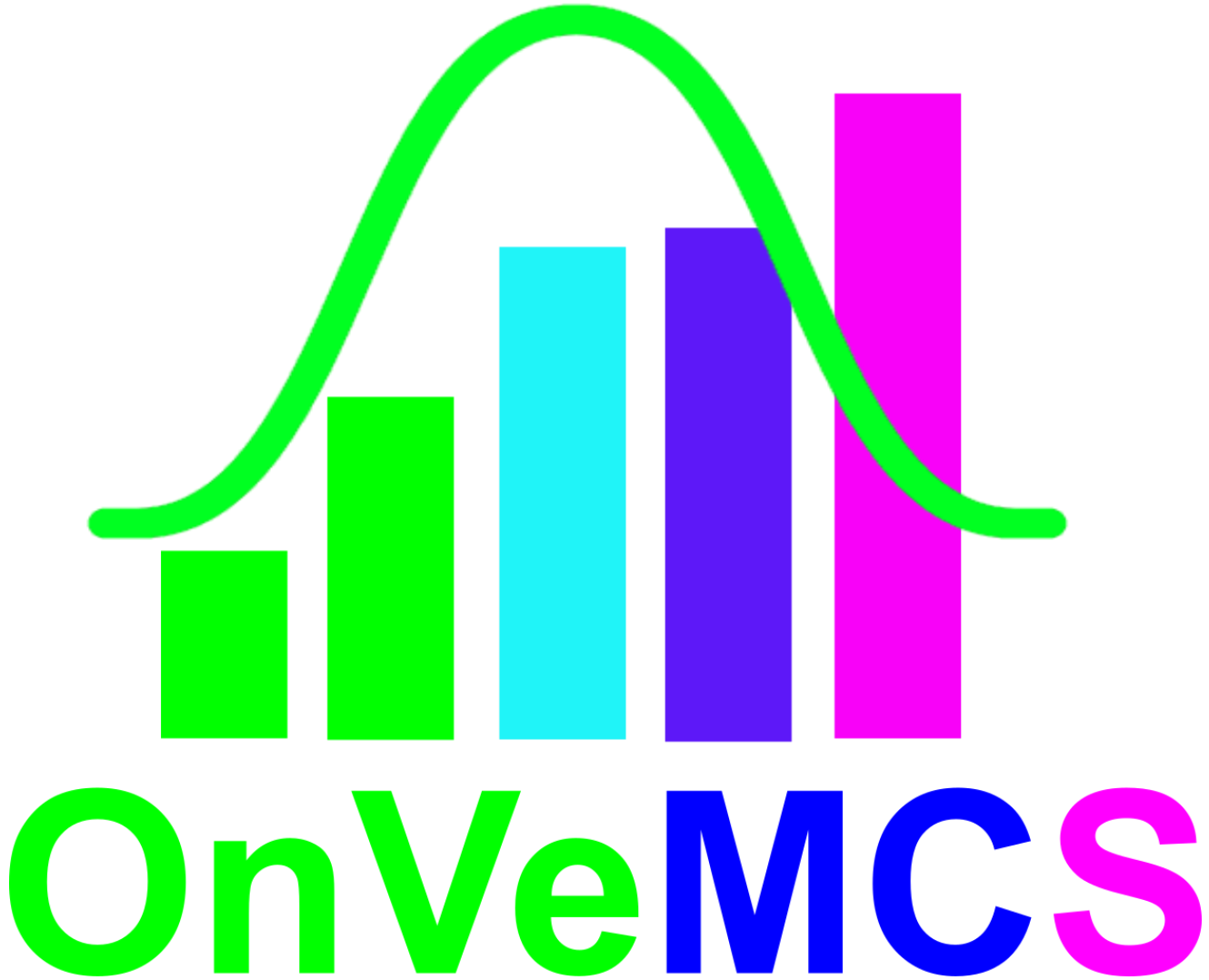
OnVeMCS User Manual

Version 1.1



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1. Introduction

OnVeMCS is a Monte Carlo simulation tool designed for probabilistic human health risk assessment. The software supports both deterministic calculations and stochastic simulations, enabling users to quantify hazard indices (HI) and cancer risks (TCR/ILCR) across multiple media and pathways. It provides flexible concentration inputs via a number of distributions, including Fixed, Normal, Lognormal, Triangular, Uniform, BetaPERT, Gamma and Weibull, allowing analysts to reflect real-world variability and uncertainty.

This manual serves as a comprehensive guide for installing, configuring and operating OnVeMCS. It summarizes key concepts (deterministic vs Monte Carlo, percentiles and exceedance probabilities, the difference between 1D and 2D Monte Carlo), describes the user interface, explains available inputs and outputs, and outlines methods and equations used in the calculations.

Use this manual as a reference when performing exposure assessments, configuring inputs, running simulations and interpreting outputs. The intended audience includes both end-users (scientists and risk assessors) and administrators responsible for deployment, licensing and data governance.

2. Quick Start

This section provides a concise end-to-end workflow. Follow these steps to run the assessment:

1. Install the software and ensure a valid licence file (see Installation & Licensing).
2. Launch OnVeMCS. From the Project ribbon (Figure 1), click **New Project** to start a new session. Upon launch you will see the initial blank screen illustrated in Figure 2.
3. Define analytes manually (via the **Manual Analyte Input** panel) or import a data table using the **Import Data** button. The import preview summarises analyte counts by medium.
4. Configure run settings: choose the scenario (e.g. Resident (Adult + Child), Worker (Outdoor + Indoor), Food Consumer), select active media (Water, Sediment, Soil, Air, Food) and pathways (Ingestion, Dermal, Inhalation), and set the number of Monte Carlo iterations. The **Run Settings** panel (Figure 3) provides these controls.
5. Click **Run simulation** to perform the simulation. A progress bar appears. For large iteration counts the run may take several minutes.
6. Review summary statistics and plots on the **Summary** and **Plots** tabs. Use interactive controls (e.g. histogram/CDF toggles) to explore results.
7. Export results to Excel via **Export results** button to obtain a multi-sheet workbook.

After completing these steps, you will have a complete risk assessment with hazard and cancer risk outputs, ready for interpretation and reporting.

