GenEst (v1.0.0) Software User Guide

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# Abstract

GenEst is a software tool for estimating bird and bat fatalities at renewable power facilities. The software package is available with a user-friendly graphic interface as well as a flexible and powerful command-line implementation. GenEst includes tools for estimating searcher efficiency, carcass persistence, and detection probability parameters from experimental field trials. Included in the software are example datasets for analyses, standard R package help files, this user guide, and vignettes detailing use at the command-line.

# 1.0 Introduction

## 1.1 Description of Product

GenEst (Generalized Estimator) is a software package designed for use by anyone analyzing data associated with estimating bird or bat fatalities at renewable power facilities, such as wind and solar farms. GenEst is written in R (R Core Team 2017) and available as a fully documented R package (<package submission information>) including a command-line interface and a user-friendly Graphic User Interface (GUI) coded using shiny (Chang et al. 2017). This User Guide focuses on the GUI version of GenEst. Vignettes within the R package detail the command-line interface.

In tracking fatalities, carcasses are usually collected during distinct searches, and searching is repeated through time. Because some carcasses are removed (via, e.g., scavengers) before searches and some carcasses are not seen by searchers even when they are present, not all carcasses that fall within a search area are found. Investigators therefore typically conduct trial experiments with placed carcasses to estimate the impact of efficiency and persistence.

-density weighted proportion

-fraction of units searched

Modules allow for estimation of searcher efficiency (Searcher Efficiency), carcass persistence (Carcass Persistence), and detection probability (Detection Probability) parameters as well as for the overall fatality estimation (Fatality Estimation).

### 1.1.1 Comparison to Other Methods

Text here describing when and why to use GenEst vs other methods. Reference to Paul’s table.

## 1.2 Installation Instructions

GenEst is available as an R package. Thus, you will need to download and install R (https://cran.r-project.org/) before using GenEst.

GenEst is available for download from the USGS GitHub repository. Within R, ensure that you have the devtools package installed and loaded into R by running

install.packages("devtools")

library(devtools)

Then download and install the GenEst package

devtools::install\_github("usgs/GenEst")

And load it into the R instance

library(GenEst)

GenEst will eventually be available from the R package repository (<http://cran.r-project.org>), at which point, the stable version of the software can be downloaded and installed locally by running

install.packages("GenEst")

And then loaded into the R instance via

library(GenEst)

Installing the GenEst package will also lead to all dependency R packages being installed and loaded into the R instance. In addition, GenEst comes with example data sets, vignettes, and help files, all located within the package folder and accessible via both the command-line and GUI routes.

## 1.3 Getting Started

Initializing the GenEst GUI is as simple as running

runGenEst()

which will launch the application in your default web browser (fig. 1). The welcome screen for the GUI has a disclaimer that must be acknowledged before proceeding. Note that opening the app ties up the active R session. As a result, if you would like to use an active R session alongside the GUI, you will need to initiate an additional R session.

## 1.4 Layout

The GUI is layed out using tabs, as shown in the top left corner of fig. 1: Home, Data Input, Analyses, and About. Once the user acknowledges the disclaimer, they are able to navigate between the tabs. The Home tab is a welcome page and the About tab includes additional information about the GUI and package. The Data Input and Analyses tabs allow active user interaction for analyses.

