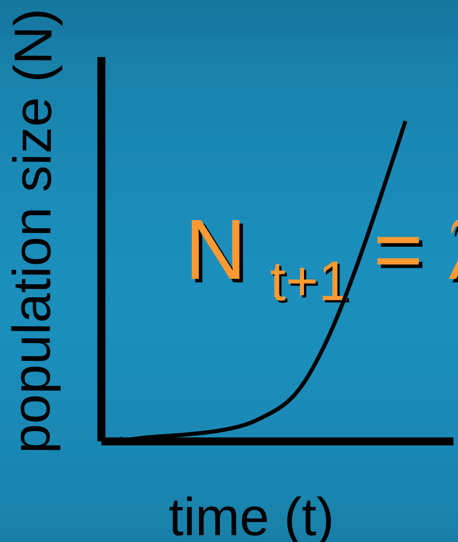
# Sensitivity Analysis of the Raccoon Rabies Model using Information Theory

E. E. Rees[1], B. A. Pond[2], R. Tinline[3], D. Murray[1], & D. Ball[3]
[1]Trent University, Peterborough, Canada; [2]Ontario Ministry of Natural Resources, Peterborough, Canada; [3]Queen's University, Kingston, Canada

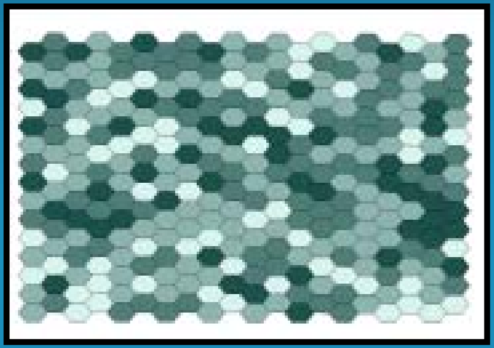
# Model Complexity

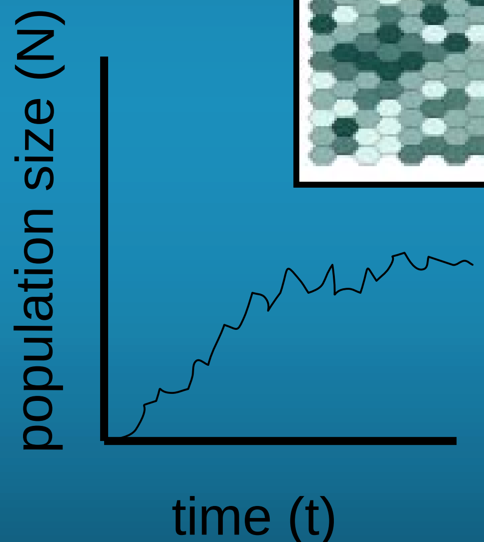
