Gamma Bomb! 2.0 – User Guide

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System Requirements: MATLAB R2012b (newer/older versions of MATLAB might not work with this program), Windows Operating System

Program Descritpion: *Gamma Bomb! 2.0 is a collection of MATLAB scripts used to fit mathematical models to Time Activity Curves derived from blood data in dynamic PET studies. Gamma Bomb! 2.0 is based off a MATLAB script called "patient_AIF_gamma_read.m" originally written by Spencer Bowen, PhD. for the Catana Lab Group in 2012.*

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Getting Started:

Thanks for choosing *Gamma Bomb! 2.0* for your blood data analysis! We hope this user guide provides you with sufficient support while using this collection of MATLAB scripts.

System Requirements:

Be sure your system adheres to the following requirements:

1. Windows Operating System (software was tested on Windows 7)
2. MATLAB version R2012b (older/newer versions of MATLAB may not be compatible)

Before continuing, please ensure you are in the "Default View" of MATLAB. (Select "Layout" > "Default" from the Toolbar.

Add Scripts to MATLAB's Current Path:

Option 1: Add Scripts to the MATLAB Root

1. Download the Gamma_Bomb_2.zip folder to the location of your MATLAB root.
    a. To locate your MATLAB root, open MATLAB and type: `matlabroot` into the command prompt.
2. Be sure to unzip all files before trying to use GammaBomb! 2.0.

Option 2: Add Scripts to a Custom Location

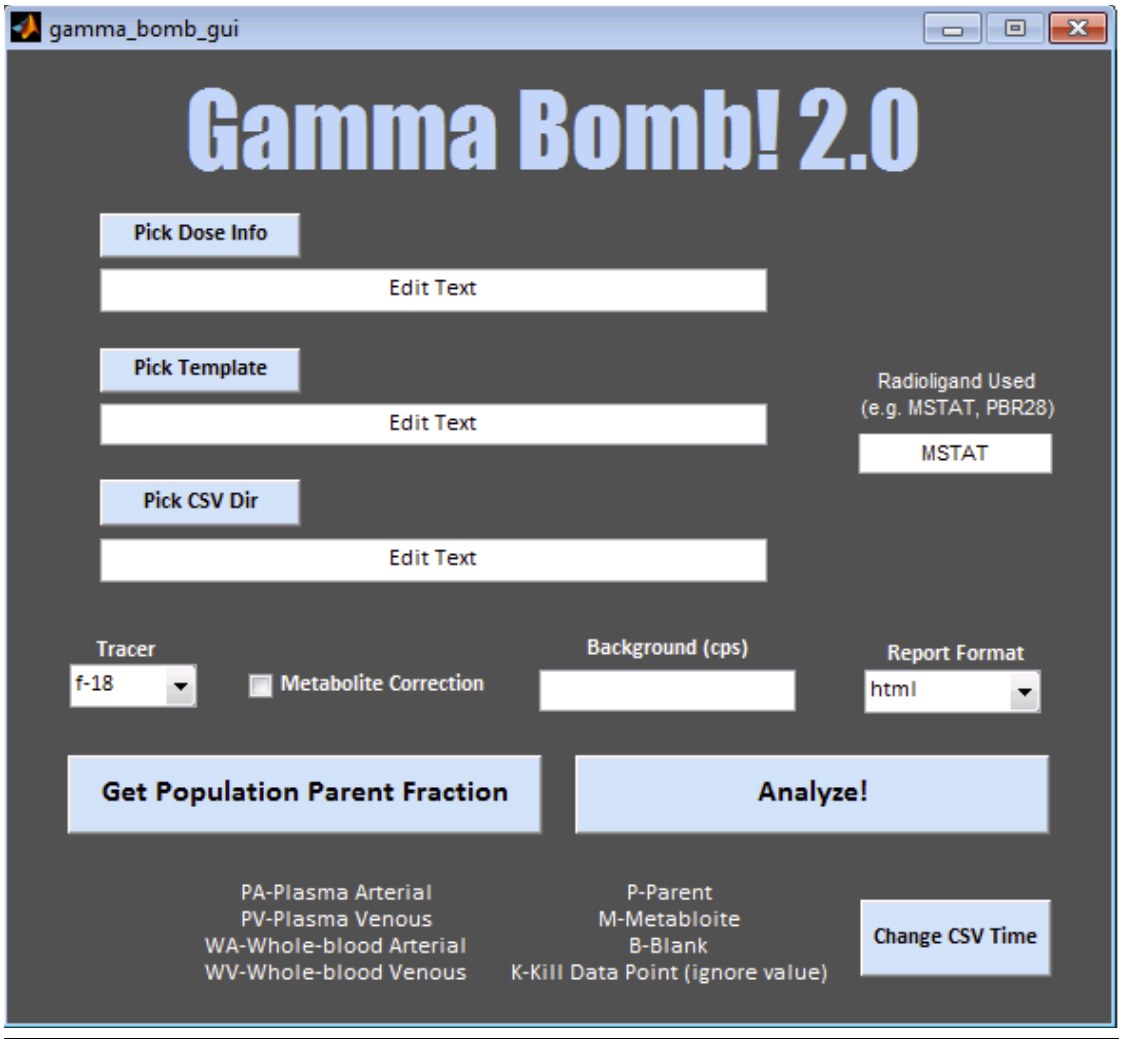
1. Download the Gamma_Bomb_2.zip folder to your custom location (i.e. C:\Documents\MyCodes)
2. Open MATLAB
3. Add your custom location to the current path.
    a. Browse for the folder where you downloaded the scripts in the left panel labeled "Current Folder"
    b. Right click on the folder and select "Add to Current Path" > "Selected Folders and Subfolders"

