the COMPUTED RESULTS Web page (Figure 12) and the processing report PDF (described in section 7 of this guide).

You can select the output data display format from the following options:

- Percent
- Decimal

If you select 'Percent' format, the program will display BOADICEA risks as percentages e.g. a probability of 1 in 50 will be expressed as 2.0 percent.

Alternatively, if you select 'Decimal' format, the program will display BOADICEA risks as decimal fractions with a value between zero and one e.g. a probability of 1 in 50 will be expressed as 0.020.

Additional information on model parameters is available in the Frequently Asked Questions section of the BOADICEA Web site.

5. COMPUTING RISKS

When you are satisfied that your input pedigree and model parameters are correct, you can proceed with a risk calculation. To compute BOADICEA risks, press the ‘Compute’ function button on the PEDIGREE TABLE VIEW Web page (Figure 6).

5.1 Pedigree validation

Before the program computes BOADICEA risks, it validates your pedigree. The pedigree validation module runs checks to ensure (as far as possible) that the input pedigree data set is valid, complete and internally consistent. The program will validate your pedigree whenever you: (1) upload it in a BOADICEA format data file, (2) edit it online and (3) compute BOADICEA risks.

If your pedigree includes family members who do not have a valid 'Year of birth' or ‘Age or age at death’, the program will generate an ERROR Web page with the following warning:

**Pedigree submit request warning**

The program has found an incomplete data record in your pedigree: a family member without cancer is missing a year of birth or age at last follow up. An individual's year of birth and age at last follow up must be specified in order for that person to be included in a calculation. As a result, family members lacking this information will be excluded from the calculation. Press 'OK' to continue.
This warning has been included to remind users that these family members will not be taken into account in the risk calculation. If you press the 'OK' function button on this Web page, the program will then submit your pedigree for processing and return a COMPUTED RESULTS Web page (Figure 12).

Figure 12. The COMPUTED RESULTS Web page.

The COMPUTED RESULTS Web page (Figure 12) displays the computed BOADICEA risks. The target is identified in the line of text across the top left-hand corner of the Web page (Figure 12), and the results are displayed as follows:

- Mutation carrier probabilities are displayed in the top left-hand table
- Current model parameter settings are displayed in the bottom left-hand table
- Breast/ovarian cancer risks are displayed in the right-hand table

The BOADICEA risks will be displayed in either 'Percent' or 'Decimal' format (described in section 4.4 of this guide). You can switch between these two output data display formats by pressing the 'Reformat' function button on the COMPUTED RESULTS Web page (Figure 12).
5.2 Graphing breast cancer risks

You can generate a graph of breast cancer risks plotted against the target's age. To do this, press the 'Graph Breast Cancer Risks' function button on the COMPUTED RESULTS Web page (Figure 12), and a graph should appear in a popup window in a few seconds (Figure 13).

Figure 13. Breast cancer risk graph. Breast cancer risks (in percent) are plotted against age in years (up to 80). The solid blue curve is the target's breast cancer risk predicted by BOADICEA on the basis of the input pedigree. The dashed black curve is the corresponding baseline breast cancer risk predicted by BOADICEA for a random individual in the general population.

The breast cancer risk graph (Figure 13) shows two curves: (1) the solid blue curve is the target's breast cancer risk predicted by BOADICEA on the basis of the input pedigree; and (2) the dashed black curve is the corresponding baseline breast cancer risk predicted by BOADICEA for a random individual in the general population.

The target's breast cancer risks (solid blue curve, Figure 13) are computed using information for all family members in the input pedigree that have a valid ‘Age or age at death’ and ‘Year of birth’.
The baseline breast cancer risks (dashed black curve, Figure 13) are computed using only the following parameters for the target: sex, age at last follow up, year of birth and age at first breast cancer diagnosis (if applicable).

- **Breast cancer risks are always expressed in percent in risk graphs**

- **If the target has already developed one breast cancer, the breast cancer risks predicted by BOADICEA (solid blue curve, Figure 13) represent the target’s risk of contralateral breast cancer**
5.3 Graphing ovarian cancer risks

You can generate a graph of ovarian cancer risks plotted against the target's age. To do this, press the 'Graph Ovarian Cancer Risks' function button on the COMPUTED RESULTS Web page (Figure 12), and a graph should appear in a popup window in a few seconds (Figure 14).