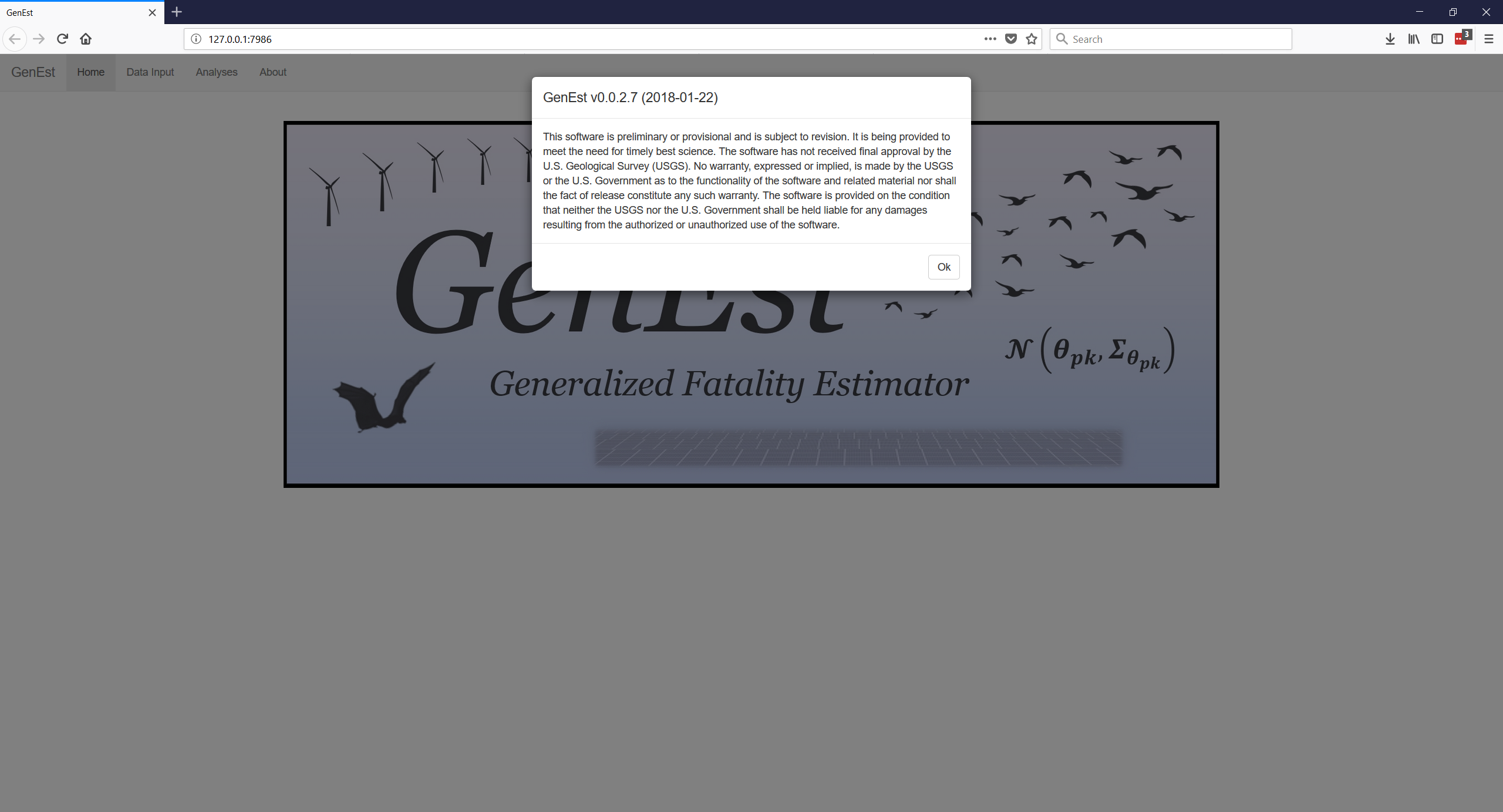


Figure 1. Welcome screen disclaimer for GenEst, as opened in Mozilla Firefox (v58.0.2).

# 2.0 Data Input

## 2.1 Data Files

Having acknowledged the disclaimer, the GUI is now able to accept data for use (fig. 2). Example data files are provided in the R package that can be used within the GUI (in the extdata subfolder in the GenEst package folder, which is located with other R package folders on the user’s computer). Clicking on the “Browse…” button allows the user to locate the files for upload.

Currently, the GUI can take one of each of four data files: Searcher Efficiency, Carcass Persistence, Search Schedule, and Carcass Observations. The files should be formatted with comma separation (either a comma separated value (.csv) or a comma delimited regular text (.txt) file). Appendix A details the necessary and available formats for each of the files. The files required to upload depend on the user’s specific desires (table 1). Upon upload, each data file becomes available for inspection (fig. 3) as well as use throughout the GUI.