## Simple Population Model

$$N_{t+1} = \lambda N$$




## Complex Individual Based Model

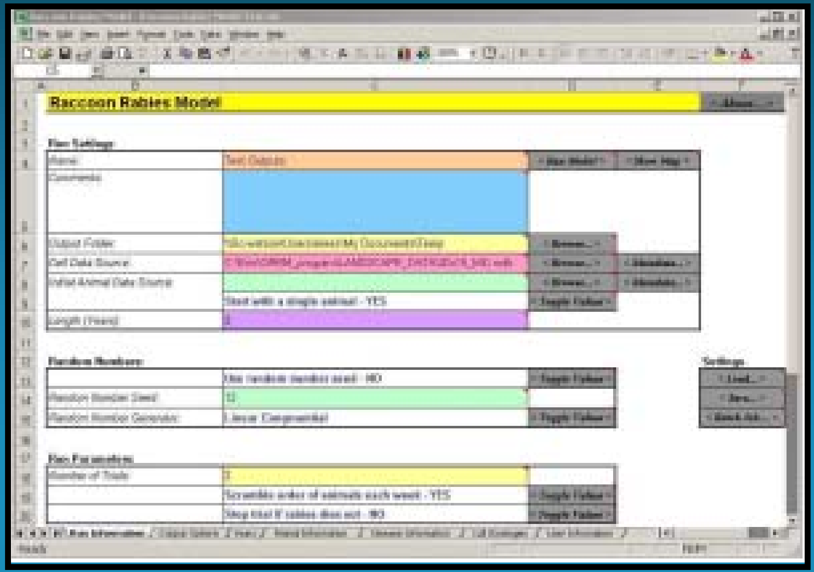




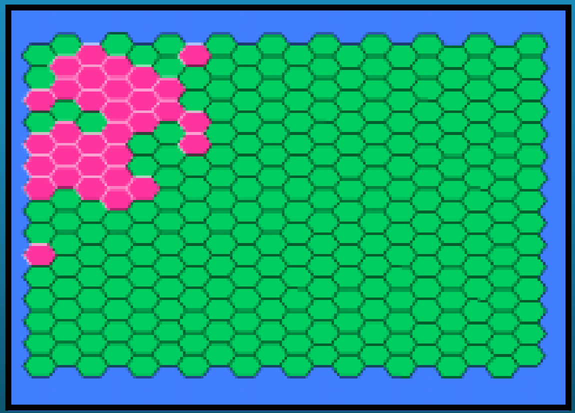

**How complex should a model be???**

# Ontario Rabies Model (ORM)

Individual-based “animal” spatial simulation disease model configured for raccoons




(MS Excel user interface)

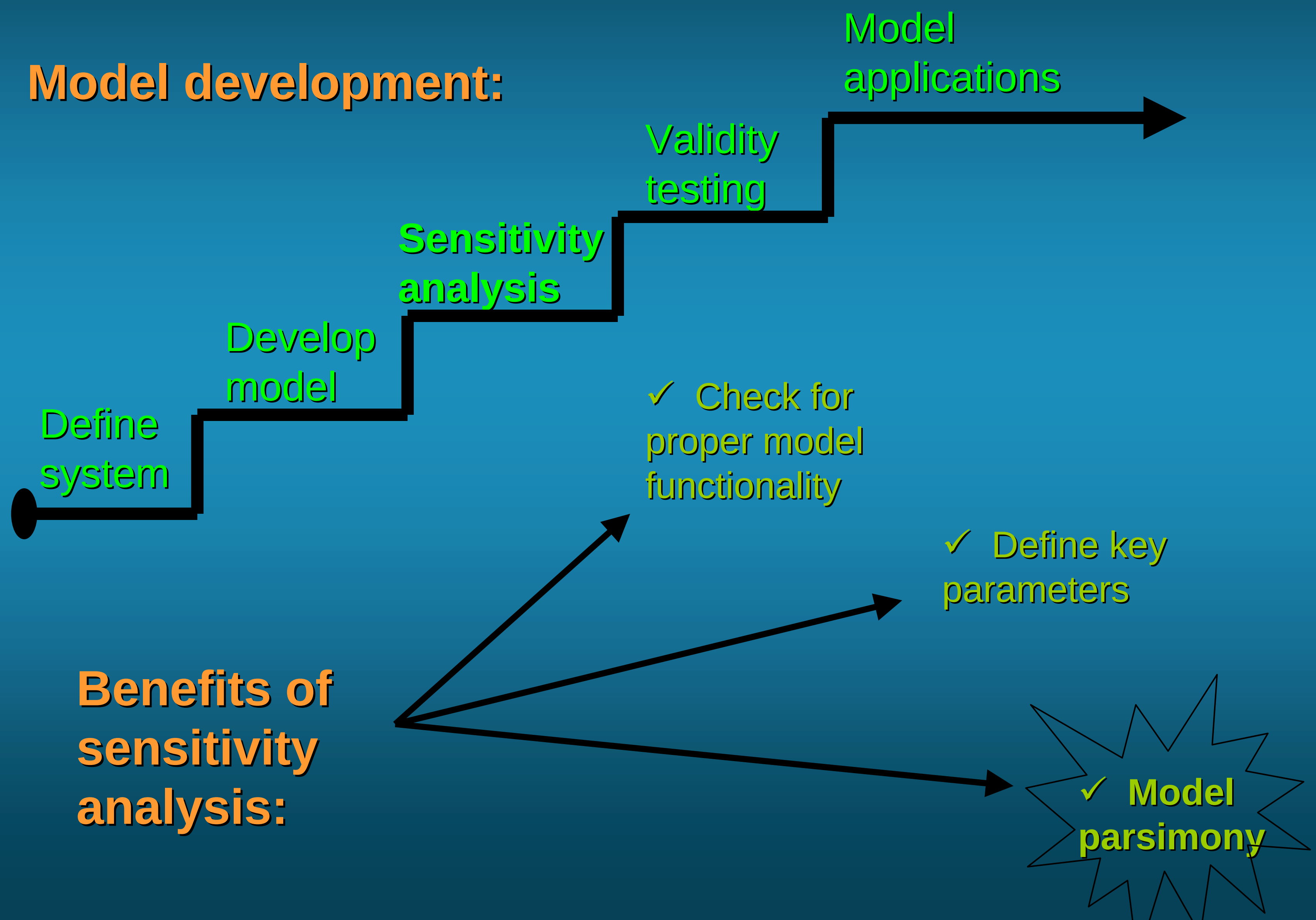


(Rabies spreading across virtual landscape)

