

BioVeL – Biodiversity Virtual e-Laboratory

Workflow Documentation

Relative importance of Chinook salmon abundance on resident Killer whale population viability pack for execution in the BioVeL Portal

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Grant Agreement No: Project Co-ordinator: Project Homepage: Duration of Project: Start Date: 283359 Mr Alex Hardisty http://www.biovel.eu 36 months Sept 2011 Aug 2014



End Date:



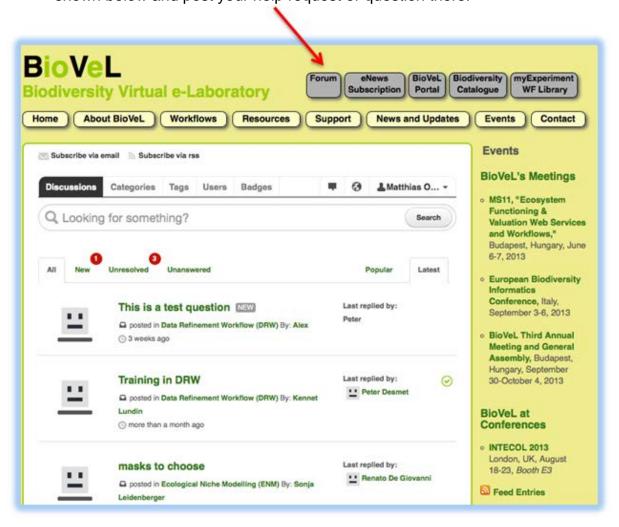
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1. Sources of help

You can obtain help with using BioVeL workflows and services from 3 places:

- 1) From the BioVeL documentation website, here: https://wiki.biovel.eu/x/BIBp
- 2) By using the BioVeL community discussion Forum on our website, www.biovel.eu. If you have questions go to the Forum by clicking the grey button shown below and post your help request or question there.



By emailing to support@biovel.eu

This documentation contains the tutorial to run two related workflows.

1. Resident killer whale-chinook salmon interactions workflow

The Resident killer whale-chinook salmon interactions workflow provides an environment to create calculate a two-sex stage-structured matrix with no density dependence and with vital rates as random variables or as functions of Chinook abundance from specific stock aggregates and to (i) quantify the differences in demographic rates between Orcinus orca population that explain population growth; (ii) to determine the relative influence of vital rates and Chinook abundance-vital rate interactions on expected population growth; (iii) to generate projections of population size at various time horizons.

2. Exploration of fishing scenarios workflow

This workflow cannot be run without running first the Resident killer whale-chinook salmon interactions workflow. The Exploration of fishing scenarios workflow needs the PostWorkspace, a zip file generated by the first workflow. See details page 39, PostWorkspace (zip file).

This workflow merges statistical inference derived from linkages between resident killer whale (RKW) vital rates (survival probability and fecundity rates) and chinook salmon abundance with demographic perturbation analysis and population viability analysis to address some of the pressing questions that have recently engaged the efforts of scientists and managers interested in: (1) the role of chinook salmon abundance in the population dynamics of RKW; and (2) how RKW population viability is expected to respond to changes in chinook mortality owing to harvest.

This workflow can be used to analyse interactions between Chinook salmon abundance from specific stock aggregates and killer whale vital rates, the effect of these interactions on killer whale population growth, and the exploration of Chinook salmon fishing scenarios on killer whale population growth and short term projections of population size. See necessary input data.

For more details about the analyses, please download:

- Sensitivity of resident killer whale population dynamics to Chinook salmon abundance (http://www.myexperiment.org/files/1307.html)
- Comparative Demography and Viability of North-eastern Pacific Resident Killer Whale Populations at Risk (http://www.myexperiment.org/files/1306.html)
- Relative importance of chinook salmon abundance on resident killer whale population growth and viability (http://onlinelibrary.wiley.com/doi/10.1002/agc.2494/abstract)

Resident killer whale-chinook salmon interactions.