![Ovarian cancer risk graph](image.png)

**Figure 14. Ovarian cancer risk graph.** Ovarian cancer risks (in percent) are plotted against age in years (up to 80). The solid blue curve is the target's ovarian cancer risk predicted by BOADICEA on the basis of the input pedigree. The dashed black curve is the corresponding baseline ovarian cancer risk predicted by BOADICEA for a random individual in the general population.

The ovarian cancer risk graph (Figure 14) shows two curves: (1) the solid blue curve is the target's ovarian cancer risk predicted by BOADICEA on the basis of the input pedigree; and (2) the dashed black curve is the corresponding baseline ovarian cancer risk predicted by BOADICEA for a random individual in the general population.

The target's ovarian cancer risks (solid blue curve, Figure 14) are computed using information for all family members in the input pedigree that have a valid ‘Age or age at death’ and ‘Year of birth’.
The baseline ovarian cancer risks (dashed black curve, Figure 14) are computed using only the following parameters for the target: sex, age at last follow up, year of birth and age at first ovarian cancer diagnosis (if applicable).

- **Ovarian cancer risks are always expressed in percent in risk graphs.**

### 6. INTERPRETING RESULTS

The **COMPUTED RESULTS** Web page (Figure 12) displays BOADICEA risks computed on the basis of your input pedigree.

#### 6.1 Mutation carrier probabilities

Mutation carrier probabilities are displayed in the top left-hand table of the **COMPUTED RESULTS** Web page (Figure 12). These figures are conditional probabilities computed on the basis of the input pedigree and are expressed as follows:

If the current output data display format (described section 4.4 of this guide) is set to 'Percent', the mutation carrier probabilities will be expressed as percentages e.g. a probability of 1 in 50 will be expressed as 2.0 percent.

Alternatively, if the current output data display format (described section 4.4 of this guide) is set to 'Decimal', the mutation carrier probabilities will be expressed as decimal fractions with a value between zero and one e.g. a probability of 1 in 50 will be expressed as 0.020.

- **If the target has had a positive genetic test, the program cannot compute mutation carrier probabilities for that individual. This is a limitation of the BOADICEA model.**

#### 6.2 Breast and ovarian cancer risks

Breast and ovarian cancer risks are displayed in the right-hand table of the **COMPUTED RESULTS** Web page (Figure 12). The risks are computed for the target at one year intervals for the next five years, and then at ages divisible by five years up to age 80. In addition, the ten year risks are also included.

These figures are conditional probabilities computed on the basis of the input pedigree and are expressed as follows:

If the current output data display format (described section 4.4 of this guide) is set to 'Percent', the cancer risks will be expressed as percentages e.g. a risk of 1 in 50 will be expressed as 2.0 percent.

Alternatively, if the current output data display format (described section 4.4 of this guide) is set to 'Decimal', the cancer risks will be expressed as decimal fractions with a value between zero and one e.g. a risk of 1 in 50 will be expressed as 0.020.
Cancer risks will only be computed if the target is a female unaffected by cancer, or a female who has developed one breast cancer.

If the target has already developed one breast cancer, the breast cancer risks predicted by the BOADICEA represent the target’s risk of contralateral breast cancer.

The cancer risks predicted by BOADICEA are ‘remaining lifetime’ risks. A remaining lifetime risk is the risk of cancer occurring between the individual’s current age and 80 (say for an individual in their 30s or 40s), conditional on the disease experience of that individual up to that point (whether she has remained unaffected or developed unilateral breast cancer).

Additional information on interpreting results is available in the Frequently Asked Questions section of the BOADICEA Web site.
7. SAVING RESULTS

When you have run a BOADICEA risk calculation, you can generate a set of output data files to save on your computer. To do this, press the ‘Generate Report’ button on the COMPUTED RESULTS Web page (Figure 12). In a few seconds, the program will return a PROCESSING REPORT Web page (Figure 15).

Figure 15. The PROCESSING REPORT Web page.

