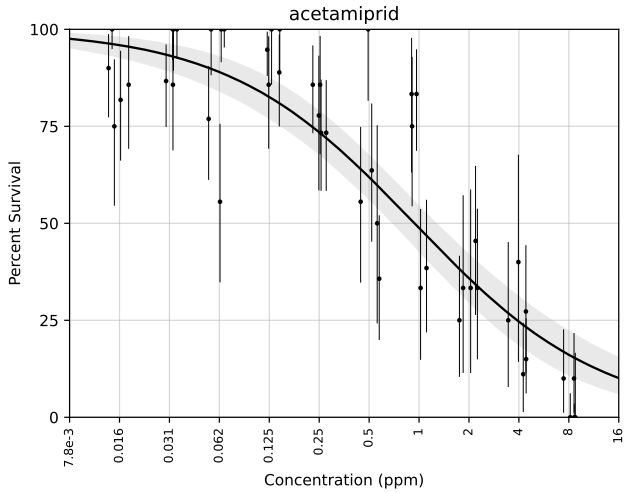
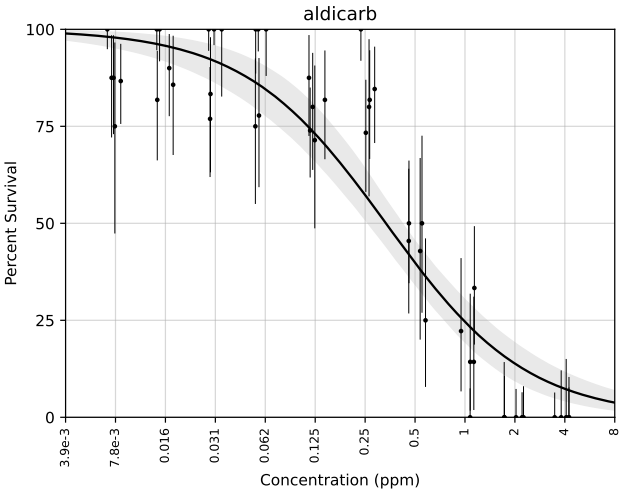
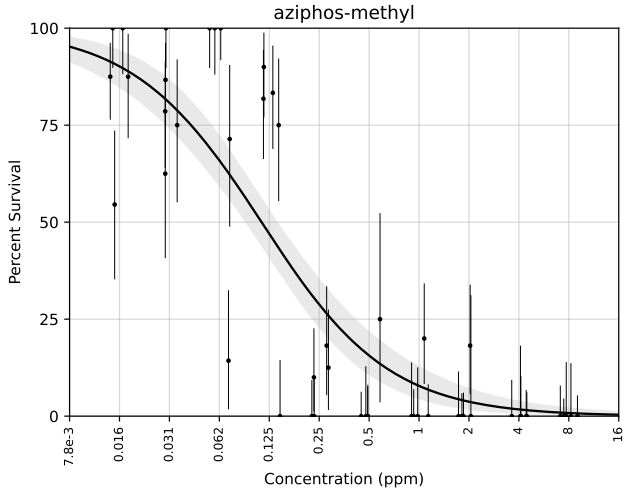


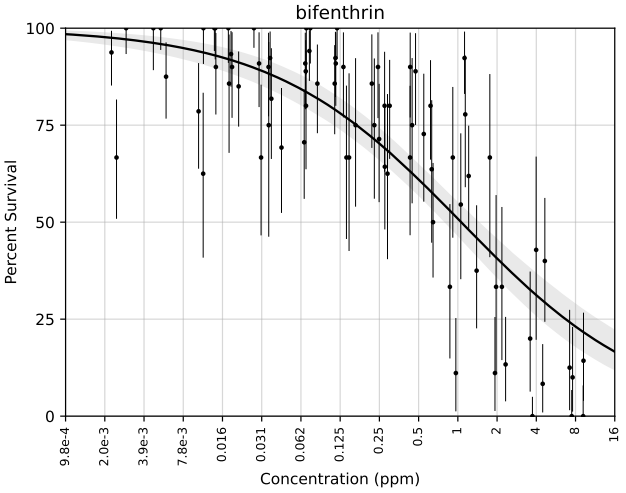
Acetamiprid LC_{50}: 0.937 ppm [0.696, 1.27]
4 biol. reps; 5 tech. reps; R^2: 0.794