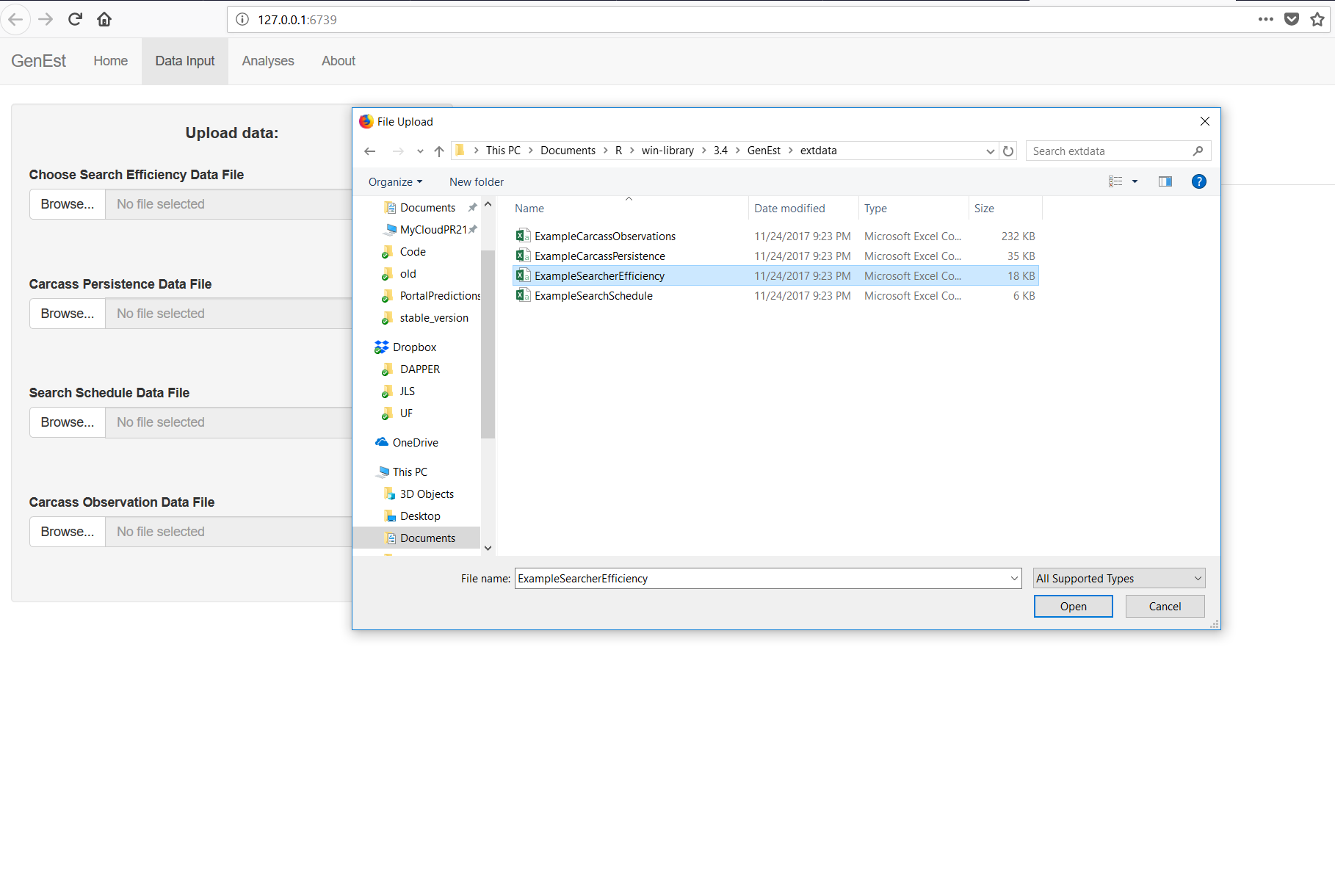


Figure 2. Browsing to the example data sets within the GenEst R package folder on a Windows (10.0.16299) machine.