The PROCESSING REPORT Web page (Figure 15) enables you to download the following files to your local computer for archival purposes:

- Processing report PDF
- Mutation carrier probabilities
- Breast/ovarian cancer risks
- Input pedigree

These options are described below.

► We strongly recommend that users save a copy of all results files for archival purposes.

7.1 Processing report PDF

The processing report PDF (Figure 16) summarises your latest risk calculation. To download the PDF, click on the link labelled here in the first line of text in the PROCESSING REPORT Web page (Figure 15), and select ‘Save Target As…’ (or similar) in your browser menu and specify an output data filename on your computer. The PDF will then be downloaded to your computer across a secure Web connection.
The processing report PDF includes the following sections:

- Risk calculation summary and pedigree table
- Pedigree drawing
- Computed results and model parameters
- Breast/ovarian cancer risk graphs

The risk calculation summary is written at the start of the report (Figure 16) and it includes the date and time of the risk calculation, the session and risk calculation numbers, and details of the input pedigree and target.

► The session number and risk calculation number uniquely identify each BOADICEA risk calculation

![Image of the processing report PDF](image)

Figure 16. The processing report PDF.

### 7.2 Mutation carrier probabilities

You can download the mutation carrier probabilities computed during the most recent processing run in a data file (see Appendix B of this guide for details of the output data format). This file includes the session number and risk calculation number, so that you can link it to the accompanying processing report PDF.
To download the mutation carrier probabilities, right click here in the second line of text on the PROCESSING REPORT Web page (Figure 15), and select ‘Save Target As…’ (or similar) in your browser menu and specify an output data filename on your computer. The data file will then will be downloaded to your computer across a secure Web connection.

7.3 Breast and ovarian cancer risks

You can download the breast/ovarian cancer risks computed during the most recent processing run in a data file (see Appendix C of this guide for details of the output data format). This file includes the session number and risk calculation number, so that you can link it to the accompanying processing report PDF.

To download the breast/ovarian cancer risks, right click here in the third line of text on the PROCESSING REPORT Web page (Figure 15), and select ‘Save Target As…’ (or similar) in your browser menu. When you have specified an output data filename, the data file will be downloaded to your computer via a secure Internet connection.

7.4 Input pedigree

You can download the input pedigree processed during the most recent processing run as a BOADICEA pedigree data file (see Appendix A of this guide for details of the output data format). This means that you can upload it, amend it online, and reprocess it again at any time in the future as more information on the family becomes available.

To download the input pedigree, right click here in the fourth line of text on the PROCESSING REPORT Web page (Figure 15), and select ‘Save Target As…’ (or similar) in your browser menu. When you have specified an output data filename, the data file will be downloaded to your computer across a secure Internet connection.

The input pedigree that you download will be the pedigree processed during the most recent processing run. Therefore, if you upload a BOADICEA pedigree data file, and amend the pedigree online and process it, the amended pedigree will be saved in the download file (not the one you uploaded originally).
8. Uploading pedigree files from your computer

You can upload BOADICEA pedigree data files that you have saved previously on your computer. To do this, select ‘Upload a pedigree file from your computer’ on the SESSION OPTION Web page (Figure 2) at the start of your session and press 'Continue' to generate a PEDIGREE FILE UPLOAD Web page (Figure 17).

![Figure 17. The PEDIGREE FILE UPLOAD Web page.](image)

Then, Press the ‘Browse…’ button on the PEDIGREE FILE UPLOAD Web page (Figure 17) to generate an additional FILE NAVIGATION window (Figure 18), which you can use to select a BOADICEA pedigree data file on your computer for processing.

► BOADICEA pedigree data filenames must include a three letter extension (e.g. ‘pedigree.txt’ or ‘pd4556.dat’). As a result, the program will generate an error if you try to upload a BOADICEA pedigree data file that does not have one.

► BWA pedigrees can include up to 275 family members
BOADICEA pedigree data files come from a variety of sources. They are usually downloaded for archival purposes at the end of a BOADICEA session. However, you can also upload BOADICEA pedigree data files that have been exported from other software packages (listed here). Similarly, in the past, some academic institutions have setup queries to export pedigrees from relational databases in the BOADICEA pedigree data file format.