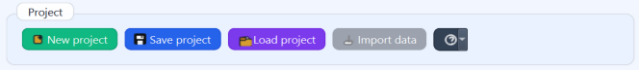


Figure 1. Project ribbon with New, Save, Load and Import buttons.

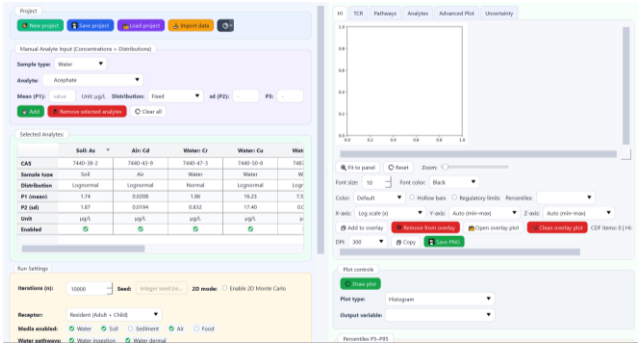


Figure 2. Initial blank screen after launching the application.

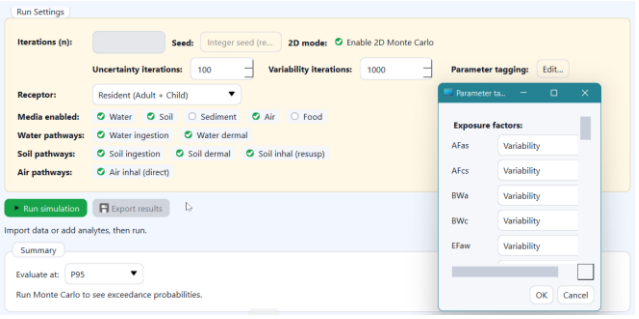


Figure 3. Run Settings panel showing scenario, media activation and iteration counts.

3. Installation & Licensing

OnVeMCS is distributed as a stand-alone Windows executable (EXE) together with a set of support files. System requirements include Windows 10 or 11, at least 4 GB of RAM and 200 MB of free disk space. To install, unzip the distribution package into a convenient folder. The software does not require a separate installer or administrator rights: simply double-click the executable to run. Projects and settings are stored in the same working folder so you can move or back up the entire folder without affecting Windows registry entries.

Some **antivirus** programs or **Windows SmartScreen** may incorrectly flag OnVeMCS.exe as suspicious because it is a newly compiled standalone executable. This is a false positive. If the application is blocked or removed, restore the file from your antivirus **Quarantine** and mark OnVeMCS.exe or its folder as **trusted/allowed**. If Windows Smart Screen appears, select **More info → Run anyway**.

Always download the application only from the official distribution source.

Licensing is enforced through a signed licence file (JSON signature). The licence file is installed to the per-user application data directory the first time you load it. On start-up the program reads the installed licence and displays the licensee name, edition (academic or commercial) and expiry date in the **About** dialog (Figure 4). Features are gated by the licence state: without a valid licence the program runs in Academic/Non-Comercial mode, disabling **Import Data** command with an expired or invalid licence it displays an error and prompts for renewal.

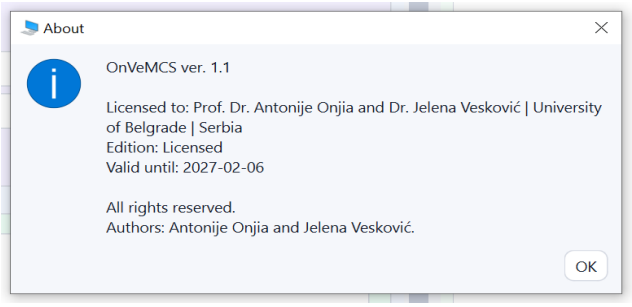


Figure 4. About dialog showing version, licence information and status.

Licence states defined in the implementation include:

1. **ACADEMIC/NON-COMERCIAL** – no licence present. The program loads projects, run simulations and export results but cannot import data.
2. **ACTIVE** – a valid licence is installed. All features are enabled, including **Import Data**.
3. **EXPIRED** – the licence has passed its expiry date. Licensed-only features are disabled until a new licence is loaded.
4. **WRONG_PC** – the licence is bound to a different machine fingerprint. Import data functionality are disabled.
5. **TIME_TAMPERED** – the system clock appears to have been rolled back relative to the licence timestamp. The program locks licensed features.
6. **INVALID/CORRUPTED** – the licence signature is invalid or the file is corrupted. No licensed features are available.

To load a licence, choose **Help → Load Licence** and browse to your licence file. Once validated, the licence is copied into your AppData folder and remains active on subsequent launches until it expires. The **Import data** button is enabled only when the licence state is **ACTIVE**. Administrators should distribute a new licence file to users before the current one expires to prevent workflow interruptions.

The licence may be academic/non-commercial or commercial, and may be time-limited or perpetual as specified in the licence agreement. The licence is bound to a specific machine fingerprint, defines activation start and expiration dates.

Unauthorised distribution, reverse engineering, decompilation, modification of the executable, or bypassing of licence enforcement mechanisms is strictly prohibited. The authors reserve the right to update licensing terms in future releases.

4. Graphical User Interface Overview

The OnVeMCS GUI is divided into several panels and tabs:

- **Project** ribbon – provides buttons for New Project, Load Project, Save Project, Import Data and Help/About. It is illustrated in Figure 1.

- **Manual Analyte Input** (left panel) – allows manual entry of analyte concentrations and distribution parameters. Screens for selecting medium, food type, analyte and specifying distribution parameters reside here.
- **Selected Analytes** – lists analytes that have been added to the current project and enables toggling them on or off.
- **Run Settings** – lets you choose the exposure scenario (e.g. worker/outdoor), activate media and pathways, and specify Monte Carlo iteration counts.
- **Summary** – displays summary statistics (percentiles) and quality assurance indicators once a simulation has completed (Figure 11).
- **Plots** – houses interactive visualisations such as histograms, cumulative distribution functions (CDFs), tornado charts and sensitivity plots. Advanced plots like risk surfaces and butterflies are accessible here when 2D Monte Carlo is enabled. Within this GUI section, users can zoom in and out, change plot colors and font sizes, overlay multiple plots for comparison, copy plots, and save them as PNG files.
- **Help/About** – provides access to the licence status and version information.