Table 1. Files needed for each analysis

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Analysis | Search Efficiency | Carcass Persistence | Search Schedule | Carcass Observations |
| Search Efficiency | x |  |  |  |
| Carcass Persistence |  | x |  |  |
| Detection Probability | x | x | x |  |
| Fatality Estimation | x | x | x | x |

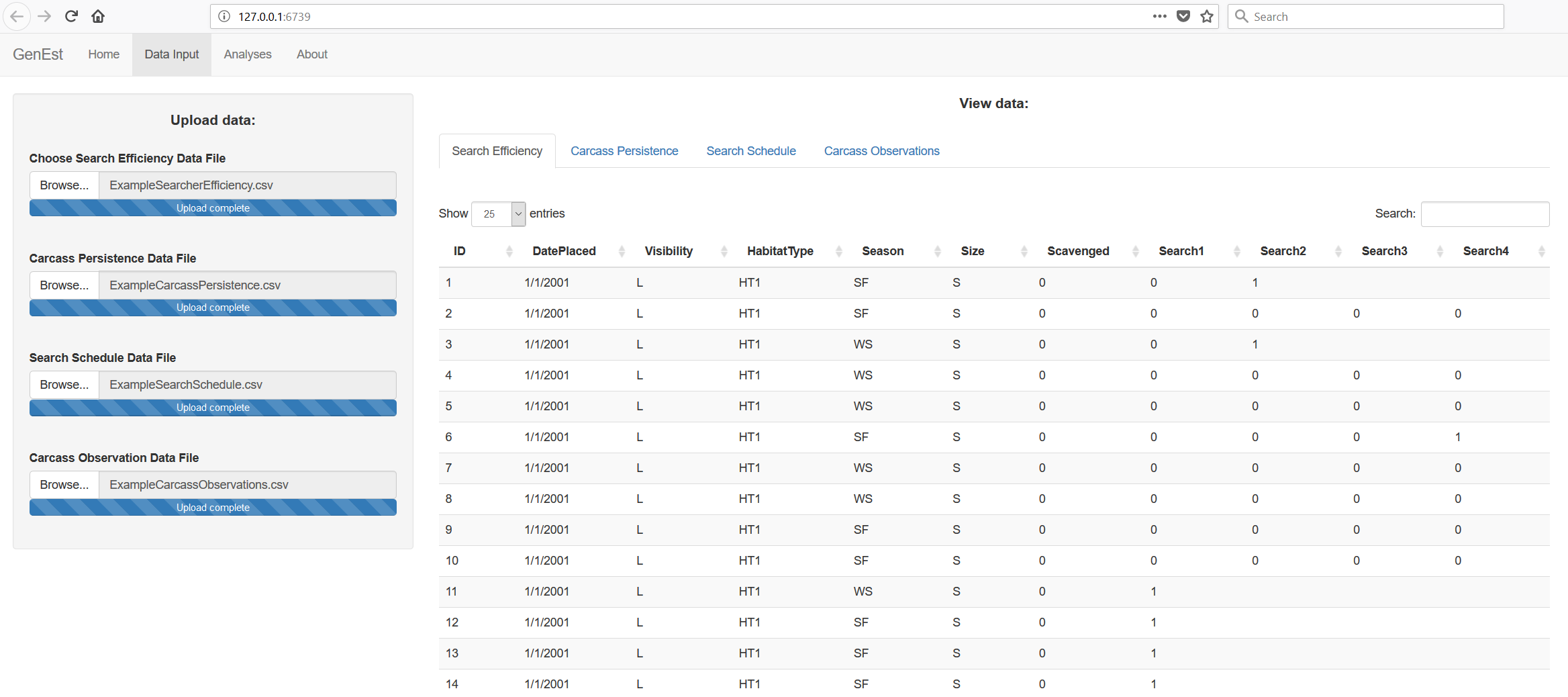


Figure 3. Visible uploaded data in the GenEst GUI.

## 2.2 General Analysis Inputs

Following upload of the data files, the user should navigate to the “Analysis” tab, and specifically to the “General Inputs” subtab, which requests two values: “Number of iterations” and “Confidence Level” (fig. 4). The “Number of iterations” controls the number of replicates used to estimate parameters, defaults to 1,000, and must be an integer value 1 or larger, with current support up to 10,000. The “Confidence Level” defines the probability used to describe the spread of distributions (for parameters and state variables), defaults to 0.9 (a.k.a. 90%) and must be between 0 and 1.