► We are unable to offer any guarantees or support for other software packages

You can upload a BOADICEA pedigree data file that contains a single pedigree or multiple pedigrees. When you upload the file, the program first runs a check to see how many pedigrees are included within it.

Uploading a single pedigree

If you upload a BOADICEA pedigree data file that contains a single pedigree, the program will first validate it. If the pedigree fails validation, the program will generate an ERROR Web page (Figure 8) describing the problem. Alternatively, if the pedigree passes validation, the program will generate a PEDIGREE TABLE VIEW Web page (Figure 6) displaying details of the first ten family members. Once the pedigree is displayed in the PEDIGREE TABLE VIEW Web page (Figure 6), you can update it and process it as normal.
Uploading multiple pedigrees

If you upload a BOADICEA pedigree data file that contains two or more pedigrees, the program will switch to the batch processing workflow (described in section 1.3 of this guide) to initiate batch jobs to validate and process each pedigree in turn. Batch processing is described in more detail in section 9 of this guide.

9. BATCH PROCESSING

The program includes a batch processing module that enables you to process up to 500 pedigrees in a single processing run. If you upload a BOADICEA pedigree data file that contains two or more pedigrees, the program will first generate a CONFIRM PEDIGREE DATA VALIDATION Web page (Figure 19).

► BOADICEA pedigree data files can contain up to 500 pedigrees
► BOADICEA pedigree data files can have a maximum size of 60 MB
► The model parameter settings used when batch processing are not recorded in the output data files. As a result, we strongly recommend that you make a record of these parameters whenever you submit a batch processing job.

When batch processing for the first time, we recommend that you begin by submitting a small test batch pedigree data file for processing first (containing say 50 pedigrees). By running an initial test in this way, you can examine the results of the pedigree data validation process (described below) to identify any potential problems with your data. Please contact us if you would like further advice on batch processing (our contact details are here).

![Figure 19. The CONFIRM PEDIGREE DATA VALIDATION Web page.](image)

Batch processing involves two separate processing tasks:

- Pedigree validation
- Pedigree processing

These activities are described below.
9.1 Pedigree validation

Before you compute BOADICEA risks, you must first validate your input pedigrees. To do this, press the 'Validate' button on the CONFIRM PEDIGREE DATA VALIDATION Web page (Figure 19). This will initiate a batch processing job that will validate each pedigree data set in your BOADICEA pedigree data file one after the other.

► Each pedigree in your BOADICEA pedigree data file must have a unique family identifier (FamID, see Appendix A of this guide).

When the batch processing job is running, the program will generate a BATCH PROCESSING JOB STATUS Web page (Figure 20) to keep you informed of progress.

![Batch Processing Job Status Web page](image)

Figure 20. The BATCH PROCESSING JOB STATUS Web page.

When the batch processing job is complete, the program will return a BATCH PROCESSING Web page (Figure 21).

![Batch Processing Web page](image)

Figure 21. The BATCH PROCESSING Web page.

The BATCH PROCESSING Web page enables you to do the following:

- Check the pedigree validation results
- Change model parameters before you compute BOADICEA risks
- Compute BOADICEA risks

These activities are described below.
Checking the pedigree validation results

To check the pedigree validation results, press the 'View Log' function button on the BATCH PROCESSING Web page (Figure 21). The program will then generate a VIEW PROCESSING LOG Web page (Figure 22).

Figure 22. The VIEW PROCESSING LOG Web page.

The VIEW PROCESSING LOG Web page (Figure 22) includes a scrollable textbox with the logfile generated by the pedigree validation batch processing job. This logfile shows which pedigrees have passed validation. A pedigree must pass validation in order for it to be submitted for further processing.

9.2 Adjusting model parameters

You can change the model parameters before you initiate a batch processing job to compute BOADICEA risks. To do this, press the ‘Model’ button on the BATCH PROCESSING Web page (Figure 21). The program will then return a MODEL PARAMETERS Web page (Figure 11, described in section 4 of this guide) to enable you to do this.