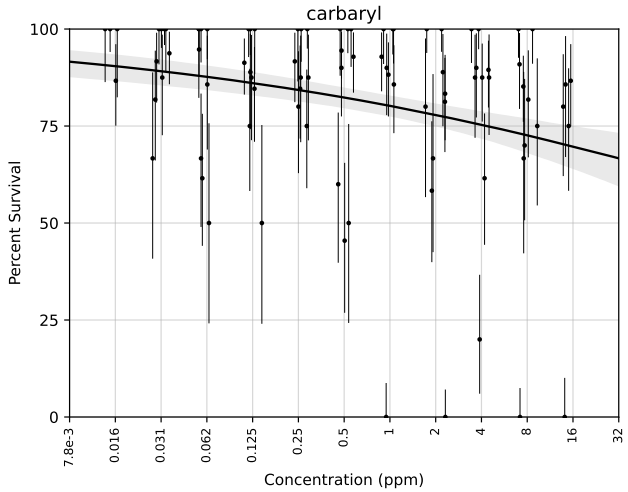
Aldicarb LC_{50}: 0.334 ppm [0.264, 0.425]
4 biol. reps; 5 tech. reps; R^2: 0.871



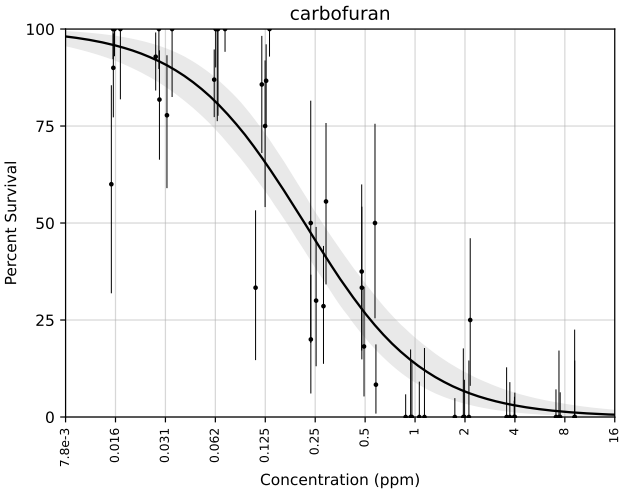
Aziphos-methyl LC_{50}: 0.112 ppm [0.0901, 0.139]
4 biol. reps; 5 tech. reps; R^2: 0.755



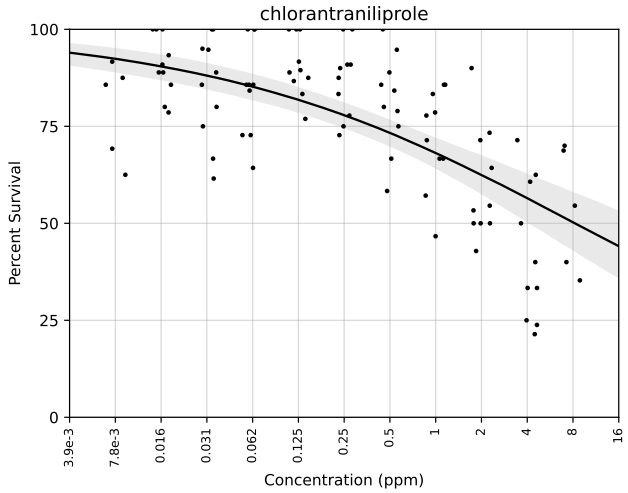
Bifenthrin LC_{50}: 1.06 ppm [0.793, 1.43]
7 biol. reps; 8 tech. reps; R^2: 0.7



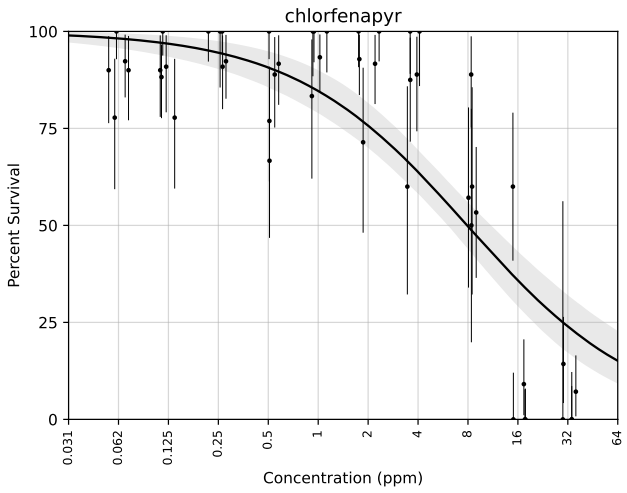
Carbaryl LC_{50}: 985 ppm [90.9, 3.18e4]
8 biol. reps; 9 tech. reps; R^2: 0.0777