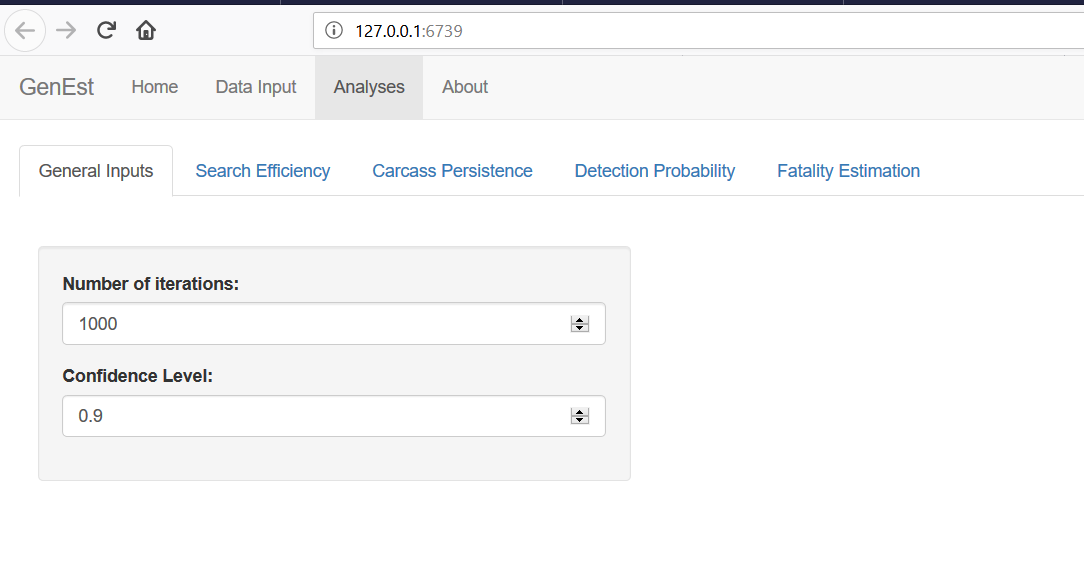


Figure 4. Required general inputs.

# 3.0 Searcher Efficiency

GenEst uses single or repeat carcass detection surveys to estimate searcher efficiency. Searcher efficiency is modeled with two parameters: , the probability that a carcass that is present is found during the first search after it landed, and , the retention of the probability that a present carcass is found on each subsequent search ( means that carcasses are only ever found on the first search and means that the detection probability does not decrease over subsequent searches). Users also have the option to fix at any acceptable level (0-1), rather than estimate it from the data. If only one survey was completed, cannot be estimated and is automatically fixed. The carcasses can be grouped into size classes and according to up to two discrete-valued predictors (e.g., season or vegetation class). The searcher efficiency parameters are estimated from the survey data using maximum likelihood methods, as implemented with custom-written functions (<insert\_final\_function\_names>) for the GenEst package. For full details, see appendix B.1.

## 3.1 Inputs

Search efficiency model inputs are available on the left-hand side panel of the Search Efficiency tab (fig. 5).

* “Choose observation columns (in order):”
  + The user is required to select the specific columns corresponding to the search efficiency trial observations
  + The columns must be in order of search.
  + At least one observation must be selected, and currently there is no maximal number of observation searches allowed.
* “Choose size class column (optional):”
  + The user is allowed to group the carcasses into size classes.
  + The same size class configuration must be present in the Searcher Efficiency and Carcass Persistence analyses in order for them to be combinable for estimation of detection probability. Further, the same size class configuration must be included in the carcass observations for the estimation of fatality.
  + This input is entirely optional.
* “Choose predictor variables (optional):”
  + The user is allowed to group the data according to up to two discrete-valued predictors.
  + The predictors selected in this analysis need to be accounted for in the carcass observations for the Searcher Efficiency model to be useable for fatality estimation.
  + The predictors selected in this analysis do not need to be used in the carcass persistence analysis.
  + This input is entirely optional.
* “Use fixed k?”

