

Fam3PRO Shiny App User Guide

Getting Started	2
Forgot Username/Password	4
Step 1 :Add/Load Pedigrees	6
Step 2: Create/Modify Pedigree	7
Step 3: Run Fam3PRO	8
Step 4: Output Results	8

Getting Started

1. Click either of the buttons to the sign-up page

PPI: PanelPRO Interface 

[Log In](#) **[Sign Up](#)** [Forgot Username or Password](#) [Bot Check](#)

Please log in

 **User Name**

 **Password**


[Log in](#)

Sign up

[Forgot Username or Password](#)

OR

2. Click the numbers and hit "Submit" to pass the bot check

PPI: PanelPRO Interface 

[Log In](#) [Sign Up](#) [Forgot Username or Password](#) **Bot Check**

Bot Check

First, let's check if you're human.

6 4

Check the numbers listed above and hit submit.

☐ 1 ☐ 2 ☐ 3 ☒ 4 ☐ 5 ☒ 6

Submit

Success, you're not a bot. You can proceed to [sign-up](#) or [recover your account information](#).

3. Enter information to finish creating a new account (“Enter manager username” is optional and can be left in blank)

Username requirements:

1. Usernames can only contain lowercase letters, numbers, and underscores (_)
2. The length of your username should be less than 60 characters

Password requirements:

1. Your password must be at least 8 character in length
2. Your password must contain one of each: lowercase letter (a-z), upper case letter (A-Z), number (0-9), symbol (example: !, @, #, \$)

PPI: PanelPRO Interface



[Log In](#) [Sign Up](#) [Forgot Username or Password](#)

Create Account

Complete the form below to create a user account.

Usernames can only contain lower case letters, numbers, and underscores (_).

New Username

Optionally, you can add one or more managers who will be able to view and download any pedigrees you save to your user account. This is useful for studies that have multiple providers enrolling patients into the same study. Your manager(s) must have already created their own user account(s) with 'manager' level permissions.

Enter managers' usernames:**Email Address****Re-enter your email address**

Passwords must be at least 8 character in length and have one of each: lowercase letter, upper case letter, number, symbol.

New Password**Re-enter New Password**

4. After the account is created, you will be guided back to the log-in page to enter your credentials. Once logging in, you will see the home page as shown below, and you are all set for using the application.

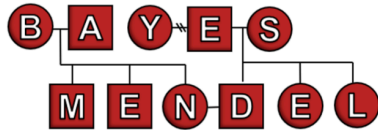
PPI: PanelPRO Interface

[Log out](#)[Home](#) [Manage Pedigrees](#) [My Account](#)

Home

What is PanelPRO?

PanelPRO, created by the BayesMendel Lab at Dana-Farber Cancer Institute, is a multi-cancer/multi-gene risk prediction model which utilizes family history to estimate the probability that a patient has a pathogenic or likely pathogenic variant (P/LP) gene variant on up to 24 different cancer susceptibility genes and, estimates a patient's future risk of cancer for up to 17 different cancer types. PanelPRO also includes the BRCApro, MMRpro, and MelaPRO risk models and users have the ability to create customized models focused on specific cancers and genes. The PanelPRO software package was written in the statistical programming language R. You can learn more about PanelPRO at the [BayesMendel lab's website](#).



Forgot Username/Password

1. Click either of the buttons to the Username/Password recovery page

PPI: PanelPRO Interface

[Log In](#) [Sign Up](#) [Forgot Username or Password](#) [Bot Check](#)

OR

Please log in

User Name

Password

[Forgot Username or Password](#)

2. Click the numbers and hit "Submit" to pass the bot check

PPI: PanelPRO Interface



[Log In](#) [Sign Up](#) [Forgot Username or Password](#) [Bot Check](#)

Bot Check

First, let's check if you're human.

6 4

Check the numbers listed above and hit submit.

☐ 1 ☐ 2 ☐ 3 ☒ 4 ☐ 5 ☒ 6

Submit

Success, you're not a bot. You can proceed to [sign-up](#) or [recover your account information](#).

3. Enter the email address used for creating the account. If you only forgot your username, the username will be directly sent to the email address. If you forgot your password or both, you will be asked to enter a recovery code that will be sent to your email address. Once the recovery code is entered, you can reset your password.

Select which credentials you need to recover:

- ☐ username
- ☐ password
- ☒ both

Submit

Thank you. If the email address provided is in our system then you will receive one email with your username and a separate email with a password recovery code.

To reset your password, enter the recovery code below and submit it.

Recovery Code

Submit Recovery Code

If you don't receive the code after two minutes, click the button below.

Send New Code

Thank you. Please reset your password below.


Enter a new password

Re-enter the new password

Reset Password

Step 1: Add/Load Pedigrees

1. Go to the **“Manage Pedigrees”** tab. You can either create a new pedigree from proband or use the default **“Example Pedigree”** as a template and make modifications on it later.
2. If you chose to load an existing pedigree, please wait for the Pedigree to load (which takes a few seconds) and click **“Get Started”** to proceed to the **“Preview”** page.