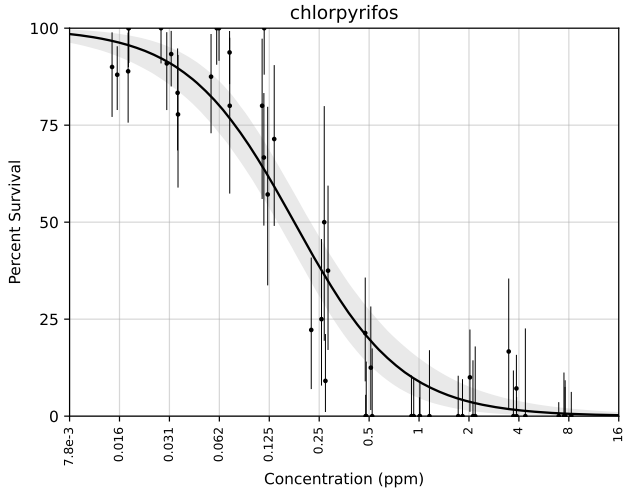
Carbofuran LC_{50}: 0.215 ppm [0.169, 0.274]
4 biol. reps; 5 tech. reps; R^2: 0.879



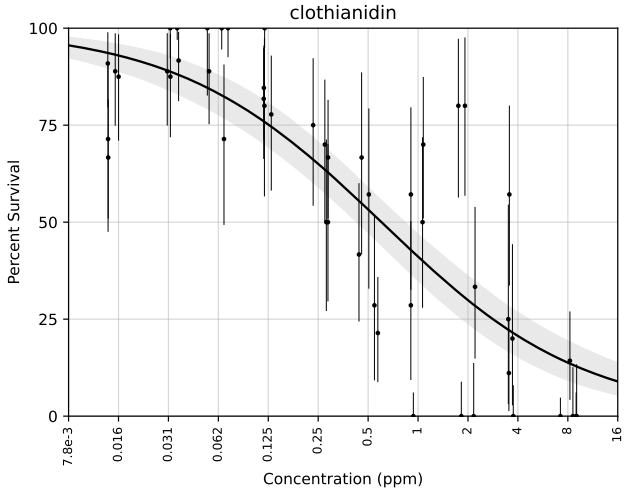
Chlorantraniliprole LC_{50}: 8.26 ppm [3.83, 22.2]
9 biol. reps; 10 tech. reps; R^2: 0.483



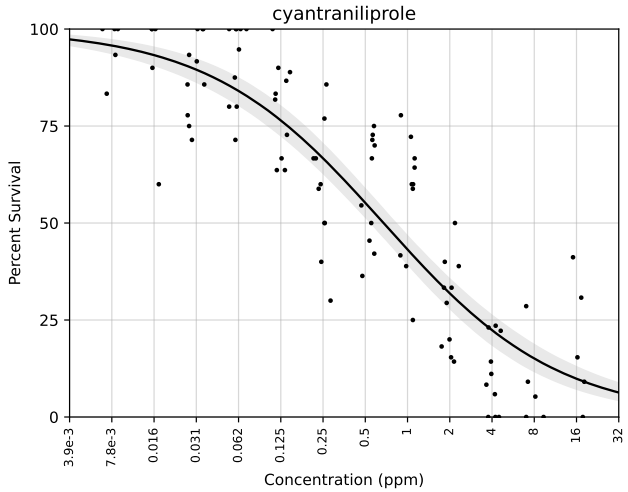
Chlorfenapyr LC_{50}: 7.93 ppm [5.98, 10.7]
4 biol. reps; 5 tech. reps; R^2: 0.71