2. Input files for tutorial

The workflow accepts input data in a .csv, coma delimited. The examples input files for the tutorial are available and described below. In this tutorial, four input files are used.

2.1 Input data

To download click here on the file name or they can be downloaded at myExperiment (http://www.myexperiment.org/packs/667.html):

Orcinus orca input data:

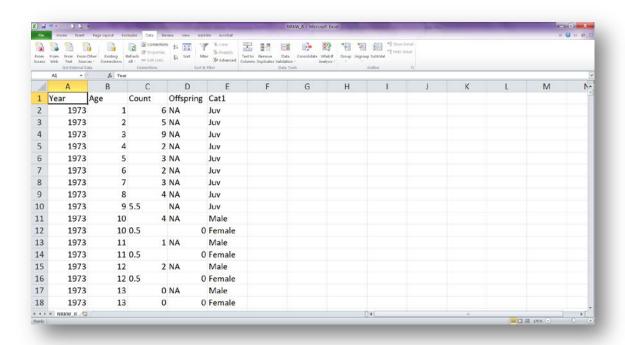
- NRKW_R or SRKW_R
- VR_combined

The following files are needed in order to get some necessary results to run (a second workflow), Exploration of fishing scenarios workflow.

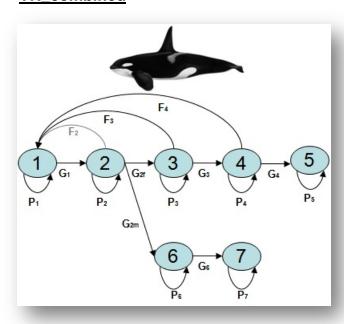
Chinook input data:

- Chinook Ab Definitions R or Chinook Ab Defs FI R
- ChinookAbundance_Data_R or ChinookAbundance_FI_R

NRKW R or SRKW R: The input data (a .csv-file) has to have the format of a table containing the *Orcinus orca* demographic data with the columns named: Year, Age, Count, Offspring and Cat1. Each year, the number of individuals per age and the number of offspring per age reproductive female category are counted (females ≥ 10 years old). IF A Female category does not have offspring equals to 0. For the called column, Cat1; Ages 1 to 9 belongs to Juv (Juveniles) and 10 to 88 (this tutorial) belongs to Female or Male. Juv and Male categories must have a NA offspring.



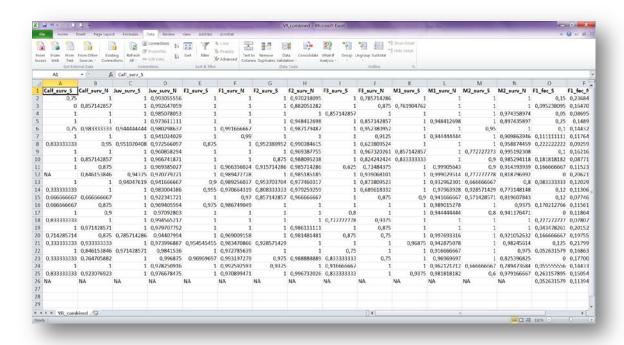
VR_combined



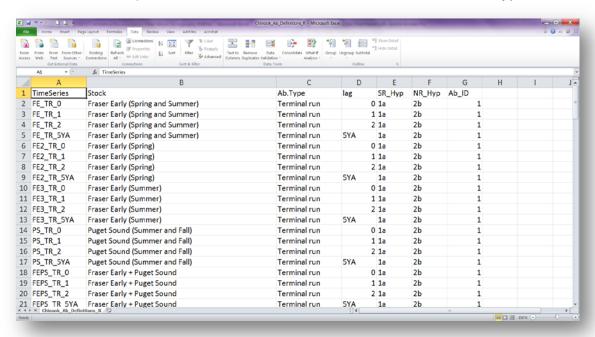
The stage-structured life cycle of resident killer whales with seven life stages:

- (1) calves; (Calf)
- (2) juveniles; (Juv)
- (3) young reproductive females; (F1)
- (4) old reproductive females; (F2)
- (5) post-reproductive females; (F3)
- (6) young mature males; and (M1)
- (7) old mature males (M2).
- Fi represent fertility; Gi represent stage transition probabilities, with female and male juvenile-to-adult transitions indicated as G2f and G2m, respectively; and, Pi represent the probability of surviving and remaining in stage i

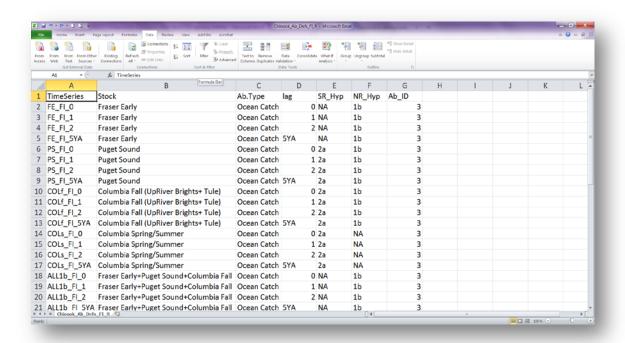
The input data (a .csv-file) has to have the format of a table containing the survival and fecundity rates per stage, per year, per population of the *Orcinus orca*. E.g. Calf_surv_S = 0, 75 will the survival value of the first year (in this case 1987) of the SRKW calves stage.



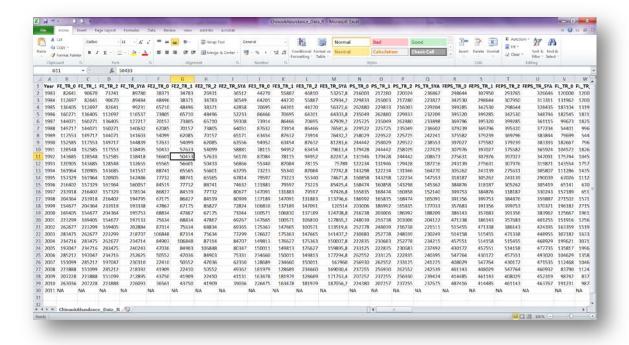
<u>Chinook Ab Definitions R:</u> Table that contains Chinook abundance definitions by stock aggregate, abundance type (TR: Terminal Run; OA: Ocean Abundance), time lag (5YA: 5-year running average), and hypothesis (SR: Southern Resident Killer Whale; NR: Northern Resident Killer Whale) and abundance ID. See below information about hypothesis.



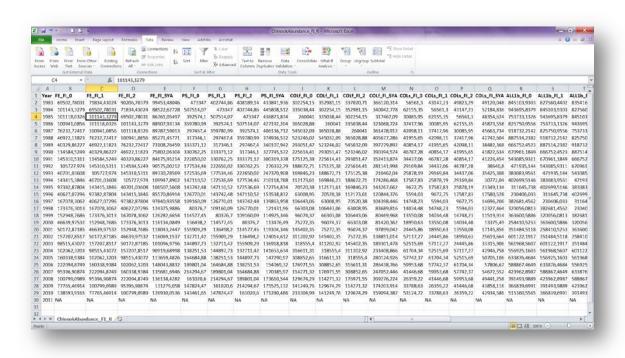
<u>Chinook Ab Defs FI R:</u> Table used to define fishery impacts (FI) on Chinook abundance by stock aggregate, time lag (5YA: 5-year running average), and hypothesis (SR: Southern Resident Killer Whale; NR: Northern Resident Killer Whale) and abundance ID. FI represent ocean catch of specific Chinook stocks or stock aggregates. See below information about hypothesis.