Simulates:

- raccoon population dynamics
- raccoon rabies viral transmission
- rabies control strategies

# Determining Complexity through Sensitivity Analysis

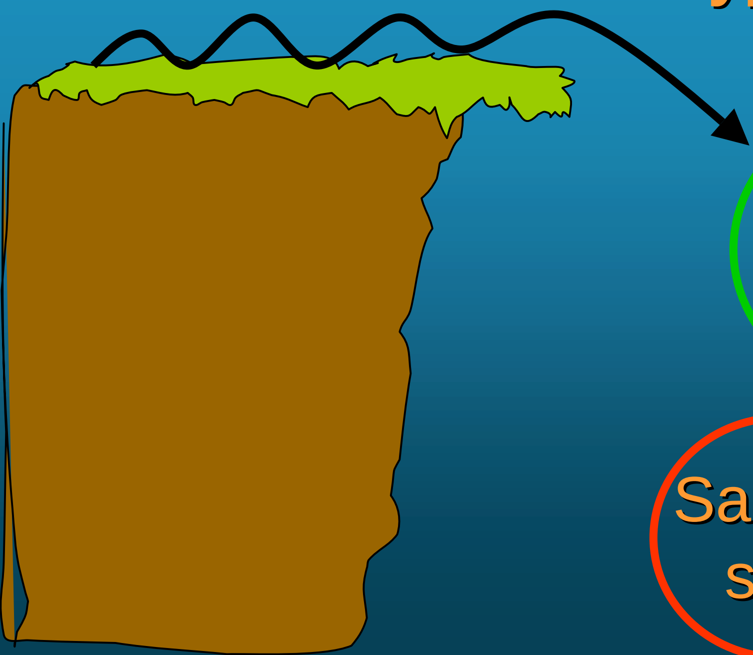


# Problems of Model Selection with Current Sensitivity Analysis Techniques

**1. Do not measure trade-off between:**

↑ realism (more parameters) ⟷ ↓ output confidence (more outcome uncertainty)

**2. Pitfalls of null hypothesis significance testing:**

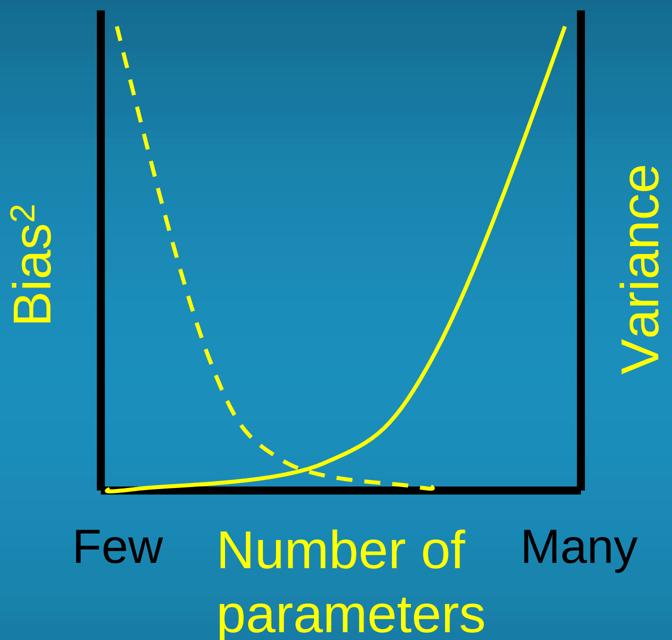


Probability (result|$H_o$)