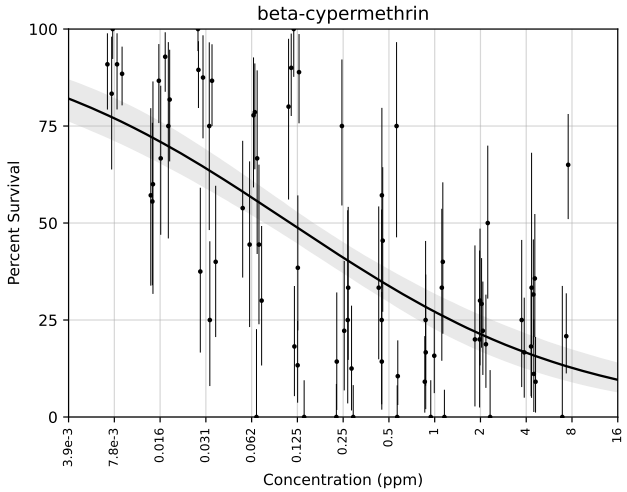
Chlorpyrifos LC_{50}: 0.177 ppm [0.143, 0.222]
4 biol. reps; 5 tech. reps; R^2: 0.918



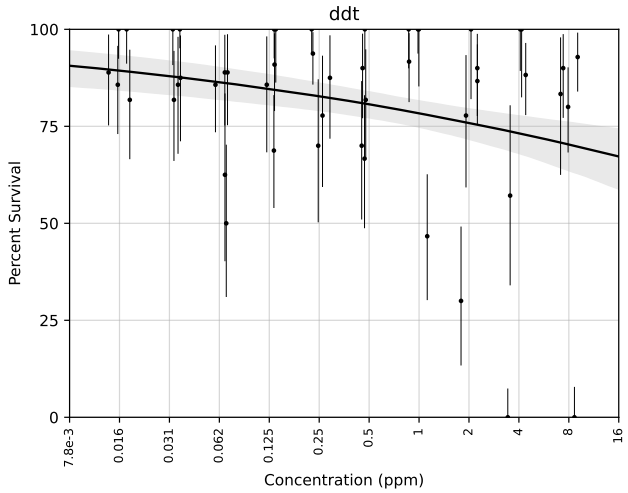
Clothianidin LC_{50}: 0.602 ppm [0.427, 0.838]
4 biol. reps; 5 tech. reps; R^2: 0.692



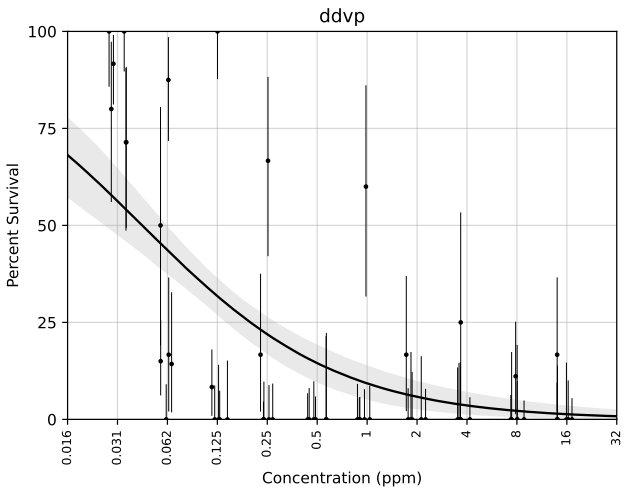
Cyantraniliprole LC_{50}: 0.675 ppm [0.548, 0.831]
9 biol. reps; 10 tech. reps; R^2: 0.797



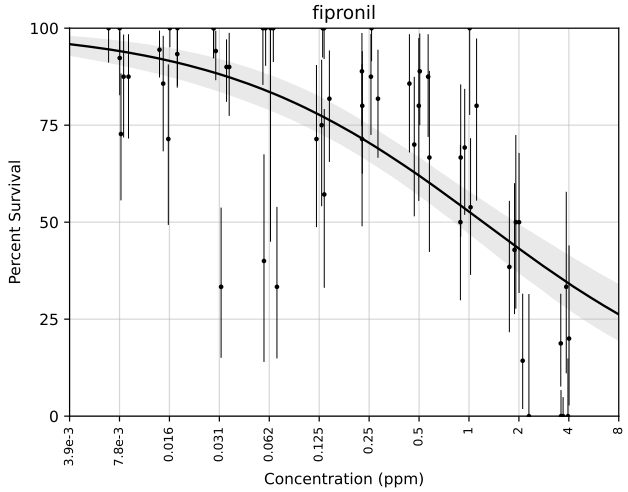
β-Cypermethrin LC_{50}: 0.112 ppm [0.0781, 0.159]
7 biol. reps; 8 tech. reps; R^2: 0.437