<u>ChinookAbundance Data R:</u> Table showing the time series of abundance (TR or OA) of all stocks and stock aggregates by time lag used in the analysis.



<u>ChinookAbundance_FI_R:</u> Table showing the time series of Fishery Impacts of all stocks by time lag used in the analysis.



2.1 Related publications

Vélez-Espino, L.A., John K.B. Ford, Eric Ward, Chuck K. Parken, Larrie LaVoy, Ken Balcomb, M. Bradley Hanson, Dawn. P. Noren, Graeme Ellis, Tom Cooney, and Rishi Sharma. 2013. Sensitivity of resident Killer Whale population dynamics to Chinook salmon abundance. Completion Report, Pacific Salmon Commission, Southern Boundary Restoration and Enhancement Fund, Vancouver BC. 191 p.

Vélez-Espino, L.A., Ford, J.K.B., Araujo, H.A., Ellis, G., Parken, C.K, & Balcomb, K. 2014. Comparative demography and viability of northeast Pacific resident killer whale populations at risk. Can. Tech. Rep. Fish. Aquat. Sci. 3084: vi + 56 p.

Vélez-Espino, L.A., John K.B. Ford, H. Andres Araujo, Graeme Ellis, Charles K. Parken and Rishi Sharma. 2014. Relative importance of Chinook salmon abundance on resident killer whale population growth and viability. Aquatic Conservation: Marine and Freshwater Ecosystems. Article first published online: 21 AUG 2014. DOI: 10.1002/aqc.2494

3. Tutorial:

The resident killer whale-chinook salmon interactions workflow provides an environment to create calculate a two-sex stage-structured matrix with no density dependence and with vital rates as random variables or as functions of Chinook abundance from specific stock aggregates and to (i) quantify the differences in demographic rates between Orcinus orca population that explain population growth; (ii) to determine the relative influence of vital rates and Chinook abundance-vital rate interactions on expected population growth; (iii) to generate projections of population size at various time horizons.

This workflow performs the following analyses:

- Vital rates estimation and probability distributions.
- · Construction of Birth-flow Matrix Model.
- Eigen analysis.
- Elasticity analysis (deterministic and stochastic).
- · Damping time.
- Stable stage distributions.
- IID projection matrices representing discrete time periods.
- Regressions between Killer Whale vital rates and stock-specific Chinook abundance.
- Elasticities of interactions between Killer Whale vital rates and stock-specific Chinook abundance.
- Retrospective perturbation analysis.
- Stochastic population growth from IID matrices and vital rate probability distributions.
- Projections of population size.

This tutorial explains the type of input data needed to run the workflow. The corresponding analysis use data from two distinct *O. orca* populations in Canada, Southern Resident Killer Whales (SRKW) and the Northern Resident Killer Whales (NRKW).

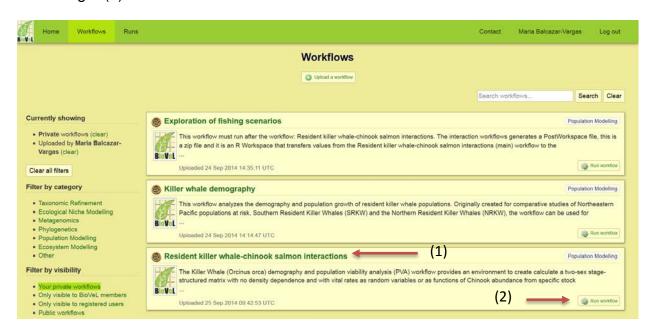
Two distinct populations of resident killer whales (Orcinus orca) in the north-eastern Pacific Ocean have been identified in Canada and the U.S. as being of conservation concern. The Southern Resident Killer Whale (SRKW) population is currently listed as endangered under the U.S. Endangered Species Act on the grounds of its small population size and vulnerability to demographic stochasticity and catastrophic events such as oil spills (NMFS 2008). In Canada, under the Species At Risk Act (COSEWIC 2008), SRKW is listed as endangered due to its small and declining population size while the Northern Resident Killer Whale (NRKW) population is listed as threatened due to its small population size. The major threats identified for these two populations are nutritional stress associated with prey and availability, particularly Chinook salmon tshawytscha) (COSEWIC 2008, Ford et al. 2010a, 2010b), pollution and contaminants, and disturbances from vessels and sound (COSEWIC 2008, NMFS 2008). An important difference in the population-size trajectories of these two populations is that, in spite of their home range overlap and potential access to similar resources, SRKW has remained at a population size of less than 100 individuals for the last four decades with an average of 85 individuals in the last decade. NRKW population size has been generally increasing for the last four decades with 268 individuals at the end of 2011.