Use the tabs at the top of the right panel to switch between Summary, Plots and other outputs. A status bar at the bottom reports the current project state, run progress and messages.

5. Inputs: Defining Analytes

Analytes define the chemical concentration inputs for the exposure assessment. You can add analytes manually or import them in bulk. When adding manually (Figure 5), follow these steps:

1. Select a medium (Water, Soil, Sediment, Air, or Food) from the drop-down.
2. If the medium is Food, choose a food type (e.g. Onion) and specify the ingestion rate (IR food in g/day) as shown in Figure 6.
3. Enter the analyte name. A CAS number is optional; synonyms appear automatically when available. The analyte entry panel with synonyms and distribution parameters is illustrated in Figure 7.
4. Choose a probability distribution for the concentration. Supported distributions include Fixed, Normal, Lognormal, Triangular, Uniform, BetaPERT, Gamma and Weibull. BetaPERT uses minimum, most-likely (mode) and maximum values; Gamma and Weibull require shape and scale parameters; Normal, Lognormal, Triangular and Uniform accept up to three parameters.
5. Specify distribution parameters:
   – For symmetric distributions (Normal, Triangular, Uniform) provide mean and standard deviation or minimum/ mode/maximum as appropriate.
   – For Lognormal distributions, P1 corresponds to the median and P2 to the geometric standard deviation; P3 is unused.
   – For BetaPERT, supply the min/mode/max values.
   – For Gamma and Weibull, supply shape and scale parameters.
   – For Fixed values supply a single constant concentration.
   The unit are set as follows: mg/kg for food, µg/L for water, mg/kg for soil/sediment, and ng/m^3 for air.
6. Click **Add** to append the analyte to the **Selected Analytes** list.

Once an analyte is in the **Selected Analytes** list (Figure 8) you can toggle it on or off using its checkbox. Disabled analytes remain in the project but do not contribute to calculations. You can also remove an analyte by selecting it and clicking **Remove selected analytes**.

The analyte drop-down is retrieved from the toxicity database and may include synonyms. Choose the entry that matches your intended medium. You may search within the drop-down by typing a few letters.

When defining analytes manually, OnVeMCS applies sensible defaults: if P2 is left blank for Normal or Lognormal distributions the program computes it as a fraction of P1 depending on the medium (for example, 0.50×P1 for water, 0.75×P1 for soil/sediment, 0.95×P1 for air/food). These defaults ensure a reasonable coefficient of variation when only a median value is specified. However, you may override them by entering your own P2.

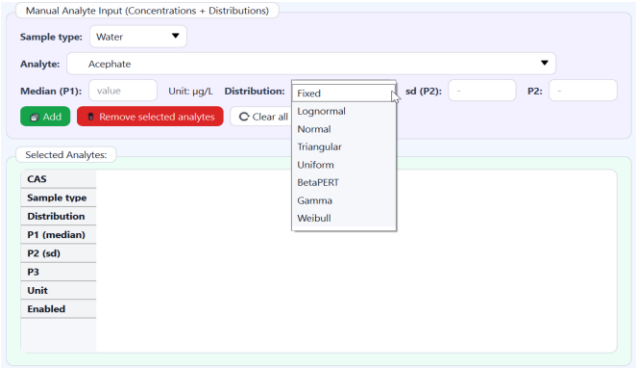


Figure 5. Distribution selector for manual analyte entry.



Figure 6. Food-specific fields for ingestion rate and food type.



Figure 7. Analyte entry panel with synonyms.



Figure 8. Selected Analytes list with enable/disable checkboxes.

6. Import Data

For larger studies it is efficient to import analytes from a spreadsheet template. OnVeMCS supports the following import format: the first three rows named as Samples, Sample type, and Units list analyte names, sample type, and concentration units, respectively, while the subsequent rows contain sample concentrations.

To import data:

1. Prepare an Excel file of the following format. The first row contains analyte names (e.g. Cd, Cr, Cu, …). The second row contains the medium for each analyte (Water, Soil, Sediment, Air or Food). The third row contains concentration units, and the subsequent rows contain sample concentrations. If health risk assessment is being done for food, the third row specifies the food type, the fourth row lists the ingestion rate (IR) in g/day for food types, while the subsequent rows contain sample concentrations for each analyte. Use blank cells for missing data.
2. Click **Import Data** in the **Project** ribbon and browse to your Excel file.
3. Review the preview window. OnVeMCS performs unit normalisation and displays the count of valid analytes per medium. The preview reports several categories: **Total analytes detected**, **Matched to OnVeTD analyte list** (those that match toxicity list entries), **CAS errors**, **Sample type errors**, and **Unit errors**. CAS errors indicate unrecognised analyte identifiers; sample type errors flag unrecognised medium codes; unit errors arise when units cannot be normalised. In the current build, the preview shows both **LENIENT** and **STRICT** counts but the strict import mode is disabled. All imports use lenient matching with synonym and whitespace normalisation.

The preview window (Figure 9) summarises the number of valid analytes by medium and flags any issues.

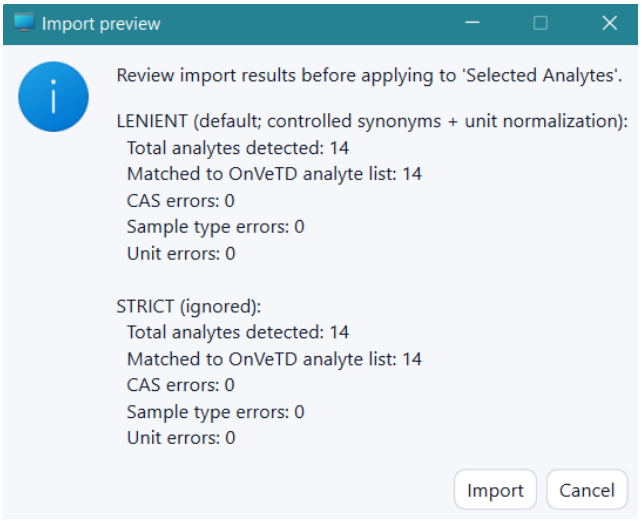


Figure 9. Import preview summarising analyte counts and medium types

4. Confirm the import. The analytes appear in the **Selected Analytes** list with distribution parameters inferred automatically.

If errors occur during import (for example, non-numeric entries, unrecognised units or inconsistent row lengths), the preview highlights

them and prevents the file from loading until corrections are made.

