RAMAS Ecotoxicology is a data analysis package used for modeling population-level ecological risk assessments. It imports data from standard laboratory bioassays, incorporates these data into the parameters of a population model, and performs a risk assessment by analyzing population-level differences between control and impacted samples.

Bioassays for assessing the impact of toxins on natural systems are usually expressed in terms of individual-level assessment endpoints such as growth, survivorship and fecundity. RAMAS Ecotoxicology translates such results into a forecast of their likely consequences at the level of the entire population. For instance, if there is an increase in mortality rate due to a contaminant, the meaning of this effect can only be determined by projecting the consequence in terms of the total population’s future abundance and vitality. It is generally important to do this projection to the population level because impacts at the organism level cannot be easily extrapolated to predict their population-level consequences. For instance, minor and inconspicuous impacts on individuals can sometimes cascade through population dynamics into significant effects at the level of the population. Conversely, seemingly major impacts on individuals may translate into only minor population-level consequences once the normal population feedbacks have been taken into account. Moreover, contradictory findings are possible at the level of the individual (e.g., decreased survival but increased fecundity) that must be resolved.

RAMAS Ecotoxicology uses stage-structured single-population models and food chain models to make the necessary projections. The software checks the validity of the input and model structure specified by the user. It uses a sophisticated second-order Monte Carlo engine to project both natural temporal variability and measurement error, and expresses its results in risk-analytic outputs such as the risk of the population’s declining to a given level.

RAMAS Ecotoxicology was developed by Applied Biomathematics with support from the Electric Power Research Institute.

Model Features
- Specify parameters as scalar numbers, intervals or distributions with automatic unit conversions and checking for dimensional consistency
- Dose-response model: Weibul, probit, logit
- Predator-prey interactions: Lotka-Volterra, Holling type II. Ratio-dependent
- Density dependence: ceiling, logistic, Ricker, Beverton-Holt
- Monte Carlo treatment of measurement error and environmental variation
- Summarize results as biomass/abundance projections and risk statistics
- Display graphs and tables, save or paste into other applications
• Comprehensive online help

**Required Data Types**
Imports data from standard laboratory bioassays and converts that relate to items such as the impact of toxins on natural systems.

**Model Outputs**
Projections of natural temporal variability and measurement error. Results are expressed in terms of analytic risk outputs, such as the risk of a population declining to a certain level.

**Hardware Requirements**
IBM PC-compatible, 486 with VGA monitor, Windows 3.1 (math coprocessor and 8Mb RAM recommended).

**Software Requirements**
None noted

**Supported Platforms**

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**Cost, Licensing and Availability**
$995 - Available from link below

**Source**
RAMAS Environmental Software

**Source URL**
http://www.ramas.com/ramas1.htm#tox