Add Data Files to MATLAB's Current Path:

1. Browse for the data files you wish to analyze in the left panel labeled "Current Folder".
2. Add the data files to the current path.
    a. Right click on the folder containing the data files and select "Add to Current Path" > "Selected Folders and Subfolders"

Open GammaBomb! 2.0

Type `gamma_bomb_gui` into the command prompt. The following window should appear:

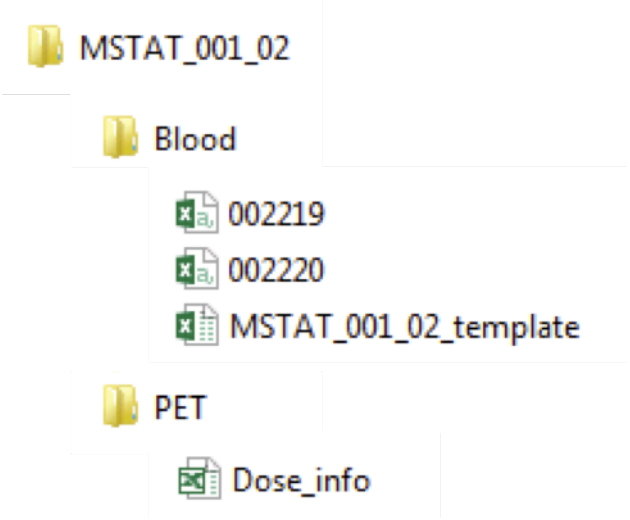


Congratulations! You have successfully opened GammaBomb! 2.0 on your computer and are ready to start analyzing data.

If the window did not appear or MATLAB displayed an error, be sure you have added the GammaBomb 2.0 scripts to your current path. Try searching your computer for "gamma_bomb_gui.m" or "gamma_bomb_gui.fig" and ensure that the location of these files has been added to the current path.

Necessary Data Files:

GammaBomb! 2.0 requires very specific types of blood data files. Before beginning analysis, be sure that your data has the following file-structure:



Necessary Files/Folders:

MSTAT_001_02 (Participant Folder) - Each participant's data files should be located in a folder. The folder name should contain the ligand name, followed by the participant number.