Uninformative

Sample size

# Overcome Problems by using Akaike's Information Criterion (AIC)



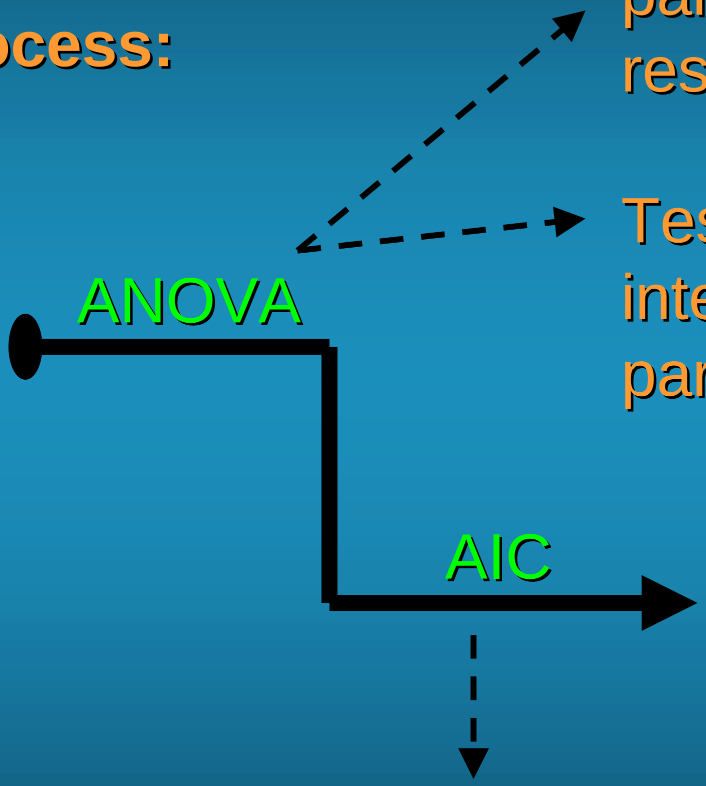

$$AIC = -2\log_e(l(\theta\,|data)) + 2K$$

Probability (result|data)

Model with the smallest AIC is the best model at approximating truth, given the other models, and the data

# Incorporating AIC into Sensitivity Analysis

**Two step process:**




Quantify effect of parameter(s) on the response variables

Test main, additive, and interaction effects of the parameters

Measure benefit of including parameter at cost of increasing outcome uncertainty

# Overview of ANOVA-AIC Sensitivity Analysis

1. **Goals:**
   - ✓ Check for proper model functionality
   - ✓ Define key parameters
   - ✓ Model parsimony

2. **Demographic sensitivity analysis:**
   - **Check demographics $1^{st}$ (in absence of rabies)**

3. **Disease sensitivity analysis:**
   - **Check disease parameters and key demographic parameters**

# Experimental Design

**Parameter inputs** → low (1/2 medium) / medium (best biological estimate) / high (2x medium)

↓

**Organise parameters into groups of 3**

↓

**Full factorial design of 3 parameters at 3 levels** → $3^3$ = 27 unique models

↓

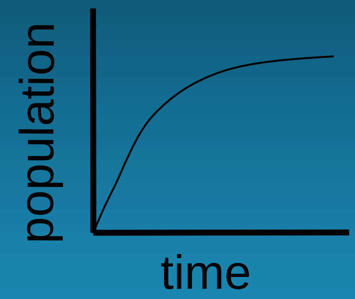
**Run each parameter set 10 times**

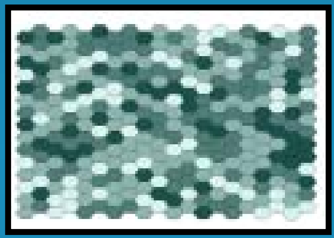
| | |
|---|---|
| M = male dispersal | l = low |
| F = female dispersal | m = medium |
| L = litter size | h = high |

| |
|---|
| MlFlLl |
| MlFlLm |
| MlFlLh |
| MlFmLl |
| MlFmLm |
| MlFmLh |
| MlFhLl |
| MlFhLm |
| MlFhLh |
| MmFlLl |
| MmFlLm |
| MmFlLh |
| MmFmLl |
| MmFmLm |
| MmFmLh |
| MmFhLl |
| MmFhLm |
| MmFhLh |
| MhFlLl |
| MhFlLm |
| MhFlLh |
| MhFmLl |
| MhFmLm |
| MhFmLh |
| MhFhLl |
| MhFhLm |
| MhFhLh |

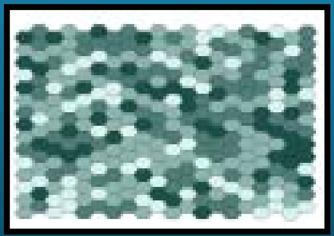
# Demographic Response Variables
# (assessing effects of parameters)

1. Total population
2. Time to stable population
3. Spatial variance: mean ratio
4. Temporal variance: mean ratio
5. Centre temporal cell variance: mean ratio
6. Moran's I



