# Graphical User Interface (GUI) Implementation for Agent-Based Microbial Radiobiology Model


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## Abstract

Sending human life to explore the Moon and Mars will be challenging. The Earth's magnetic field naturally protects life from deep-space particle radiation that will pose health risks to humans in deep space. Current research is insufficient as it can only report cell damage in the form of bulk growth curves. AMMPER (Agent-based Model for Microbial Populations Exposed to Radiation) is an open-source, agent-based, computational model designed to simulate the effects of deep-space radiation on individual yeast cells (*Saccharomyces cerevisiae)* to facilitate interpretation of biological radiation experiments. Version 1.0 of the code ran in a console, limiting the program's accessibility. Here we present a graphical user interface (GUI) for AMMPER, developed internally by converting input points and UI files, designing an application and logo, and expanding program packages. Additionally, optical assistance corresponding with simulation parameters has been integrated. Future work will include creating a bit installer and runtime environment for AMMPER to increase ease of download and use. Ultimately, the creation of the GUI has two main goals: to facilitate the integration of computational models into the work of researchers in microbial radiobiology, and to act as an interactive and visual resource for space biology education.


## Background

**Deep Space Radiation & Biology**

- Modern human spacecraft is protected by our planet's magnetic field in an area called Low Earth Orbit (LEO)[5]
- Outside of the LEO exists ionizing radiation, a causation of cause DNA damage and oxidative stress,[5] specifically:
  - Galactic Cosmic Radiation (GCR), chronic and carcinogenic
  - Solar Particle Events (SPE), sporadic and unpredictable
- Deep space exploration is dangerous and expensive; often, computational modeling acts as an alternative research resource
- There are no computational models, to our knowledge, that report damage on the individual cell level as opposed to bulk growth curves, as cell damage is naturally heterogeneous,[5] prompting the creation of Agent-based Model for Microbial Populations Exposed to Radiation (AMMPER) by Amrita Singh and Daniel Palacios

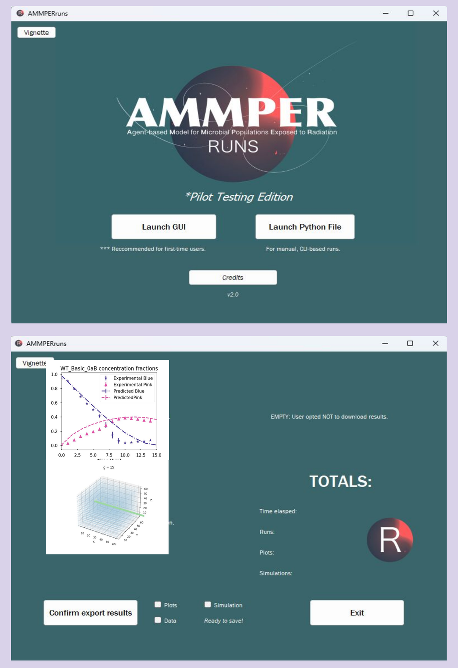
**AMMPER v1.0**

- Uses yeast (*S. cerevisiae*) as a model for the impact of radiation of eukaryotic cells
- Integrates data from BioSentinel, the first biological CubeSat to fly beyond the LEO, and the RITRACKS library, which explores radiation dispersion and energy in three dimensions, to explore the impact of deep space radiation
- Coded in Python and offers several simulation types (150MeV Proton, NSRL GCRSim, Deep Space, Gamma), the radiation dosage (if applicable), cell type (Wild Type, rad51), and ROS Model (Basic, Complex)[5]

**Statement of Purpose**

- Version 1.0 ran in a purely console-oriented interface,[5] limiting its use to those with computational knowledge
- A graphical user interface (GUI) acts as the mediator between a system's hardware and software and the human attempting to operate it[2]
- AMMPER's GUI converts input points into values using object-oriented programming (OOP) and modularization in Python

## Future Directions & Release



While the AMMPER GUI is an improvement for the user experience of the software, there are several other areas for potential software enhancement:

- Multi-run version (pictured to the left)
- Bit installer
- Machine learning integration
- Vignette/tutorial feature
- Installation & comprehensive use guide