Blood Folder – This folder should be located inside the participant folder and should contain all blood data files.

002219 & 002220 – These are CSV files that contain radioactive count data. They should be numbered sequentially. At least one is needed, but there is no limit to the number of CSV files allowed. All CSV files should be located in the Blood folder.

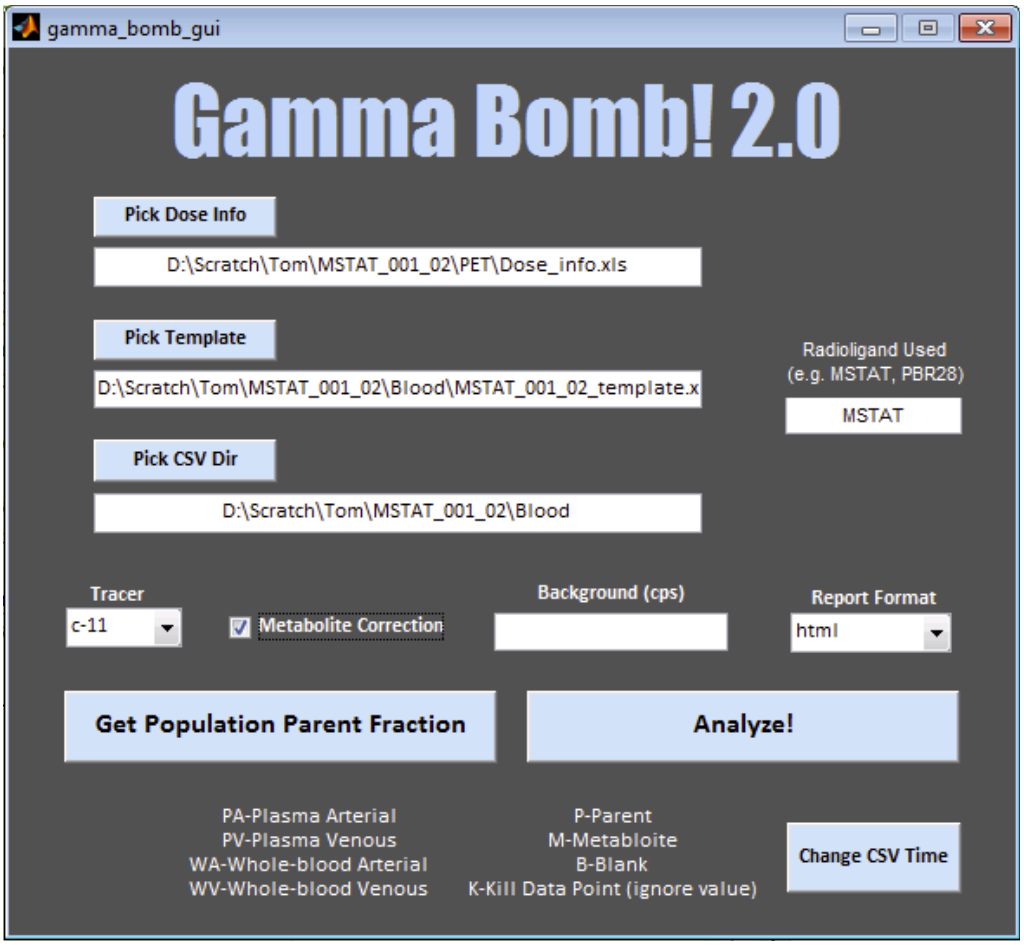
MSTAT_001_02_template – This Excel file is a template file showing what was contained in each of the tubes the chemist tested. This should be located in the Blood folder.

PET Folder – This folder is located in the Participant folder and contains the Dose Info file.

Dose_info – This Excel file contains demographic information about the participant and some basic information about the scan (e.g. Time of Injection). It should be located in the PET folder.

Filling Out the GUI

To begin analyzing data, fill out all necessary info on the GammaBomb! 2.0 GUI and then click the “Analyze!” button. The following graphic shows an example of a GUI that has been filled out and is ready for data analysis.