9.3 Computing risks

Once you have validated your pedigrees, you can initiate a batch processing job to compute BOADICEA risks by pressing the 'Compute' function button on the BATCH PROCESSING Web page (Figure 21). The program will then generate another BATCH PROCESSING JOB STATUS Web page (Figure 20) to keep you informed of progress.
9.4 Saving results

When the batch processing job has finished, the program will return a BATCH PROCESSING REPORT Web page (Figure 23).

![BOADICEA Batch Processing Report](image)

**Figure 23. The BATCH PROCESSING REPORT Web page.**

You can use the BATCH PROCESSING REPORT Web page (Figure 23) to download the following data files to your local computer for archival purposes:

- Input pedigrees
- Mutation carrier probabilities
- Breast and ovarian cancer risks

These options are described below.

**Input pedigrees**

You can download the pedigrees that passed validation and were submitted for processing in the BOADICEA pedigree data file format (see Appendix A of this guide for details of this output data format). To download this data file, right click [here](#) in the first line of text on the BATCH PROCESSING REPORT Web page (Figure 23), and select ‘Save Target As...’ in your browser menu.

**Mutation carrier probabilities**

You can download the mutation carrier probabilities computed for each pedigree that passed validation in a data file (see Appendix B of this guide for details of the output data format). To download these data, right click [here](#) in the second line of text on the BATCH PROCESSING REPORT Web page (Figure 23), and select ‘Save Target As...’ in your browser menu.
Breast and ovarian cancer risks

You can download the breast and ovarian cancer risks computed for each pedigree that passed validation in a data file (see Appendix C of this guide for details of the output data format). To download these data, right click [here](#) in the fourth line of text on the **BATCH PROCESSING REPORT** Web page (Figure 23), and select ‘Save Target As…’ in your browser menu.

### 10. LOGGING OUT

The **PROCESSING REPORT** Web page (Figure 15) enables you to save your results at the end of the online processing workflow (Figure 1). Similarly, the **BATCH PROCESSING REPORT** Web page (Figure 23) enables you to save your results at the end of the batch processing workflow (Figure 1).

Once you have saved your results, if you press the 'Next Pedigree' function button on either of these Web pages, the program will reset your session and generate a **SESSION OPTION** Web page (Figure 2).

Alternatively, if you press the 'Logout' function button, the program will terminate your session and generate a **SESSION COMPLETED** Web page (Figure 24).

![SESSION COMPLETED Web page](#)

**Figure 24. The SESSION COMPLETED Web page.**

When you reset your session or logout, all clinical data files created during the session (pedigree file, processing report PDF, BOADICEA output files etc) are deleted from the BWA server. If you fail to logout (e.g. if you close your browser window by mistake, or your computer network goes down), then all data files created during the session will be deleted from the BWA server 24 hours later. This helps us to conform to the [UK Data Protection Principles](#).
References

Appendix A
BOADICEA pedigree data file format (continued on next page)

The BOADICEA import/export pedigree data format is a simple TAB-delimited text format. BOADICEA pedigree data files consist of two header records followed by a series of pedigree data records, one for each family member. The pedigree data records include 32 parameters (data columns) separated by one or more TAB (or whitespace) characters. For clarity, parameters 1-19 are described on this page, and parameters 20-32 are described overleaf.

This screenshot shows parameters 1-19 in a sample BOADICEA pedigree data file:

<table>
<thead>
<tr>
<th>BOADICEA import pedigree file format 4.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>FamID</td>
</tr>
<tr>
<td>-------</td>
</tr>
<tr>
<td>54273</td>
</tr>
<tr>
<td>54273</td>
</tr>
<tr>
<td>54273</td>
</tr>
<tr>
<td>54273</td>
</tr>
<tr>
<td>54273</td>
</tr>
<tr>
<td>54273</td>
</tr>
<tr>
<td>54273</td>
</tr>
<tr>
<td>54273</td>
</tr>
<tr>
<td>54273</td>
</tr>
<tr>
<td>54273</td>
</tr>
<tr>
<td>54273</td>
</tr>
</tbody>
</table>

The first header record specifies the format number: "BOADICEA import pedigree file format 4.0"

The second header record specifies the column names as shown above (and overleaf): "FamID Name Target IndivID FathID ..."