**AMMPER Source Code**

## GUI Phases

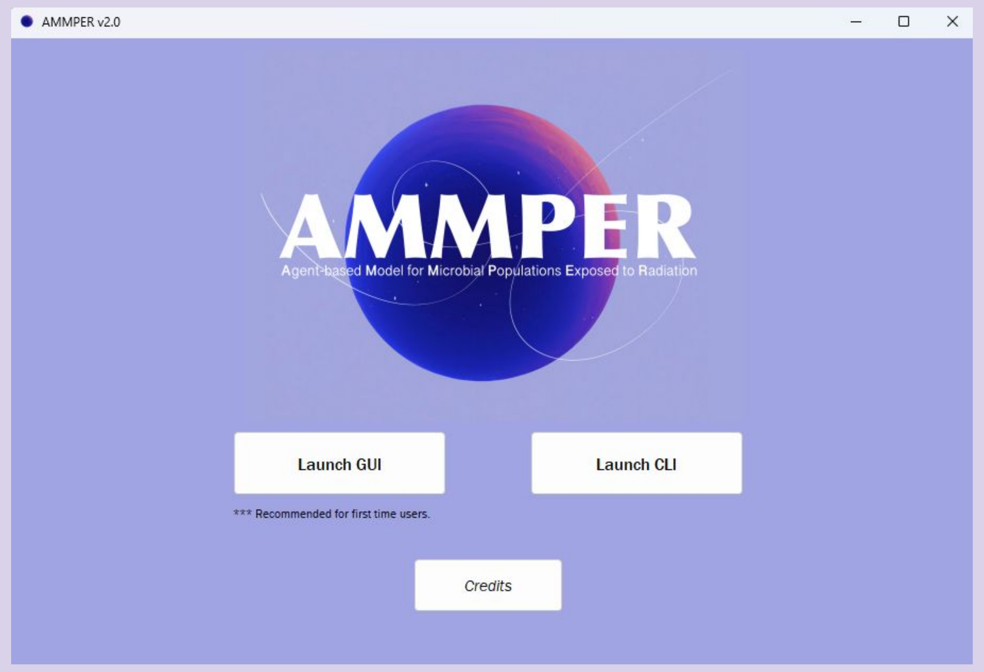



*Figure 1.* Graphical user interface launch screen.


*Figure 2.* Parameter adjustment screen.


*Figure 3.* Loading screen.

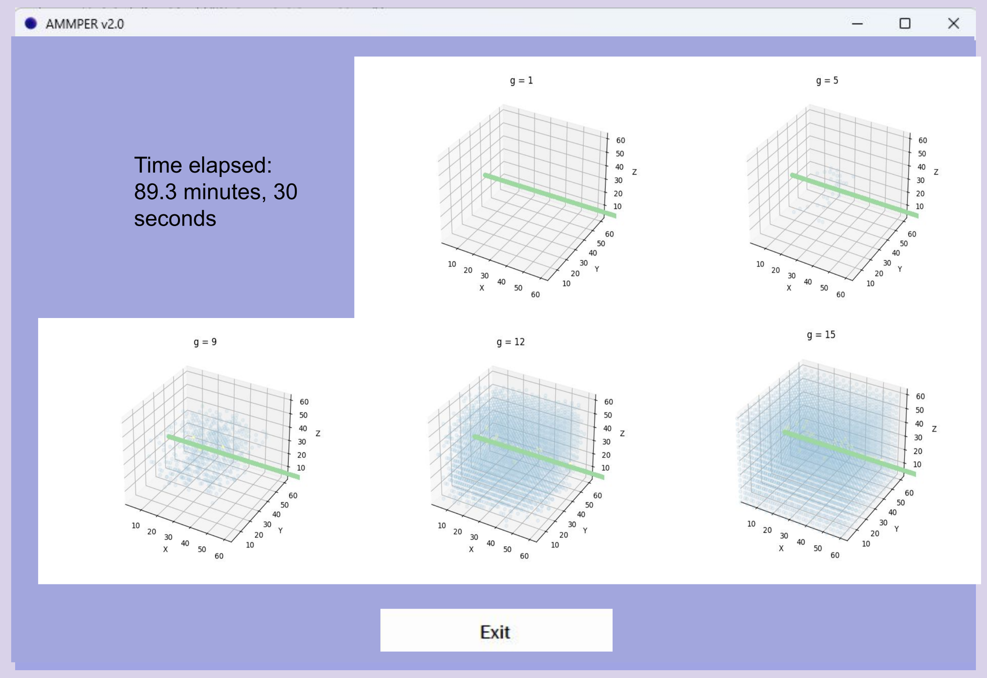



*Figure 4.* Ending screen.