Pick Dose Info: Choose an Excel file (should be located in the PET folder) that includes necessary demographic information. It will probably be called “Dose_info.xls”

Pick Template: Choose an Excel file (should be located in the Blood folder). The first sheet of this file should show a grid outlining what was contained in each tube. The codes for this file are explained on the bottom of the Gamma Bomb! GUI (PA, PV, WA, etc.)

Pick CSV Dir: Select the directory of the CSV file(s) that contain blood data (CSV files should be located in the Blood folder).

Tracer: Select the radiotracer used for this participant (C-11 or F-18).

Metabolite Correction: Check this box if you wish to incorporate metabolite correction into the Time Activity Curve Models.

Background (cps): Enter a number here if you have already calculated the background necessary to compute parent fraction statistics. (If you have not already calculated this, the computer will figure it out for you.)

Report Format: Select whether you wish to generate a final report in PDF, HTML, or both formats.

Change CSV Time: Click this button to generate new CSV files with different time stamps.

Radioligand Used: In this box, type the name of the radioligand used (e.g. MSTAT, PBR28, etc.). The name of the radioligand is not needed for any data analysis, but will appear in the final report. The name typed in this box should match the name of the ligand on the participant's main data folder. By default, this box will read "MSTAT".

Get Population Parent Fraciton: Click this button to generate a Parent Fraction curve from participants' data that has already been analyzed. See the "Get Parent Fraction Data from a Population" section of this User Guide for more information.

Analyze!: Click this button to begin data analysis.

Shortly after clicking "Analyze!," a message should appear summarizing some basic information and data from the study. If all of this information seems to be correct, click "Ok" to continue with data analysis. If something seems off exit the window, double check that all of your data files are correct, and try analyzing again.

If previous data analysis has already been performed on the current data, a dialogue box will appear to warn you that all previous analysis will be overwritten. Select "yes" to continue and overwrite all previous analyses. Select "no" to exit the program.

Data Output & the Final Report

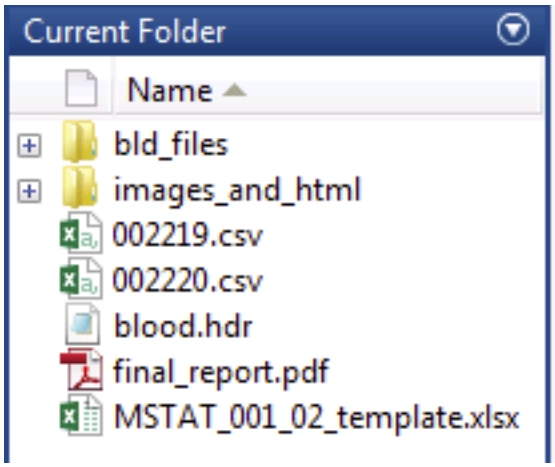
Data Analysis of a single participant using GammaBomb! 2.0 typically takes between 5-10 minutes. Throughout the data analysis, many statistics and output messages will appear on the screen. After all analysis is complete, the following message will appear in MATLAB's command prompt window:

```
*****ANALYSIS COMPLETE*****
```

IMPORTANT: While the computer is analyzing the data, many graphs and figures will pop up on the screen. These graphs and figures are converted to .png and .bmp images via screenshot, so it is suggested that you not have any other programs open on the computer while GammaBomb 2.0 is running.

Output Files:

After analysis is complete, the following files and folders will now be located in the participant's Blood folder:



bld_files: This folder contains all the generated bld data files. These typically include parentfraction.bld, plasma_art.bld, plasma_art_Feng.bld, etc. These data files contain data from TAC and Parent Fraction fits/models.

images_and_html: This folder contains all the images generated by the report. .BMP images are of graphs. .PNG images are of LaTex equations that are shown in the final report. This folder will also contain "final_report.html", the HTML version of the final report. The HTML final report must remain in the same folder as the images in order for the images to be visible in the report.