PPI: PanelPRO Interface  **Dana-Farber**
Cancer Institute [Log out](#)

[Home](#) [Manage Pedigrees](#) [My Account](#)

Manage My Pedigrees

[Create or Load](#) [Preview](#) [Copy](#) [Download](#) [Delete](#)

Create New or Load Existing Pedigree

Working pedigree: no pedigree has been loaded or created yet.

To get started, you will either need to create a new pedigree using our pedigree builder or load an existing pedigree from your user account.

Select a start-up option:

☐ Create new

☒ Load existing

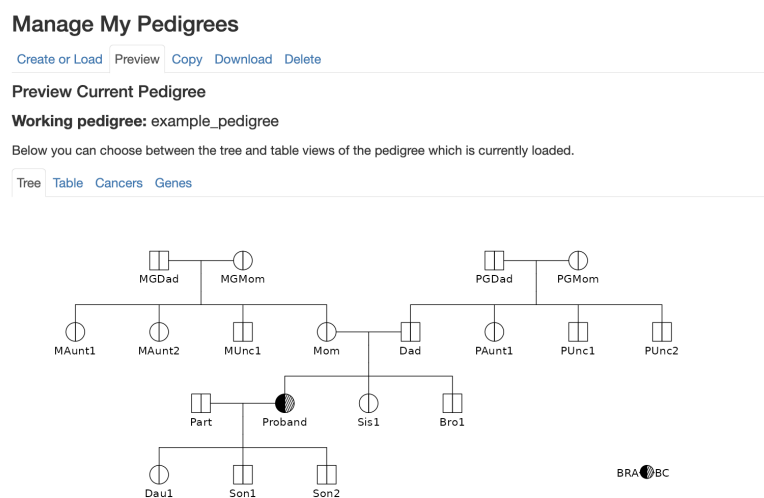
Select a user account:

Select a pedigree to load:

Clicking the button below will load your selected pedigree and will take you to the create/edit pedigree screen to view and/or edit your pedigree.

[▶ Get Started](#)

3. The **“Preview”** page allows you to look at the visualized pedigree. If you are a manager, you can load or use the **“Copy”** and **“Delete”** tab to copy/delete pedigrees from the associated accounts. The **“Download”** tab currently supports users downloading the pedigrees in either .csv or .rds format.



Note: the image above will only display a maximum of 4 cancer types.

Step 2: Create/Modify Pedigree

The “Create/Modify Pedigree” tab allows addition/deletion to elements in the working pedigree and display the pedigree in an interactive mode. Once you finish editing the pedigree, make sure to click “**Update and Save Pedigree**” to save your changes if storing pedigree information is allowed, or your changes will be lost. *Please double check your eligibility for saving the pedigrees with your organization!*

[Home](#) [Manage Pedigrees](#) [Create/Modify Pedigree](#) [PanelPRO](#) [My Account](#)

Select a relative to edit:

Proband (Proband)

Update and Save Pedigree

Tree [Table](#) [Cancers](#) [Genes](#)

Demographics [Cancer Hx](#) [CBC Risk](#) [Tumor Markers](#) [Surgical Hx](#) [Genes](#)

Proband's Demographics

Enter the proband's demographic information below.

Unique Pedigree ID:

example_pedigree

Sex assigned at birth:

Female

Check here if deceased:
☐ Deceased

Current Age (1 to 89):

50

Race:

White

Hispanic Ethnicity:

Hispanic

Ancestry (check all that apply):
☒ Ashkenazi Jewish
☒ Italian

Download Image

Note: the tree above only displays PanelPRO cancers. Unknown cancer ages will show as 0. Gene tests, surgical history, and tumor markers are not displayed.

- **Left Panels:**

1. Tree: an interactive tree that can be dragged around, where users can zoom in/out, show the pedigree in full screen, manually adding/deleting nodes.
2. Table: displaying the pedigree information as a dataframe, including all the basic information for all nodes in the pedigree.
3. Cancers: displaying only the nodes with cancer diagnoses and relevant information (age of diagnosis, other cancer).
4. Genes: showing the gene testing results for each gene variant and each node.

- **Right Panels:**

1. Demographics: panel for modifying demographic information for each node (to switch proband and relatives, use the drop-down tab above the panels: **“Select a relative to edit”**).
2. Cancer Hx: allows users to manually add cancer history for the proband and relatives, including cancer types diagnosis age (which can be left in blank if unknown).
3. CBC risk: allows users to specify the contralateral breast cancer risk for a node by choosing the answers for the questions below:

[Demographics](#) [Cancer Hx](#) [CBC Risk](#) [Tumor Markers](#) [Surgical Hx](#) [Genes](#)

Proband's Contralateral Breast Cancer Risk

Was the 1st breast cancer pure invasive, mixed invasive and DCIS, or unknown?

Pure invasive ▼

Was the 1st breast cancer treated with anti-estrogen therapy?

No ▼

Is there a personal history of high risk pre-neoplasia (ie atypical hyperplasia or LCIS?)

Unknown ▼

What were the BI-RADS breast density results?

b - scattered areas of fibroglandular density ▼

What was the size of the 1st breast tumor?