Parameters 1-19 on the pedigree data records are defined as follows:

1. FamID: Family/pedigree ID, character string (maximum 13 characters)
2. Name: First name/ID of the family member, character string (maximum 8 characters)
3. Target: The family member for whom the BOADICEA risk calculation is made, 1 = target for BOADICEA risk calculation, 0 = other family members.
4. IndivID: Unique ID of the family member, character string (maximum 7 characters)
5. FathID: Unique ID of their father, 0 = no father, or character string (maximum 7 characters). Each family member must have either: (1) no parents specified (e.g. see '103' above), or (2) both parents specified (e.g. see '302' above).
6. MotMID: Unique ID of their mother, 0 = unspecified, or character string (maximum 7 characters)
7. Sex: M or F
8. MZtwin: Identical twins, 0 = not an identical twin. Use one of these characters to identify MZ twins: 1 2 3 4 5 6 7 8 9 A (e.g. see '301' and '302' above)
9. Dead: The current status of the family member, 0 = alive, 1 = dead
10. Age: Age at last follow up, 0 = unspecified, integer = age at last follow up
11. Yob: Year of birth, 0 = unspecified, or integer (consistent with Age if the person is alive)
12. 1stBrCa: Age at first breast cancer diagnosis, 0 = unaffected, integer = age at diagnosis, AU = unknown age at diagnosis (affected unknown)
13. 2ndBrCa: Age at contralateral breast cancer diagnosis, 0 = unaffected, integer = age at diagnosis, AU = unknown age at diagnosis (affected unknown)
14. OvCa: Age at ovarian cancer diagnosis, 0 = unaffected, integer = age at diagnosis, AU = unknown age at diagnosis (affected unknown)
15. ProCa: Age at prostate cancer diagnosis 0 = unaffected, integer = age at diagnosis, AU = unknown age at diagnosis (affected unknown)
16. PanCa: Age at pancreatic cancer diagnosis 0 = unaffected, integer = age at diagnosis, AU = unknown age at diagnosis (affected unknown)
17. Ashkn: Ashkenazi status, 0 = not Ashkenazi, 1 = Ashkenazi
18. BRCA1t: BRCA1 genetic test type, 0 = untested, S = mutation search, T = direct gene test
19. BRCA1r: BRCA1 genetic test result, 0 = untested, P = positive, N = negative

... (remaining columns described overleaf)
Appendix A
BOADICEA import/export pedigree data format (continued from previous page)

This screenshot shows parameters 20-32 in a sample BOADICEA pedigree data file:

<table>
<thead>
<tr>
<th></th>
<th>BRCA2t</th>
<th>BRCA2r</th>
<th>PALB2t</th>
<th>PALB2r</th>
<th>ATMt</th>
<th>ATMr</th>
<th>CHEK2t</th>
<th>CHEK2r</th>
<th>ER</th>
<th>PR</th>
<th>HER2</th>
<th>CK14</th>
<th>CK56</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>S</td>
<td>P</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>3</td>
<td>0</td>
<td>0</td>
<td>T</td>
<td>N</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

Parameters 20-32 on the pedigree data records are defined as follows:

20. **BRCA2t**: BRCA2 genetic test type, 0 = untested, S = mutation search, T = direct gene test
21. **BRCA2r**: BRCA2 genetic test result, 0 = untested, P = positive, N = negative
22. **PALB2t**: PALB2 genetic test type, 0 = untested, S = mutation search, T = direct gene test
23. **PALB2r**: PALB2 genetic test result, 0 = untested, P = positive, N = negative
24. **ATMt**: ATM genetic test type, 0 = untested, S = mutation search, T = direct gene test
25. **ATMr**: ATM genetic test result, 0 = untested, P = positive, N = negative
26. **CHEK2t**: CHEK2 genetic test type, 0 = untested, S = mutation search, T = direct gene test
27. **CHEK2r**: CHEK2 genetic test result, 0 = untested, P = positive, N = negative
28. **ER**: Estrogen receptor status, 0 = unspecified, N = negative, P = positive
29. **PR**: Progestrogen receptor status, 0 = unspecified, N = negative, P = positive
30. **HER2**: Human epidermal growth factor receptor 2 status, 0 = unspecified, N = negative, P = positive
31. **CK14**: Cytokeratin 14 status, 0 = unspecified, N = negative, P = positive
32. **CK56**: Cytokeratin 56 status, 0 = unspecified, N = negative, P = positive