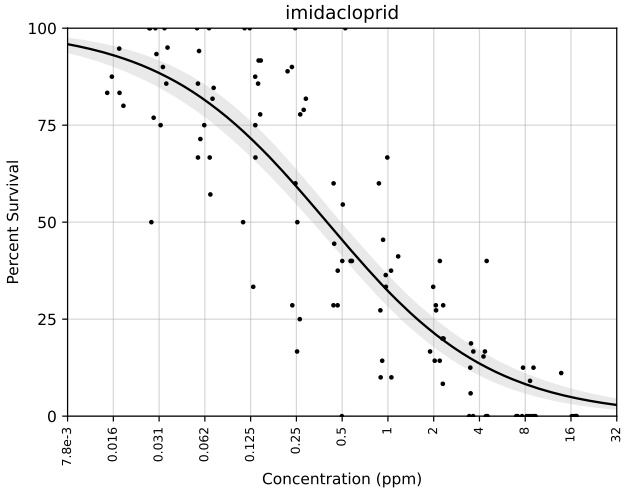
DDT LC_{50} cannot be estimated with the given data.
4 biol. reps; 5 tech. reps; R^2: 0.0763



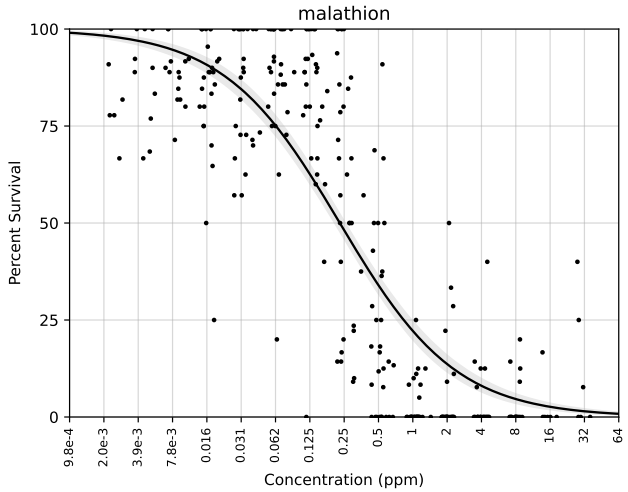
DDVP LC_{50}: 0.0441 ppm [0.0282, 0.0641]
5 biol. reps; 6 tech. reps; R^2: 0.468



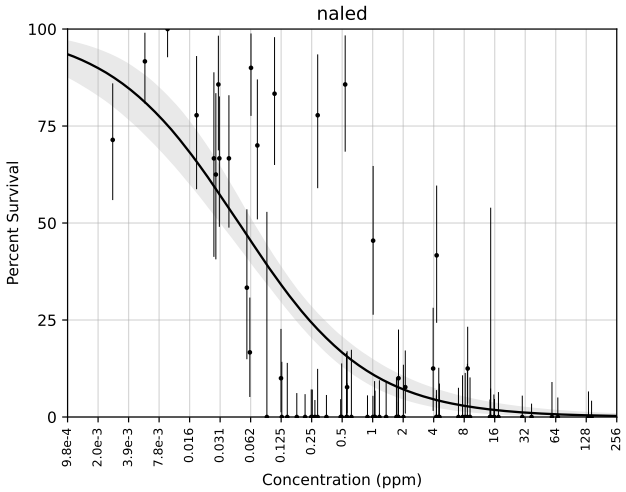
Fipronil LC_{50}: 1.22 ppm [0.802, 1.85]
5 biol. reps; 6 tech. reps; R^2: 0.529



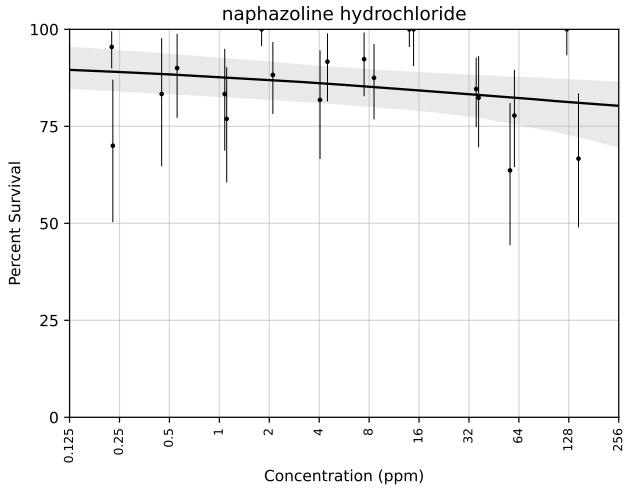
Imidacloprid LC_{50}: 0.398 ppm [0.322, 0.485]
9 biol. reps; 11 tech. reps; R^2: 0.771