When preparing data for import, remove leading and trailing spaces from analyte names, ensure units are spelled correctly, and avoid hidden characters in cells. However, if in your import file one analyte header contained a leading space (" Cr") and the intake-rate row label contained a zero-width character, these issues are automatically corrected in lenient mode but would cause strict mode to reject the file if enabled. Consistent formatting and use of official analyte names reduce import problems.

7. Run Settings and Monte Carlo Simulation

Run settings govern how OnVeMCS performs the Monte Carlo simulation. Figure 3 shows the run settings panel, and Figure 10 shows the progress indicator during a run.

- **Receptor** – choose an exposure receptor (Resident, Worker – outdoor/indoor, Food Consumer). Each receptor type determines default body weight, exposure duration, inhalation rate and other factors.
- **Consumer groups** – for food scenarios you can select subgroups (Infant, Toddler, Child, Adult, …) which adjust body weight and intake rates accordingly.
- **Media enabled** – tick which media (Water, Soil, Sediment, Air, or Food) are active in the current run. Only enabled media contribute to the hazard and risk calculations.
- **Pathways** – select the exposure pathways (ingestion, dermal, inhalation) relevant to the scenario. For food, ingestion is typically the only pathway; for soil/sediment, ingestion, dermal and inhalation (resuspension) may be enabled, while for water ingestion and dermal pathways are relevant. If the air is selected, the only pathway is inhalation.
- **Iterations (n)** – the number of Monte Carlo draws per analyte. A higher value yields smoother distributions but increases runtime; values of 10 000–20 000 are typical for stable percentiles in 1D runs.
- **Seed** – an optional numeric seed used to initialise the random number generator. Providing a seed ensures reproducible runs. Leaving it blank causes the program to choose a random seed.
- **2D Mode** – performs two-dimensional Monte Carlo simulation. When enabled, you specify an **Uncertainty iterations** number (outer loop) and **Variability iterations** number (inner loop). Each outer sample draws uncertain parameters (e.g., exposure factors, analyte concentrations), and then runs n inner variability simulations.
- **Parameter tagging** – an optional dialog allows you to designate which exposure factors are treated as *uncertain*. Tagged parameters are sampled once per outer iteration (uncertainty), while untagged parameters vary across the inner iterations (variability). Use this feature to separate uncertainty from variability in 2D runs.

Use the **Run simulation** button to execute the simulation. While running, a progress bar and status message appear (Figure 10).

Guidance: start with a moderate n (e.g. 2000–5000) to test your inputs. Increase **n** or **enable 2D Monte Carlo** for final analyses when uncertainty quantification is needed.

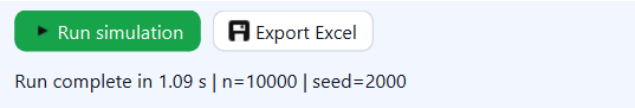


Figure 10. Status indicator during Monte Carlo simulation

8. Outputs and Basic Plots

When a run completes, OnVeMCS fills the Summary and Plots tabs with results. Figure 11 shows the **Summary** tab after a run, and Figures 12–19 illustrate the basic plots.

- **Summary and Percentiles** tabs – lists HI (Hazard Index) and TCR/ILCR (Total Cancer Risk) metrics for each scenario combination. Tables report the mean, median and percentiles and flag exceedances of the HI=1 threshold or TCR limits.
- **Histograms** – show the frequency distribution of HI or TCR. A vertical line at HI=1 indicates the non-cancer screening threshold (Figure 12). Lines at 1E-6 and 1E-4 mark lower and

upper cancer-risk bounds on TCR histograms (Figures 12 and 13).

- **Cumulative Distribution Functions (CDFs)** – plot the probability that HI or TCR is below a given value. You can toggle between histogram and CDF using the plot type selector (Figures 14 and 15).
- **Pie** (Pathways and Analytes) – break down total risk by exposure pathway (Figure 16) or by analyte (Figure 17), helping identify major contributors.
- **Sensitivity plots** – depict the percentage of variance explained for each input parameter, ranking variables by their influence (Figure 18).
- **Tornado charts** – present a sorted bar chart of sensitivity results highlighting the variables that cause the largest change between P05 and P95 (Figure 19).

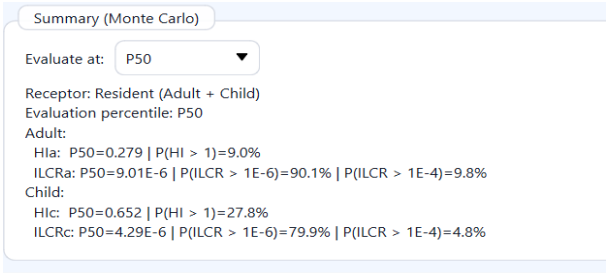


Figure 11. Summary tab with total HI and TCR metrics after a simulation.

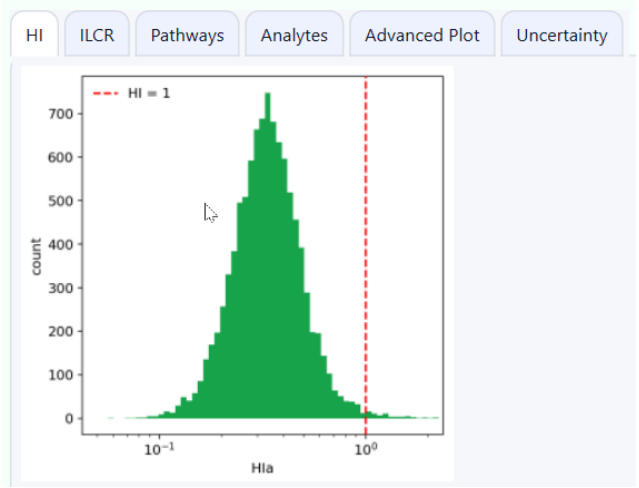


Figure 12. HI histogram with reference line at HI=1.