In your browser (preferably Firefox or Chrome) navigate to the <u>BioVeL Portal</u> page (<u>http://portal.biovel.eu</u>/) and log in with your username and password (1). You will need to register if you have not already done so.

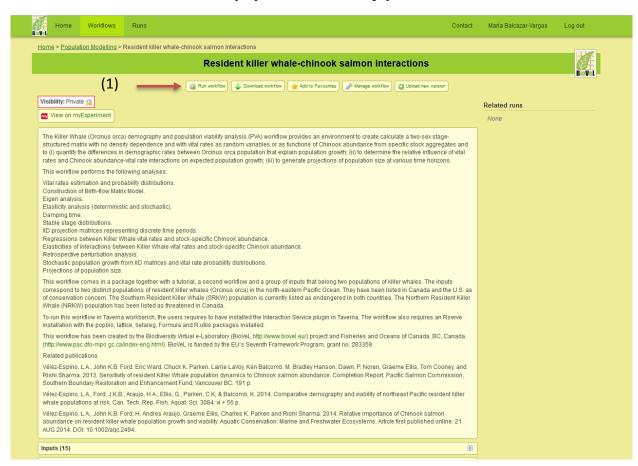
Choose the Population Modelling analysis and click, this will show you a list of relevant analysis:



On the resulting page choose the workflow *Resident killer whale-chinook salmon interactions* (1) you can also directly run the workflow using the 'Run workflow' button at the bottom-right (2).



On the resulting page click on the 'Run Workflow' button at the top (1).



On the next page you can edit the name of the workflow run to make it easier for you to identify it later (e.g. Resident Killer whale-Chinook salmon interactions_1).

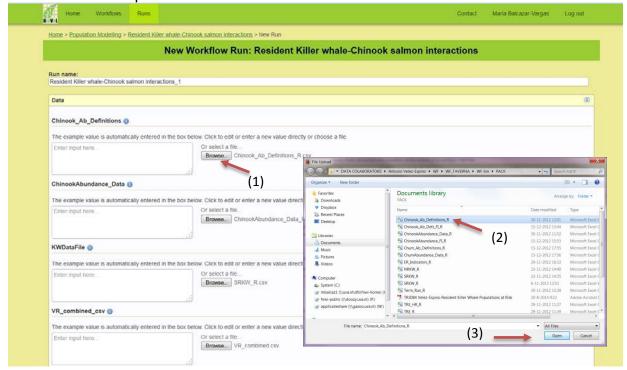


3.1 Input Ports

3.1.1 Data

<u>Chinook Ab Definitions:</u> it's a .csv file. Chinook abundance definitions by stock aggregate, abundance type (TR: Terminal Run; OA: Ocean Abundance), time lag (5YA: 5-year running average), and hypothesis (SR: Southern Resident Killer Whale; NR: Northern Resident Killer Whale) and abundance ID. See below information about hypothesis. Here, two files can be used as input: Chinook_Ab_Definitions_R.csv *or* Chinook_Ab_Defs_FI_R.csv

To open the file. Click in Browse (1), a window dialog appears and the user selects the file e.g. Chinook_Ab_Definitions_R.csv, (2) and then clicks the Open button (3). Repeat this action for all the input DATA.