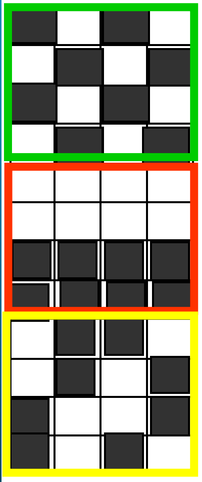
V:M = 0 → uniform
V:M = 1 → random
V:M > 1 → clumped



< 0 → not like neighbours

0 → "like" with "like"

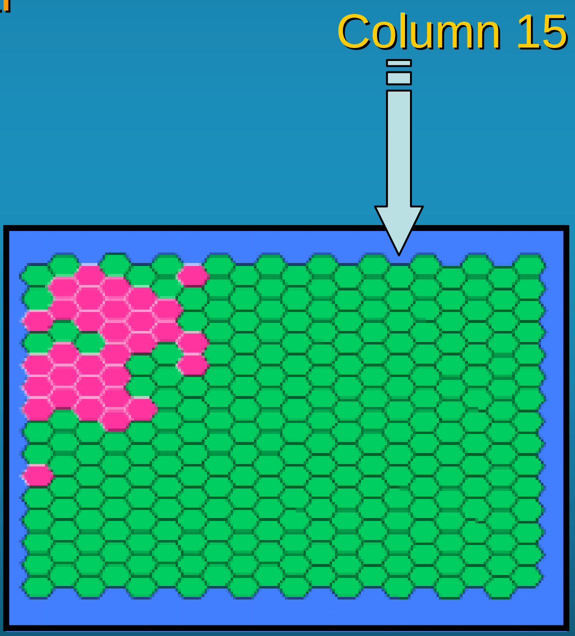
> 0 → random



Select representative response variables or some effects might be missed!

# Disease Response Variables
# (assessing effects of parameters)

1. Total population
2. Spatial variance: mean ratio
3. Total number of rabies cases after 1 year
4. Maximum number of rabies cases
5. Time to maximum number of cases
6. Disease persistence
7. Disease duration
8. Rate of spread
9. Mean distance of spread




(15 x 20 virtual landscape)

Select representative response variables or some effects might be missed!

# ANOVA-AIC Sensitivity Analysis

1. Perform ANOVA on 27 unique models of each sensitivity testing group

recall…

| |
|---|
| MlFlLl |
| MlFlLm |
| MlFlLh |
| MlFmLl |
| MlFmLm |
| MlFmLh |
| MlFhLl |
| MlFhLm |
| MlFhLh |
| MmFlLl |
| MmFlLm |
| MmFlLh |
| MmFmLl |
| MmFmLm |
| MmFmLh |
| MmFhLl |
| MmFhLm |
| MmFhLh |
| MhFlLl |
| MhFlLm |
| MhFlLh |
| MhFmLl |
| MhFmLm |
| MhFmLh |
| MhFhLl |
| MhFhLm |
| MhFhLh |

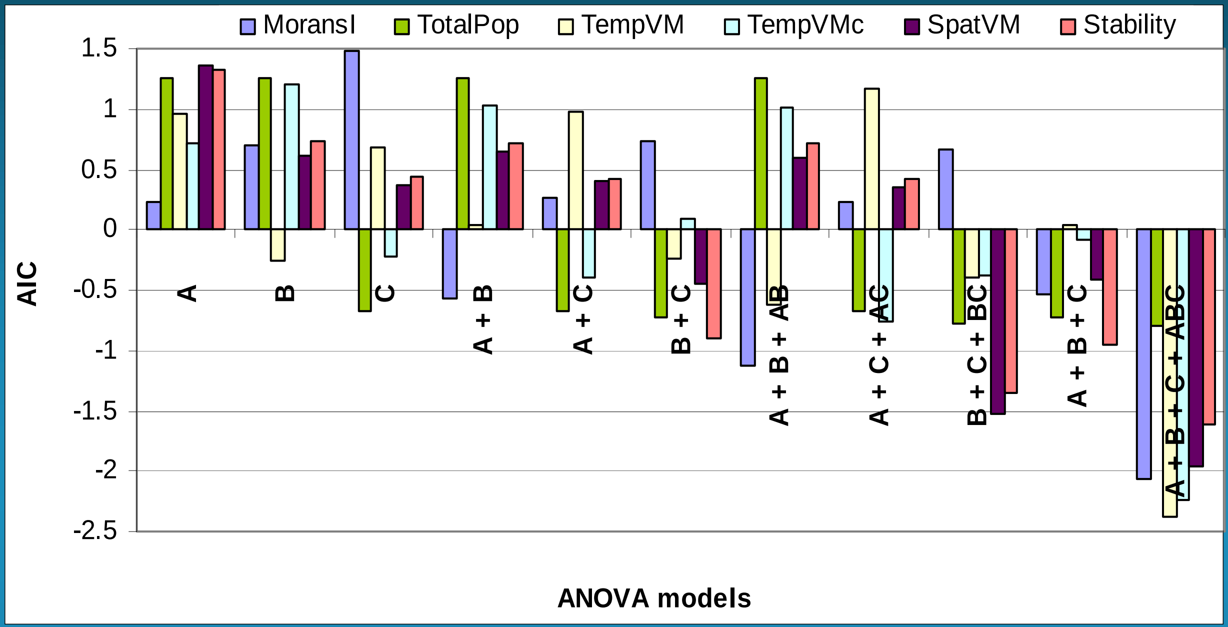
2. Generate a mean square error term (MSE) for 11 ANOVA models