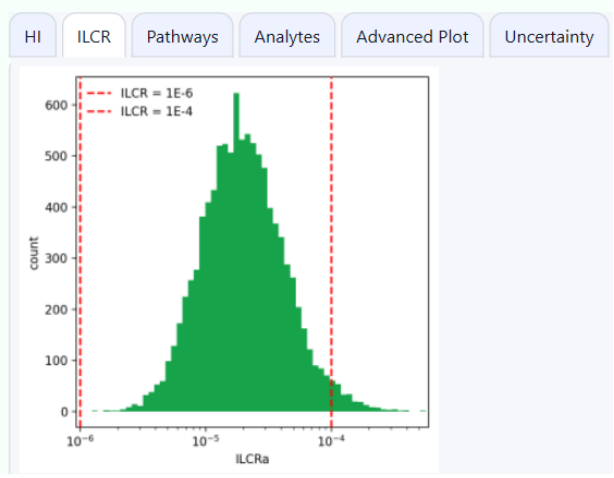


Figure 13. TCR histogram with reference lines at 10^{-6} and 10^{-4}.

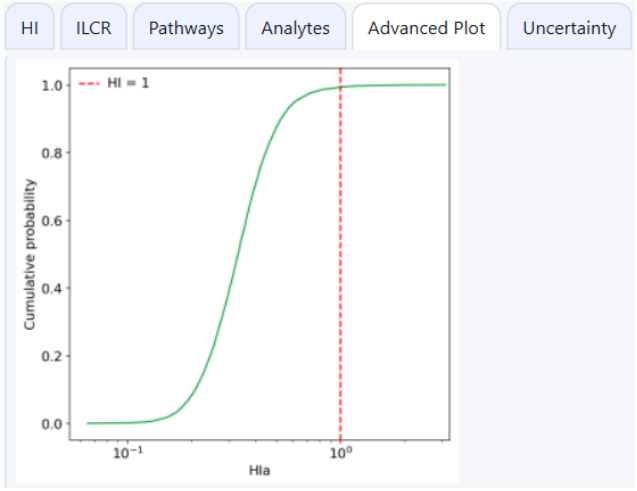


Figure 14. HI CDF illustrating the probability distribution of mon-carcinogenic risk.

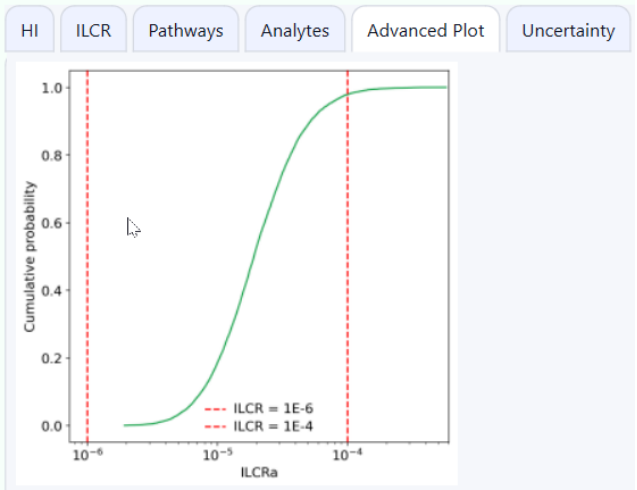


Figure 15. TCR CDF showing the probability distribution of cancer risk.

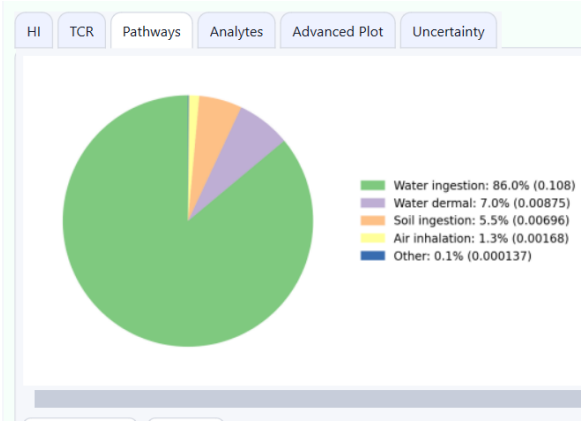


Figure 16. Pie chart showing contribution by exposure pathway.

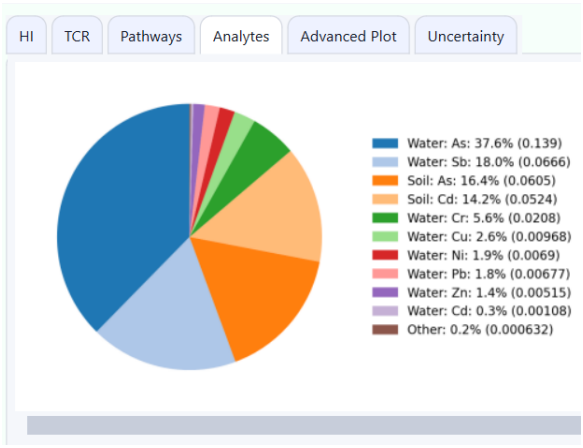


Figure 17. Pie chart showing contribution by analyte.

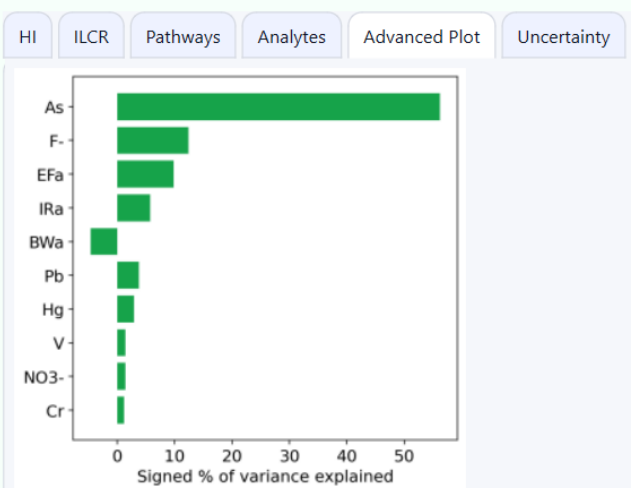


Figure 18. Sensitivity plot highlighting influence of each input variable.