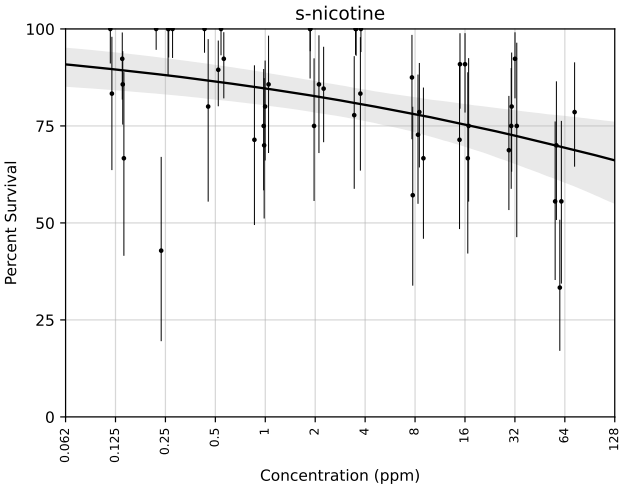
Malathion LC_{50}: 0.229 ppm [0.205, 0.255]
16 biol. reps; 31 tech. reps; R^2: 0.742



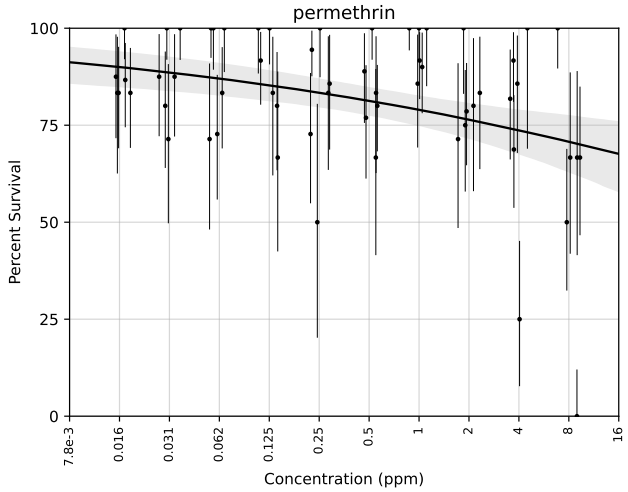
Naled LC_{50}: 0.0478 ppm [0.0325, 0.0677]
7 biol. reps; 7 tech. reps; R^2: 0.566



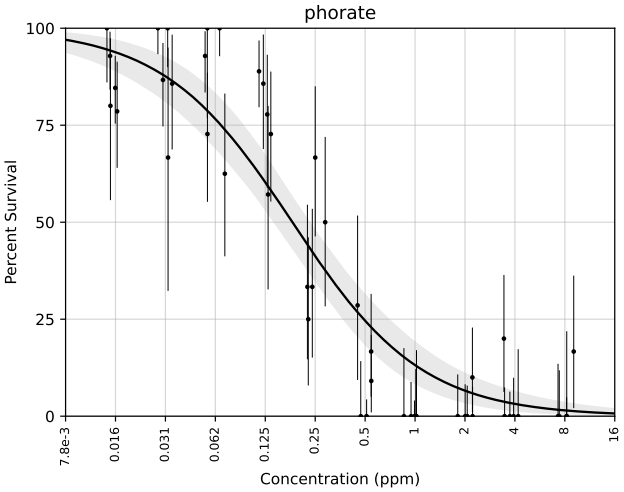
Naphazoline hydrochloride LC_{50} cannot be estimated with the given data.
2 biol. reps; 2 tech. reps; R^2: 8.88e-3