CSV & XLS files: These are the original data files that were in the Blood folder and were used for analysis.

blood.hdr: This file contains some generic information about the study (e.g. Time of Injection, BAT offset, Duration of the study, etc.)

final_report.pdf: This is a PDF summary of the data analysis. It will appear here if the PDF format was selected in the GammaBomb! 2.0 GUI.

Additional Files: If you navigate into the participant's PET folder, you will notice that several .hdr files and a PDF file have appeared there. The .hdr files were used to calculate the Bolus Arrival Time (BAT) and the PDF file shows a graph of the BAT.

The Final Report:

The 3-6 page final report will be in either PDF or HTML format (or both) and will contain several sections:

Participant Information: This section contains demographic information about the participant as well as general information about the study.

Time Activity Curve (TAC) Models: This section contains information about the models used to fit the Time Activity Curve. Currently, GammaBomb! 2.0 uses a Feng Model and a Linear to 3-Exponential Model to fit the TAC. The report shows how many outliers were omitted from analysis, shows graphs of each of the models, and gives a "fit metric" for each of the models. The fit metric describes the amount of space between the raw data and the fit. A fit metric closer to zero indicates a better fit.

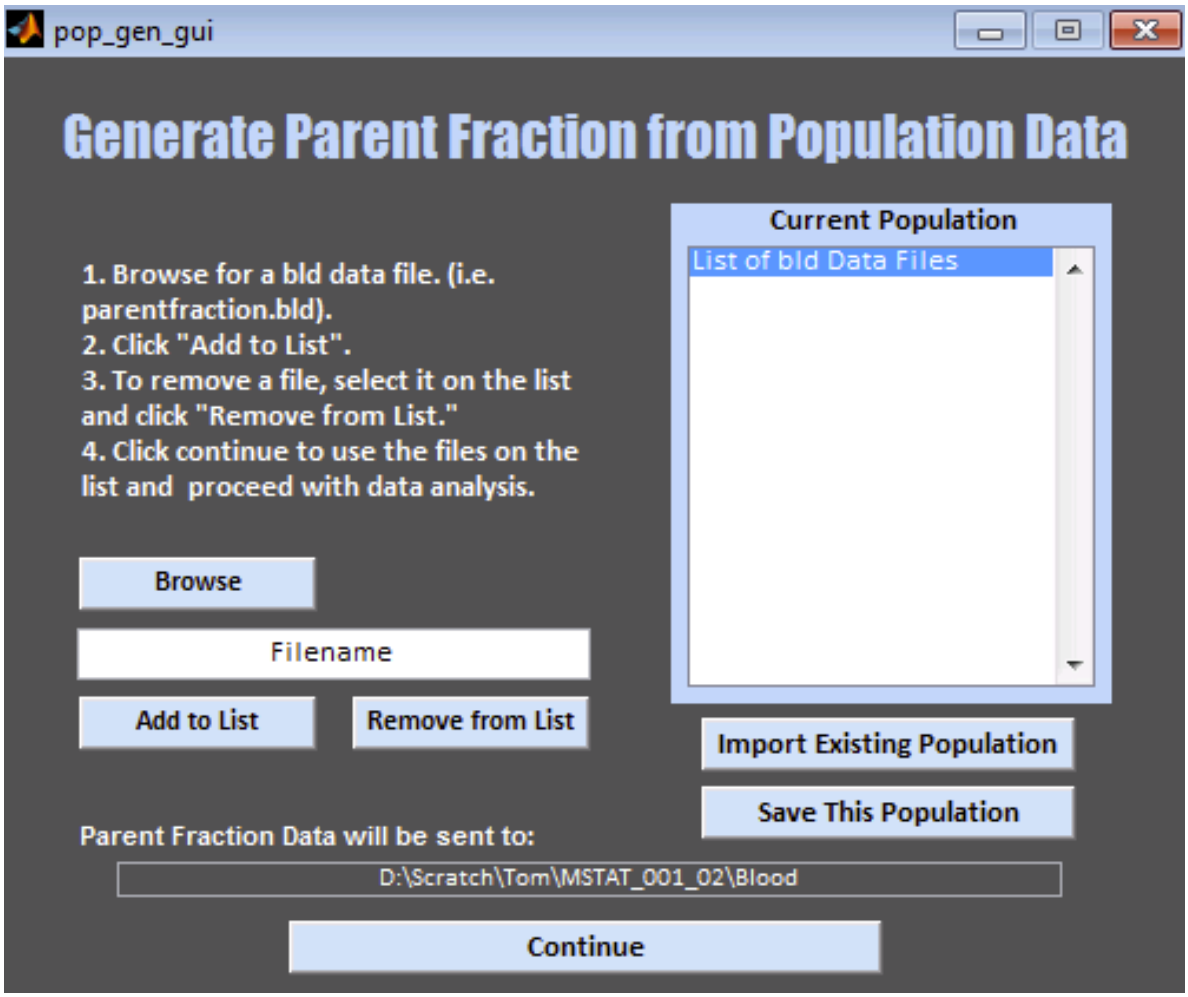
Summary of Parent Fraction Fit Statistics: This section shows a data table that lists the R-square, Adjusted R-Square, and Degrees of Freedom (DFE) for each of the Parent Fraction Fits. Currently, GammaBomb! 2.0 fits Parent Fraction Data to four models: Hill, Linear to Exponential (Lin2Exp), Exponential (Exp), and Power. This section also lists which model was the best fit of the parent fraction data based on r-squared value.