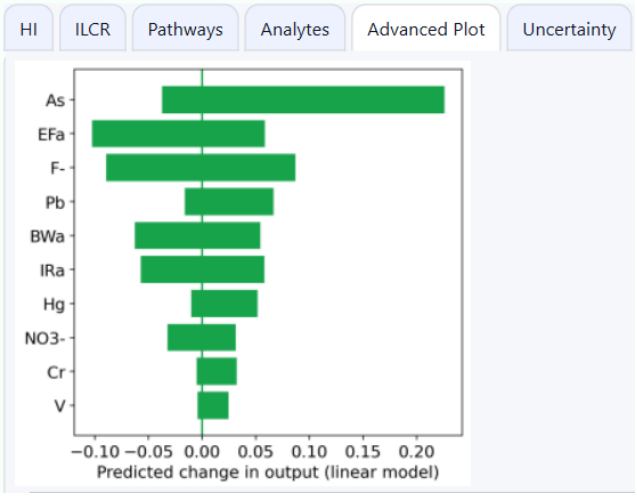


Figure 19. Tornado chart ranking variables by impact on output variance.

9. Advanced Plots and Uncertainty Analysis

When a two-dimensional (2D) Monte Carlo run is performed (outer loop m > 1), additional plots become available. Figures 20–25 illustrate these advanced outputs.

- **Uncertainty** ribbons – display confidence bands around the CDF of HI or TCR, capturing uncertainty in percentile estimates. In 1D mode is not available (Figure 20), while in 2D mode is presented as shown in Figure 21. Use this plot to gauge the uncertainty in percentile estimates: a narrow ribbon means little uncertainty, while a wide ribbon means percentile estimates vary across outer iterations.
- **Nested CDFs** – overlay CDFs from each outer sample to visualise variability and identify potential multimodality (Figure 22). When these curves are widely dispersed, the uncertainty component dominates, while when they cluster tightly together with sharp steps, variability dominates.
- **CDF with confidence bands** – combines the standard CDF with uncertainty ribbons in a single plot for easier interpretation (Figure 23).
- **Risk Surface** plots – depict the joint distribution of two variables, such as HI and TCR, across outer and inner loops. You can view the surface as a 3D wireframe. Axis scaling controls (Auto, Robust, Log) for the X, Y and Z

axes allow you to focus on specific ranges (Figure 24). The X-axis represents the variability percentile (0–100 %), the Y-axis represents the uncertainty confidence (0–100 %) and the Z-axis shows the risk metric (HI or TCR).

- **Butterfly** plots – show how much the model output changes when each individual input parameter is varied to its lower and upper bound while all other parameters are kept at their baseline values, thereby visualizing the relative local sensitivity of the model to each parameter (Figure 25). It splits the contributions of uncertainty and variability for each input factor. The left side (negative direction) shows variability contributions, and the right side (positive direction) shows uncertainty contributions. The length of each bar corresponds to the magnitude of its effect on the output metric. This diagnostic helps you identify which parameters drive population heterogeneity (variability) and which drive uncertainty.

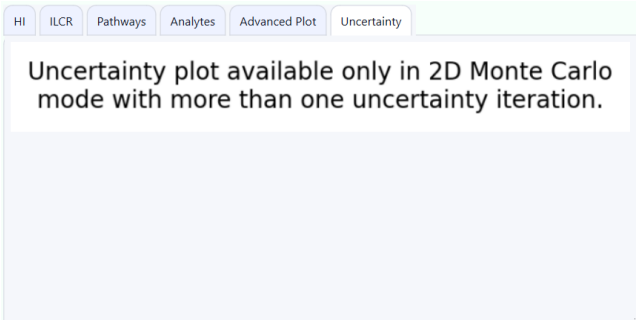


Figure 20. Uncertainty ribbon plot placeholder (1D mode).

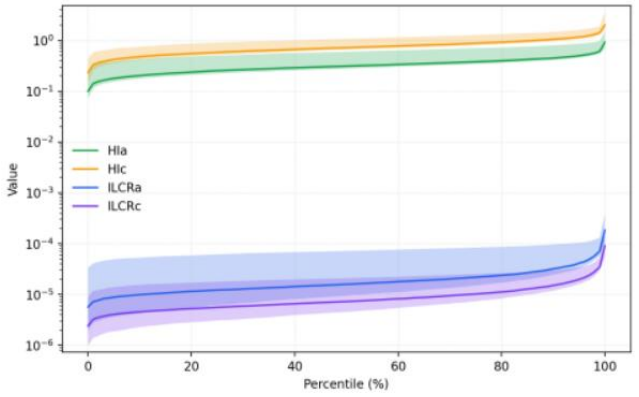


Figure 21. Uncertainty ribbon plot after a 2D Monte Carlo run.

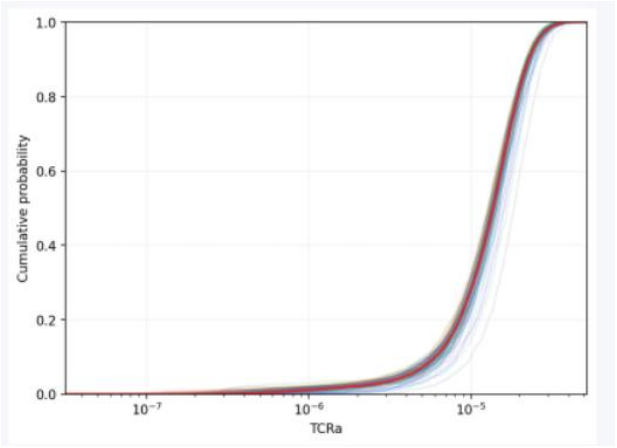


Figure 22. Nested CDFs for TCR illustrating variability across outer samples.

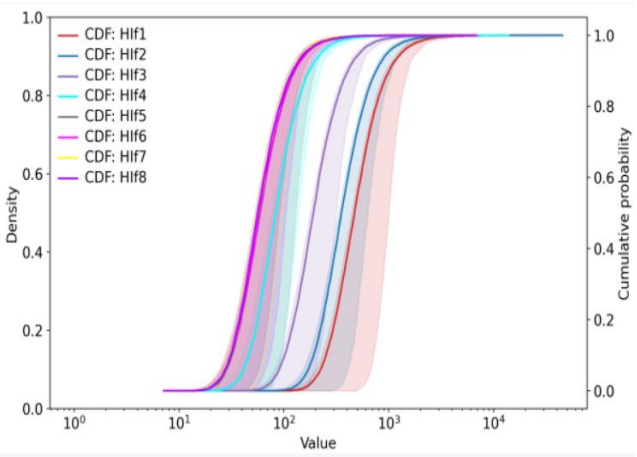


Figure 23. HI CDF with confidence bands.