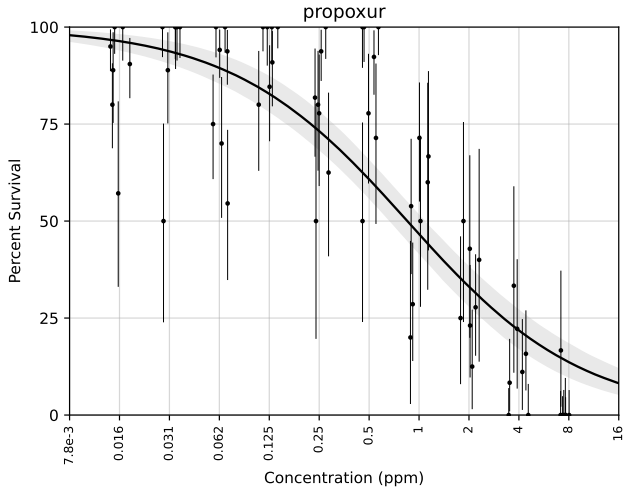
***S*-nicotine** LC_{50}: 2.98e3 ppm [121, 2.21e6]
4 biol. reps; 5 tech. reps; R^2: 0.211



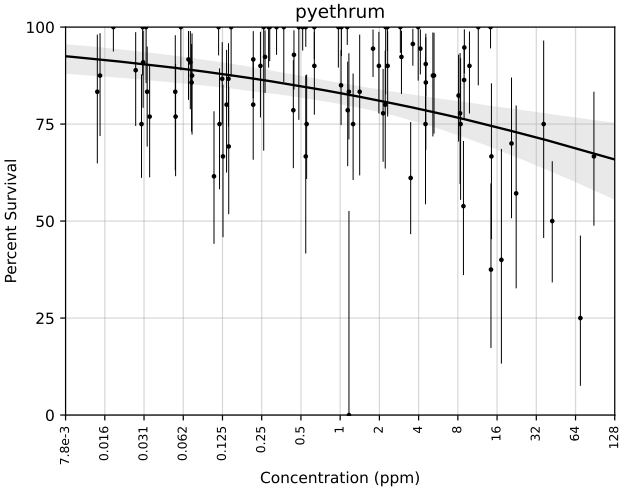
Permethrin LC_{50} cannot be estimated with the given data.
5 biol. reps; 6 tech. reps; R^2: 0.133



Phorate LC_{50}: 0.182 ppm [0.143, 0.233]
4 biol. reps; 5 tech. reps; R^2: 0.883



Propoxur LC_{50}: 0.85 ppm [0.669, 1.08]
6 biol. reps; 7 tech. reps; R^2: 0.761



Pyethrum LC_{50}: 4.08e3 ppm [145, 1.14e6]
8 biol. reps; 9 tech. reps; R^2: 0.138

Data analysis was performed using the statistics module for the Merlin Data Analysis program. Live/dead counts from the bioassay were used to generate new survival probabilities using a Beta prior. The user-specified prior is Heldane's prior, the improper prior Beta$(0, 0)$, (set by `BETA_PRIOR`) and 3840 bootstrap iterations were used (set by `BOOTSTRAP_ITERS`).When either the live count or dead count was equal to 0, the prior the distribution Beta$(0.25, 0.25)$ (set by `BETA_PRIOR_0`) was used to avoid the sunrise problem. Correlation between wells in a replicate was modelled by generating multivariate normal random variables with correlation $\rho = 0.1$ (set by `RHO`), which were then converted to quantiles, and then back-converted to probabilities in the appropriate beta distribution.

Each iteration of bootstrapped dose-response data was fit to the curve

$$\theta_i = \frac{1}{(1 + \exp(b_0 + b_1 x_i))}$$

by maximizing the log-likelihood function. This is equivalent to solving the problem

$$\underset{b_0, b_1}{\operatorname{argmax}} \left(-\frac{b_0^2 + b_1^2}{2\sigma^2} + \sum_{i=1}^{n} p_i \xi_i - \sum_{i=1}^{n} \ln(1 + \xi_i) \right)$$

where

$$\xi_i = e^{b_0 + b_1 x_i}.$$

A scale parameter may be included by setting `CURVE_TYPE = ls3` in the `analysis_config.txt` file. Priors on parameters were $(b_0, b_1) \sim \mathcal{N}(\mathbf{0}, \sigma I_2)$, where $\sigma = 1000.0$, as defined by `LL_SIGMA` in the `analysis_config.txt` file. Optimization of the log-likelihood function was performed using the optimized vector Broyden-Fletcher-Goldfarb-Shanno (BFGS) algorithm using a C interface to the GNU Scientific Library.

Credible intervals for the data points are shown at the 80% level when fewer than 10 replicates are used. The best-fit line is calculated as the median value of all fitted curves at a given concentration. The error region for the curve respresents a 95% confidence region, as determined by quantiles of predicted survivals at each concentration.