We created the AMMPER GUI with the software engineering design principle known as Human-Computer Interaction (HCI), which focuses on how humans and hardware interact with each other[1]. This is often found in the form of a graphical user interface (GUI), which converts input point for a program through the use of buttons, windows, and control panels.[2] Additionally, the concept of kineticons (kinetic icons) is implemented through the visualization screen[1], as well as the addition of paged display and quick buttons for energy efficiency.[4]

We programmed the GUI using Python libraries in the VSCode IDE. The GUI was generated using the Qt Creator platform into an XML which was converted to Python script using a console-based compiler. Then the GUI was made operational by connecting the functionality of the original AMMPER code to the buttons on the GUI. AMMPER is compatible with Windows and Mac devices.

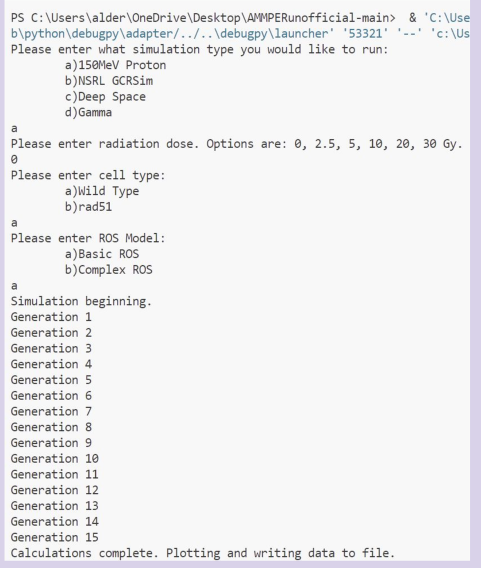
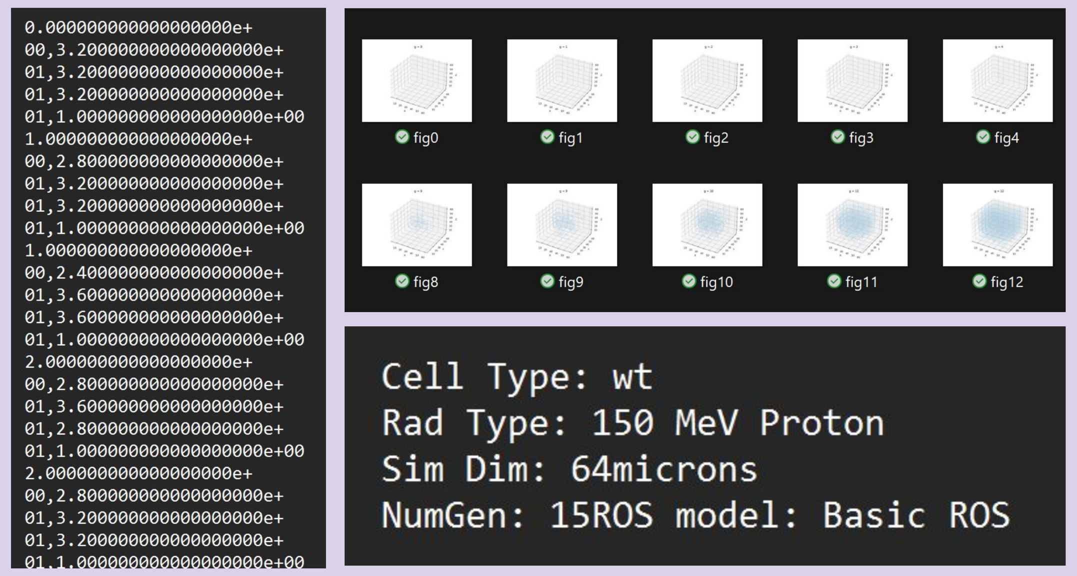


*Figure 5.* AMMPER v1.0 parameters.




*Figures 5, 6 & 7.* Data extraction from AMMPER v1.0 for comparison.