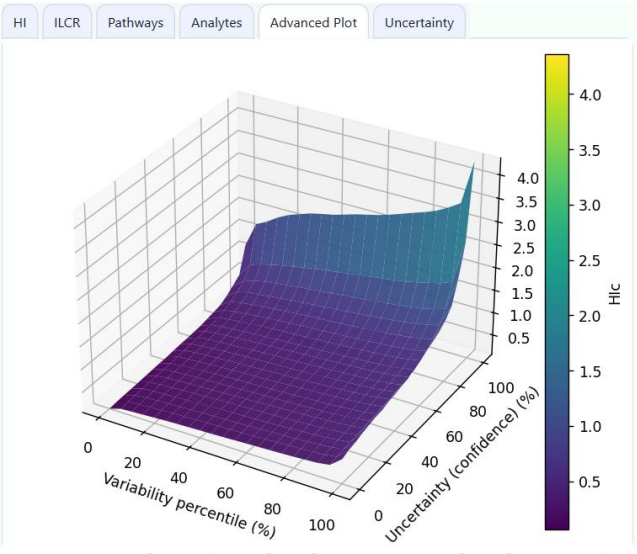


Figure 24. Risk Surface plot showing joint distribution of HI and TCR



Figure 25. Butterfly plot showing the model output changes.

10. Exporting Results to Excel

To document and share results, OnVeMCS can export the entire project into a multi-sheet Excel workbook. Click **Export Excel** from the left panel after running a simulation to generate an export file. Figure 26 shows an overview of the exported workbook and its sheet structure.

The exported workbook includes the following sheets:

- **HI,ILCR** – raw Monte Carlo output arrays for HI and TCR/ILCR for each scenario combination. When 2D Monte Carlo is enabled the sheet includes percentile bands *(__cdfband_low* and *__cdfband_high*) for each percentile.
- **Percentiles_P5_P95** – summarises percentiles (P05 through P95) for each metric.
- **Deterministic** – lists deterministic calculations using median input values and, when applicable, per-sample deterministic results.
- **Uncertainty_Intervals** – provides lower and upper percentile bounds for specified risk levels (e.g. P05, P95) across outer loops.
- **Summary_Stats_with_Uncertainty** – merges mean, median and percentile statistics with uncertainty intervals into one table.
- **Probability_of_Exceedance** – calculates the probability that HI exceeds 1.0 or that TCR/ILCR exceeds risk thresholds (e.g. 1E-6, 1E-4).
- **CI_Other_Percentiles** – provides additional percentile bands beyond the default set (e.g. P50, P90, P95, and P99).
- **Outer_Scenarios** – lists summary statistics (mean, P05, P50, P95, P99) for each outer iteration.
- **Risk_Surface** – contains a gridded representation of the risk surface for 2D runs, including the X and Y grid coordinates and risk values.
- **Butterfly** – stores the data plotted in butterfly plots.
- **Analytes** – lists all analyte definitions and distributions as stored in the project file.
- **Exposure_Factors** – documents the exposure factors used for each scenario and consumer subgroup (e.g. body weight, exposure duration, averaging time).
- **Pie_Pathways** and **Pie_Analytes** – summarise contributions in a format suitable for pie charts.
- **Sensitivity** and **Tornado** – contain the underlying data used in the sensitivity and tornado plots.
- **HQCR_adult_res** and **HQCR_child_res** – scenario-specific tables for HQ and CR outputs (sheet names vary by scenario).

Column names and sheet structures correspond directly to the figures shown in the GUI. Extra plot-series columns (e.g., *__hist_x*, *__hist_counts*, *__cdf_x*, *__cdf_y*, *__cdfband_low*, *__cdfband_high*) are included so that advanced users can reconstruct plots in Excel or other software.

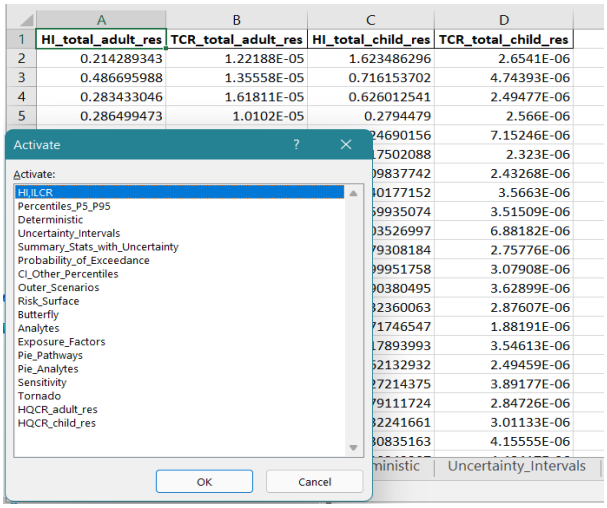


Figure 26. Overview of the exported Excel workbook and sheet structure

11. Methods & Equations

OnVeMCS implements well-established human health risk assessment equations grounded in U.S. EPA guidance. In this section the key formulas and parameter distributions are presented. Exposure calculations are performed per pathway and per analyte. For water two exposure pathways are specific: ingestion and dermal pathways. For soil/sediment, there are three exposure pathways: ingestion, dermal, and inhalation. If the medium is air or food, only inhalation and ingestion are present as exposure pathways, respectively. Non-carcinogenic risk is quantified through **hazard index** (HI), while carcinogenic risk is quantified through **total carcinogenic risk** (TCR) or **incremental lifetime cancer risk** (ILCR). In all cases, first, the **Average Daily Dose** (ADD) (for food Estimated Daily intake (EDI)) is computed, as shown below for each medium type.