| Main Effects Models | Additive Effects Models | Interaction Effects Models |
|---|---|---|
| A | A + B | A + B + AB |
| B | A + C | A + C + AC |
| C | B + C | B + C + BC |
| | A + B + C | A + B + C + ABC |

3. Use the MSE to calculate an AIC value

$$AIC = n\log_e(MSE \times errorDF / n) + 2K$$

# Results



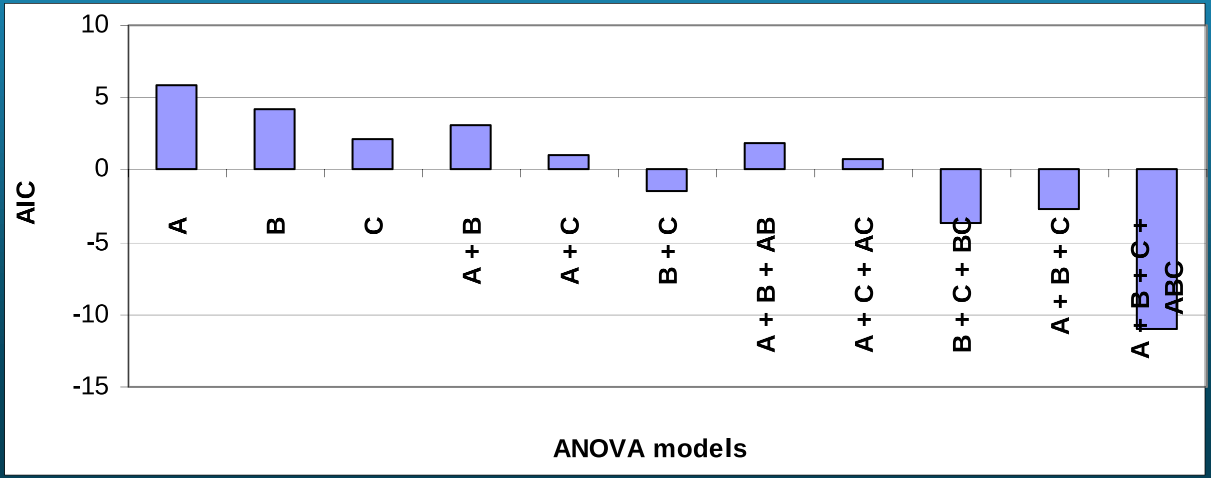

Example of demographic sensitivity analysis group:

A = male dispersal

B = female dispersal

C = litter size

pooled AIC




**A + B + C + ABC always the best! (accounted for the most variation)**

# Conclusions

**ORM modelling conclusions:**

- Demonstrated expected functionality
- Identified key parameters (e.g. litter size)
- Model is parsimonious

**AIC sensitivity analysis conclusions:**

- ✓ **Overcomes pitfalls of null hypothesis significance testing**
- ✓ **Measures whether inclusion of a parameter to improve model fit outweighs cost of increased outcome uncertainty**
- ✓ **Still yields benefits of other sensitivity analysis techniques**

# Acknowledgments


Rick Rosatte, Kirk Sobey, and the Ministry of Natural Resources, Rabies Research and Development Unit

Bradley White, Christopher Kyle, Catherine Cullingham, Annamaria Szanto from the NRDPFC, Trent University


TRENT UNIVERSITY

NATURAL RESOURCES DNA Profiling & Forensic Centre

ONTARIO NATURAL RESOURCES

Queen's UNIVERSITY