Unknown ▼

4. Tumor Markers: allows input for test results of any tumor markers for the related cancer of the node.
5. Surgical Hx: allows input for a node's surgical history and the age at the specific surgery procedure.
6. Genes: allows users to enter and edit germline gene test results based on the instructions. Users can create/edit panels, edit panel results, and view results in a summary table.

Step 3: Run Fam3PRO

1. Hover to the “Fam3PRO” tab, you will see the current version of the Fam3PRO package running and the name of the working pedigree.
2. Click “Show Fam3PRO” Documentation if you want to learn further details of the Fam3PRO.
3. There are different options of model specifications available: PanPRO22 (default), BRCAPRO, BRCAPRO5, BRCAPRO6, MMRPRO, PanPRO11. Detailed cancer types and genes for each model are shown in respective specifications.
4. Adjust model parameters for maximum simultaneous mutations and year interval for future cancer risk.
5. Click “Run Fam3PRO”. You will see a notification below about the estimated time for completion based on the active processes running at the time (**please do not close the window**). An email will be sent after the result is ready.

[Home](#) [Manage Pedigrees](#) [Create/Modify Pedigree](#) **PanelPRO** [My Account](#)

PanelPRO

version: 1.1.0

Working pedigree: test

[Run PanelPRO](#) [PanelPRO Results](#)

Instructions

Specify the model parameters below then hit the 'Run PanelPRO' button at the bottom of the page. For more information on the parameters click on the 'Show PanelPRO Documentation' button.

[Show PanelPRO Documentation](#)

Basic Settings

Model Specification ('model_spec'):

PanPRO22

This model specification includes:

18 Cancers: Brain, Breast, Colorectal, Endometrial, Gastric, Kidney, Leukemia, Melanoma, Ovarian, Osteosarcoma, Pancreas, Prostate, Small Intestine, Soft Tissue Sarcoma, Thyroid, Urinary Bladder, Hepatobiliary, Contralateral

22 Genes: ATM, BARD1, BRCA1, BRCA2, BRIP1, CDH1, CDK4, CDKN2A, CHEK2, EPCAM, MLH1, MSH2, MSH6, MUTYH, NBN, PALB2, PMS2, PTEN, RAD51C, RAD51D, STK11, TP53

Maximum simultaneous mutations allowed per individual ('max.mut'):

2

Year interval for future cancer risk (1 to 10) ('age.by'):

5

Advanced Settings

Note: running PanelPRO generally takes about 2-3 minutes but may take 10 minutes or longer for large pedigree with many unknown ages. The blue status bar at the top of the screen will stop cycling once the analysis is complete.

[Run PanelPRO](#)

Step 4: Check Output Results

1. After running the Fam3PRO, you will receive an email notification when the process finishes. You will be automatically directed to the page with a cancer risk probability plot. If you have multiple processes running under one account, you will receive the email notification when the last process is complete.

PanelPRO result is ready Inbox x

hereditarycancer+noreply@ds.dfci.harvard.edu

to me ▼

Dear User,

The job you submitted to PanelPRO is complete.

You can now return to the site and check your results.

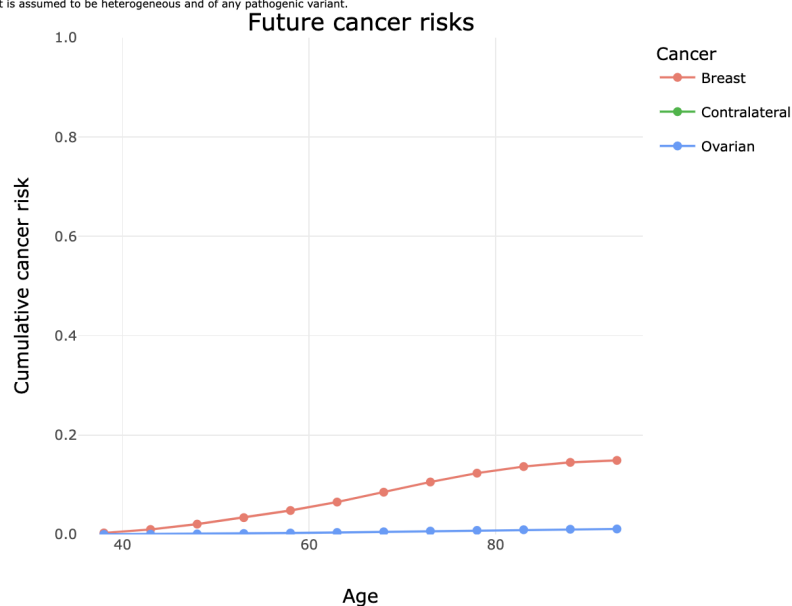
Thanks,

The BayesMendel Lab at Dana-Farber Cancer Institute

2. You can switch between the tabs to look at the carrier probabilities and cancer risks in a table or a plot.

Variability in estimates may arise from an imputation process for missing ages.
The range of estimates is indicated by error bars or (lower, upper) estimates.

If the hetero/homogeneity or variant of the gene has not been specified,
it is assumed to be heterogeneous and of any pathogenic variant.



Thank you for using Fam3PRO!