- **Water medium**:

$$ADD_{ing} = \frac{C \times IngR \times EF \times ED}{BW \times AT}$$

$$ADD_{derm} = \frac{C \times SA \times Kp \times ET \times EF \times ED \times CF}{BW \times AT}$$

- **Soil/sediment medium:**

$$ADD_{ing} = \frac{C \times RBA \times IngR \times EF \times ED \times CF}{BW \times AT}$$

$$ADD_{derm} = \frac{C \times SA \times AF \times ABS \times EF \times ED \times CF}{BW \times AT}$$

Only for soil:

$$EC_{inh} = \frac{C \times EF \times ED \times \frac{ET}{24} \times \left(\frac{1}{VF} + \frac{1}{PEF}\right)}{AT}$$

- **Air medium:**

$$EC_{inh} = \frac{C \times \frac{ET}{24} \times EF \times ED}{AT}$$

- **Food medium:**

$$EDI_{ing} = \frac{C \times IngR \times EF \times ED \times CF}{BW \times AT}$$

The ADD (or EDI or EC) computation is based on the concentration of the analyte (mg/L; mg/kg; mg/m^3) and exposure parameters: IngR is the ingestion rate (L/day), InhR is the inhalation rate (m^3/day), EF is the exposure frequency (days/years), ED is the exposure duration (years), BW is the average body weight (kg), ET is exposure time (h/day), RBA is relative bioavailability (unitless), AT is the average exposure time (h/day), SA is the exposed skin area (cm^2), Kp is the dermal permeability coefficient (cm/h), CF is the unit transfer factor (L/cm^3), AF is the adherence factor (mg/cm^2/day), ABS is the dermal absorption factor (unitless), PEF is the particulate emission factor (m^3/kg), and VF is volatilization factor (m^3/kg).

Second, HI and TCR/ILCR are calculated as a sum of all **hazard quotients** (HQ) and **cancer risks** (CR) across all analytes and pathways for a given scenario, respectively. To compute HQ and CR, reference dose (or reference concentration for air) (RfD, mg/kg/day; RfC, μg/m^3) and cancer slope factor (SF, (mg/kg/day)$^{-1}$) are necessary. If the medium is air, instead of cancer slope factor, inhalation unit risk (IUR, μg/m^3) is used.

Equations for HQ, HI, CR, and TCR/ILCR calculations are provided below for each medium.

- **Water medium:**

$$HQ_{ing} = \frac{ADD_{ing}}{RfD_{ing}}$$

$$HQ_{derm} = \frac{ADD_{derm}}{RfD_{derm}}$$

$$HI = \sum(HQ_{ing} + HQ_{derm})$$

$$CR_{ing} = ADD_{ing} \times SF_{ing}$$

$$CR_{derm} = ADD_{derm} \times SF_{derm}$$

$$ILCR = \sum(CR_{ing} + CR_{derm})$$

- **Soil medium:**

$$HQ_{ing} = \frac{ADD_{ing}}{RfD_{ing}}$$

$$HQ_{derm} = \frac{ADD_{derm}}{RfD_{derm}}$$

$$HQ_{inh} = \frac{EC_{inh}}{RfC}$$

$$HI = \sum(HQ_{ing} + HQ_{derm} + HQ_{inh})$$

$$CR_{ing} = ADD_{ing} \times SF_{ing}$$

$$CR_{derm} = ADD_{derm} \times SF_{derm}$$

$$CR_{inh} = EC_{inh} \times IUR$$

$$TCR = \sum(CR_{ing} + CR_{derm} + CR_{inh})$$

- **Air medium:**

$$HQ_{inh} = \frac{ADD_{inh}}{RfC_{inh}}$$

$$HI = \sum(HQ_{inh})$$

$$CR_{inh} = ADD_{inh} \times IUR$$

$$TCR = \sum(CR_{inh})$$

- **Food medium:**

$$HQ_{ing} = \frac{EDI_{ing}}{RfD_{ing}\ (or\ TDI, ADI, \dots)}$$

$$HI = \sum(HQ_{ing})$$

$$CR_{ing} = EDI_{ing} \times SF$$

$$TCR = \sum(CR_{ing})$$

An HI less than 1 suggests exposures are unlikely to cause non-cancer health effects, whereas values above 1 indicate potential concern.

A TCR/ILCR below 1×10^{-6} is considered negligible, between 1×10^{-6} and 1×10^{-4} acceptable, while above 1×10^{-4} is unacceptable.

OnVeMCS uses toxicity data (e.g. RfD, SF, IUR, Kp, TDI, ADI) from the USEPA, EFSA, and JECFA/JMPR toxicity databases, and the data predominantly used in the scientific literature (Miletić et al. 2023, https://doi.org/10.3390/met13071266; Vesković et al. 2025, https://doi.org/10.3390/w17192901). Furthermore, when performing probabilistic health risk assessment, concentrations and exposure parameters are used as distributions. All exposure parameter values and their distributions are summarized in the exported excel file. In the software, a lowercase letter next to each parameter indicates whether it refers to adults (a), children (c), indoor workers (wi), or outdoor workers (wo), as well as the relevant medium: water (w), soil (so), sediment (se), air (a), or food (f).

12. Troubleshooting & FAQ

Common issues and their remedies include:

- Import errors – Ensure the Excel template has no blank headers and that units are specified. Use numeric values only.
- Simulation runs slowly – Reduce the number of iterations. Close other applications to free memory.
- Plots appear blank – Confirm that the run completed successfully and that at least one analyte and pathway are enabled.
- Licence expired – Contact the administrator for an updated licence file. Without a valid licence the Import Data functions are disabled.
- Unexpectedly high risk values – Check units and distribution parameters for each analyte. Verify that intake rates and exposure factors correspond to the selected scenario.

Further assistance is available via the Help menu. The **About** dialog lists the software version and support contact information.

13. Disclaimer (Limitation of Liability)

OnVeMCS is a scientific research and decision-support tool intended for probabilistic human health risk assessment. The software implements established risk assessment equations and statistical sampling methods. However, it does not replace professional judgement, regulatory review, or site-specific expert evaluation.

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16. Citation Policy

When OnVeMCS is used in scientific publications, technical reports, regulatory submissions, theses, or conference presentations, the software should be cited appropriately.

In a peer-reviewed publication, the OnVeMCS software is described citing the associated publication in addition to the software version. The citation should include the software name and version number. This ensures reproducibility and scientific transparency.

Recommended citation format:

Onjia, A., & Vesković, J. (2026). OnVeMCS: A Standalone Software for Monte Carlo Simulation and Sensitivity Analysis of Risks from Multi-Pathway Human Exposure via Soil, Sediment, Water, Air, and Food. *Environments*, *13*(6), 332. https://doi.org/10.3390/environments13060332.