In the above screenshot, the first pedigree data record includes a positive BRCA2 genetic test (mutation search), and the last pedigree data record includes a negative PALB2 genetic test (direct gene test).
Appendix B
BOADICEA mutation carrier probabilities export data file format (continued on next page)

The BOADICEA mutation carrier probabilities export data format is a simple TAB-delimited text format. It consists of a single header record and a single data record with 20 parameters (data columns) separated by one or more TAB (or whitespace) characters. For clarity, parameters 1-10 are described on this page, and parameters 11-20 are described on the next page.

This screenshot shows parameters 1-10 in a sample BOADICEA mutation carrier probabilities export data file:

<table>
<thead>
<tr>
<th>FamID</th>
<th>Date</th>
<th>Time</th>
<th>SessionNum</th>
<th>CalNum</th>
<th>Name</th>
<th>IndivID</th>
<th>Version</th>
<th>BRCA1(dec)</th>
<th>BRCA1(%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:31:32</td>
<td>bd246bac22f7ae</td>
<td>6</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>0.2203</td>
<td>22.0</td>
</tr>
</tbody>
</table>

The header record includes the column names shown above (and overleaf): 'FamID  Date  Time  SessionNum...'

Parameters 1-10 on the pedigree data records are defined as follows:

1. FamID: Family/pedigree identifier
2. Date: Day of risk calculation in DD/MM/YY format
3. Time: Time of risk calculation in HH:MM:SS format
4. SessionNum: Session number, a unique number generated when the user logs onto the server
5. CalNum: Risk calculation number, increments throughout the current session each time the use runs a risk calculation
6. Name: Firstname/ID of the target
7. IndivID: Unique identifier of the target
8. Version: BWA software version number
9. BRCA1(dec): BRCA1 mutation carrier probability in decimal format (floating point number between 0.0 and 1.0)
10. BRCA1(%): BRCA1 mutation carrier probability in percent format (floating point number between 0.0 and 100.0)
This screenshot shows parameters 11-20 in a sample BOADICEA mutation carrier probabilities export data file:

<table>
<thead>
<tr>
<th>BRCA2 (dec)</th>
<th>BRCA2 (%)</th>
<th>PALB2 (dec)</th>
<th>PALB2 (%)</th>
<th>ATM (dec)</th>
<th>ATM (%)</th>
<th>CHEK2 (dec)</th>
<th>CHEK2 (%)</th>
<th>NoMutation (dec)</th>
<th>NoMutation (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.2809</td>
<td>28.1</td>
<td>0.0006</td>
<td>0.1</td>
<td>0.0019</td>
<td>0.2</td>
<td>0.0026</td>
<td>0.3</td>
<td>0.4936</td>
<td>49.4</td>
</tr>
</tbody>
</table>

Parameters 11-20 on the pedigree data records are defined as follows:

11. BRCA2 (dec)  | BRCA2 mutation carrier probability in decimal format (floating point number between 0.0 and 1.0)
12. BRCA2 (%)   | BRCA2 mutation carrier probability in percent format (floating point number between 0.0 and 100.0)
13. PALB2 (dec) | PALB2 mutation carrier probability in decimal format (floating point number between 0.0 and 1.0)
14. PALB2 (%)   | PALB2 mutation carrier probability in percent format (floating point number between 0.0 and 100.0)
15. ATM (dec)   | ATM mutation carrier probability in decimal format (floating point number between 0.0 and 1.0)
16. ATM (%)     | ATM mutation carrier probability in percent format (floating point number between 0.0 and 100.0)
17. CHEK2 (dec) | CHEK2 mutation carrier probability in decimal format (floating point number between 0.0 and 1.0)
18. CHEK2 (%)   | CHEK2 mutation carrier probability in percent format (floating point number between 0.0 and 100.0)
19. NoMutation (dec) | Probability of no mutation in decimal format (floating point number between 0.0 and 1.0)
20. NoMutation (%) | Probability of no mutation in percent format (floating point number between 0.0 and 100.0)
Appendix C

BOADICEA breast and ovarian cancer risks export data file format

The BOADICEA breast and ovarian cancer risks export data format is a simple TAB-delimited text format. It consists of a single header record and a series of data records (one for each year) with 13 parameters (data columns) separated by one or more TAB (or whitespace) characters.