## AMMPER Output

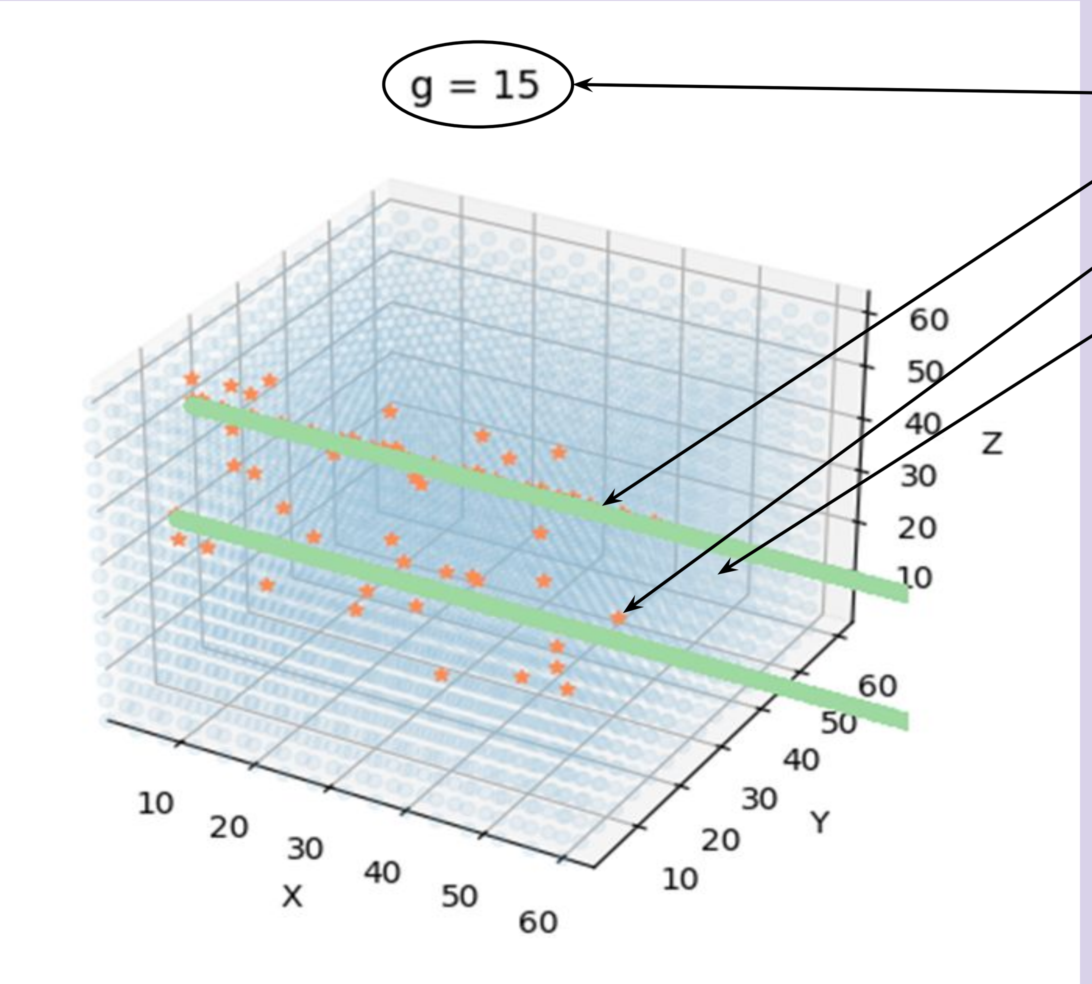



*Figure 5.* 150 MeV Proton simulation output. Image credit to Daniel Palacios.

### Key

Generation number (g = 15)

Radiation event

Dead cells

Healthy cells

### Analysis

- Example of a 150 MeV Proton simulation in AMMPER
- Simulates the impact of radiation events on healthy *S. cerevisiae* cells
- Output is generated and saved to the device in fifteen sequences, according to the generation of cell replication

## References & Acknowledgements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[5]Singh, A., Lera, M. P., Santa Maria, S., & Lee, J. A. (2023)Agent-based Model for Microbial Populations Exposed to Radiation (AMMPER) simulates yeast growth for deep-space experiments. bioRxiv: 2023.10.29.564630. doi:10.1101/2023.10.29.564630



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