## 3.2 Outputs

Outputs are available on main panel of the Search Efficiency tab (fig. 5), with tabs corresponding to each of four specific output screens: Data, Model Table, Figure, and Model Selection.

### 3.1.1 Data

Text.

### 3.1.1 Model Table

Text.

### 3.1.1 Figure

Text.

### 3.1.1 Model Selection

Text.

# 4.0 Carcass Persistence

Text.

## 4.1 Subsection

Text.

### 4.1.1 Example subsubsection

Text.

# 5.0 Detection Probability

Text.

## 5.1 Subsection

Text.

### 5.1.1 Example subsubsection

Text.

# 6.0 Fatality Estimation

Text.

## 6.1 Subsection

Text.

# 7.0 Worked Examples

## 7.1 Example 1

Text.

### 7.1.1 Example subsubsection

Text.

## 7.2 Example 2

Text.

### 7.2.1 Example subsubsection

Text.

# 8.0 Conclusions

Text.

(1)

Text.

Text in appendix A.

Text referencing a figure (fig. 1).

Text including a reference (Huso and Dalthorp, 2014). More text with a reference (Huso and others, 2012). Text with multiple references (Bispo and others, 2012; Warren-Hicks and others, 2013).

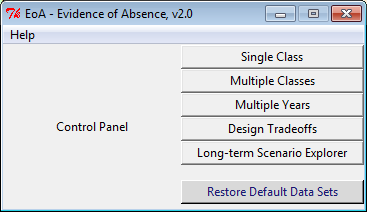
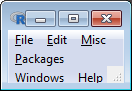
 

Figure 2. Screen captures of the EoA control panel and the minimized R console.

#### Option: An unnumbered but linked header

Text referencing a table (table 1).

Table 1. Example format of carcass persistence data.

[CPmin represents the last time a carcass was observed. CPmax represents the time when a carcass was first noted as missing. Times are recorded in days elapsed since the carcass was placed in the field. For carcasses that are scavenged some time before the first carcass check, CPmin = 0 and CPmax = time of the first carcass check. For carcasses that are known to have been scavenged at an exact time (for example, a coyote is seen removing the carcass), CPmin = CPmax = time of the scavenging event. For carcasses that are still present at the end of the field study, CPmin = time of final carcass check and CPmax = Inf (which is case sensitive)]

|  |  |
| --- | --- |
| CPmin | CPmax |
| 0.95 | 5.99 |
| 4.93 | 6.85 |
| 12.03 | 12.03 |
| 0 | 3.11 |
| 0 | 0.11 |
| 22.1 | Inf |
| 20.82 | Inf |

# Acknowledgments

Text

# References Cited

Chang, W., Cheng, J., Allaire, J.J., Xie, Y., and McPherson, J., 2017, shiny: web application framework for R, version 1.0.5, <https://CRAN.R-project.org/package=shiny>.

R Core Team, 2017, R: A language and environment for statistical computing, v3.4.3: R Foundation for Statistical Computing, Vienna, Austria, [https://www.R-project.org/](%20https:/www.R-project.org/).

# Appendix A. Input File Formats

This appendix details the formats of the input files for the GenEst GUI.

## A.1 Search Efficiency

With text!

## A.2 Carcass Persistence

With text!

## A.3 Search Schedule

With text!

## A.4 Carcass Observations

With text!

# Appendix B. Analytical Details

This appendix provides additional information regarding the analyses underlying the GenEst software.

## B.1 Search Efficiency

With text!

## B.2 Carcass Persistence

With text!

## B.3 Search Schedule

With text!

## B.4 Carcass Observations

With text!

1. DAPPER Stats. [↑](#footnote-ref-1)
2. U.S. Geological Survey. [↑](#footnote-ref-2)
3. Oregon State University. [↑](#footnote-ref-3)
4. WEST. [↑](#footnote-ref-4)
5. Duke University. [↑](#footnote-ref-5)
6. oikostat. [↑](#footnote-ref-6)