This screenshot shows a BOADICEA breast and ovarian cancer risks export data file:

<table>
<thead>
<tr>
<th>FamID</th>
<th>Date</th>
<th>Time</th>
<th>SessionNum</th>
<th>CalNum</th>
<th>Name</th>
<th>IndivID</th>
<th>Version</th>
<th>Age</th>
<th>BrCaRisk(dec)</th>
<th>BrCaRisk(%)</th>
<th>OvCaRisk(dec)</th>
<th>OvCaRisk(%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>21</td>
<td>0.0001</td>
<td>0.0</td>
<td>0.0000</td>
<td>0.0</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>22</td>
<td>0.0004</td>
<td>0.0</td>
<td>0.0000</td>
<td>0.0</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>23</td>
<td>0.0008</td>
<td>0.1</td>
<td>0.0000</td>
<td>0.0</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>24</td>
<td>0.0013</td>
<td>0.1</td>
<td>0.0001</td>
<td>0.0</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>25</td>
<td>0.0020</td>
<td>0.2</td>
<td>0.0001</td>
<td>0.0</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>30</td>
<td>0.0107</td>
<td>1.1</td>
<td>0.0003</td>
<td>0.0</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>35</td>
<td>0.0316</td>
<td>3.2</td>
<td>0.0018</td>
<td>0.2</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>40</td>
<td>0.0632</td>
<td>6.3</td>
<td>0.0066</td>
<td>0.7</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>45</td>
<td>0.1065</td>
<td>10.7</td>
<td>0.0167</td>
<td>1.7</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>50</td>
<td>0.1586</td>
<td>15.9</td>
<td>0.0282</td>
<td>2.8</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>55</td>
<td>0.2097</td>
<td>21.0</td>
<td>0.0459</td>
<td>4.6</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>60</td>
<td>0.2977</td>
<td>25.8</td>
<td>0.0698</td>
<td>7.0</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>65</td>
<td>0.3072</td>
<td>30.7</td>
<td>0.0894</td>
<td>8.9</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>70</td>
<td>0.3561</td>
<td>35.6</td>
<td>0.1060</td>
<td>10.6</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>75</td>
<td>0.3963</td>
<td>39.6</td>
<td>0.1213</td>
<td>12.1</td>
</tr>
<tr>
<td>bwa4-19-2</td>
<td>06/01/16</td>
<td>14:01:58</td>
<td>bd246bac22f7ae</td>
<td>5</td>
<td>301</td>
<td>1</td>
<td>v4beta9</td>
<td>80</td>
<td>0.4313</td>
<td>43.1</td>
<td>0.1356</td>
<td>13.6</td>
</tr>
</tbody>
</table>

The header record includes the column names shown above: 'FamID Date Time SessionNum..'

The data record parameters are defined as follows:

1. FamID: Family/pedigree identifier
2. Date: Day of risk calculation in DD/MM/YY format
3. Time: Time of risk calculation in HH:MM:SS format
4. SessionNum: Session number, a unique number generated when the user logs onto the server
5. CalNum: Risk calculation number, increments throughout the current session each time the user runs a risk calculation
6. Name: Firstname/ID of the target
7. IndivID: Unique identifier of the target
8. Version: BWA software version number
9. Age: Age in years for the breast and ovarian cancer risk prediction
10. BrCaRisk(dec): Breast cancer risk in decimal format (floating point number between 0.0 and 1.0)
11. BrCaRisk(%): Breast cancer risk in percent format (floating point number between 0.0 and 100.0)
12. OvCaRisk(dec): Ovarian cancer risk in decimal format (floating point number between 0.0 and 1.0)
13. OvCaRisk(%): Ovarian cancer risk in percent format (floating point number between 0.0 and 100.0)