Parent Fraction Fits: This section displays graphs of each of the parent fraction fits.

Histograms for Parent Fraction Data Points: This section shows a histogram for each of the parent fraction data points. The title of each histogram indicates the time stamp for the data point. Blue bars on the histograms signify parent data. Red bars signify metabolite data. Before plotting, data are adjusted by background subtraction and decay correction.

Using Population Data:

GammaBomb! 2.0 is capable of using a custom population of participants to generate a Parent Fraction curve. To access the population-selection tool, click “Get Population Parent Fraction” on the main GUI. The following window will open:



Creating a Custom Population:

1. To create a population, begin by clicking “Browse” to search for existing .bld files that contain parent fraction data.
2. Once a file is selected, its name should appear in the box that currently says “Filename.”
3. Click “Add to List” to add the file to the population list.
   Note: each file can only be added once to the list. As each file is added, it should appear on the list under “Current Population.”
4. If you wish to remove a data file from the list, highlight it and click “Remove from List.”

Saving the Current Population:

1. Once two or more participants have been added to the population, you can click "Save this Population" to save the list of data files.
2. A dialogue box will appear asking you to name the population file and to select where it should be saved.
3. The list of data files will be saved as a .bld file.

Importing an Existing Population:

1. Perhaps you would like to use the same population of parent fraction data for several participants. To load an existing population, click "Import Existing Population" and browse for the desired .bld file.
2. The .bld file selected should contain the names of several other .bld files that contain parent fraction data.

Troubleshooting:

1. The GammaBomb! 2.0 GUI does not appear when I type `gamma_bomb_gui.`

Enusre that the GammaBomb! 2.0 scripts have been added to the current MATLAB path. See page 3 for details.

2. At the very end of analysis, some red errors pop up in the MATLAB command window. Everything seems to be fine, but this concerns me.

This is normal and has to do with the display of LaTex equations in the HTML final report.

3. The program seems to freeze and is taking a long time to analyze the data.

This is normal. During the beginning of analysis, the computer must estimate the Bolus Arrival Time (BAT) which involves some heavy math. Later, the computer needs to calculate many integrals which also takes some time. If you do not see the `*****ANALYSIS COMPLETE*****` message, then the data is still being analyzed. If the data has been undergoing analysis for more than 10 minutes, try restarting GammaBomb! 2.0 or double check that your input files are correct.