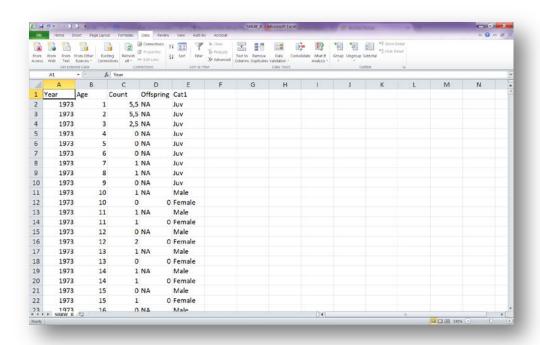


<u>ChinookAbundance Data:</u> it's a .csv file. Time series of abundance (TR or OA) of all stocks and stock aggregates by time lag used in the analysis. Here, two files can be used as input: ChinookAbundance_Data_R.csv *or* ChinookAbundance_FI_R.csv

To open the file. Click in choose file, a window dialog appears and the user selects the file e.g. ChinookAbundance_Data_R.csv and then clicks the Open button.

<u>KWDataFile:</u> it's a .csv file. Population File. This is a .csv file with the census data (i.e., counts) by age and group (juvenile, male or female) for the study population. For animals of uncertain year of death, amortized partial values were used. For instance, an animal with probable death over a span of two years was counted as 0.5 for the first year and 0.0 for the second year. Here, two files can be used as input: SRKW_R.csv or NRKW_R.csv

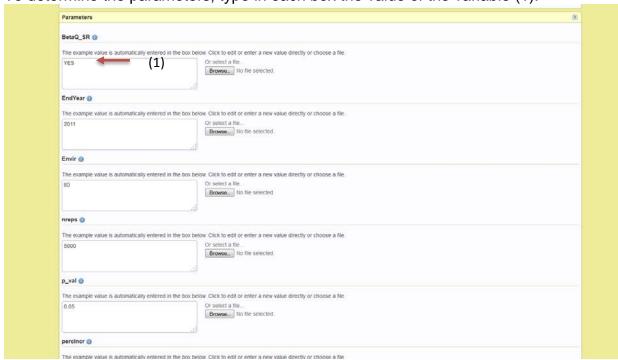
To open the file. Click in choose file, a window dialog appears and the user selects the file e.g. SRKW_R.csv and then clicks the Open button.



<u>VR combined:</u> Time series of vital rates (fecundity and survival by life stage) for both populations. To open the file. Click in choose file, a window dialog appears and the user selects the file e.g. VR_combined.csv and then clicks the Open button.

3.1.2 Parameters

To determine the parameters, type in each box the value of the variable (1).



<u>BetaQ SR:</u> defines if the simple regressions should be run with a Beta: YES or Linear model: NO.

e.g.: YES

EndYear: Last year to be considered in the analysis.

e.g.: 2011

ENVIR: Type of environmental stochasticity used for projection of population size. Two types available: IID (identically and independently distributed) or VR_Random (vital rates as random variables). For IID, various matrices are generated from vital rates representative of discrete time periods specified by the user (see "Study_period_year_x"). These matrices are drawn randomly for projections. For VR_Random, vital rates are randomly drawn from their probability distributions parameterized with mean and variances from the entire study time period (see Output Port "Stats_by_Category").

e.g.: IID

NREPS: Number of replications for projections of population size

e.g.: 5000.

p.val: p- value for the regression.

e.g.: 0.05

percincr: Percentage increment of Chinook abundance (0.1 = 10%).

e.g.: 0.1

population: It is the name of the analysed population.

e.g.: SRKW

<u>Sims:</u> Number of simulations that are used for generation of stochastic vital rate elasticities. This input indicates the number of stochastic matrices generated from randomly drawn vital rates. After computing population growth and elasticities for each of these matrices, a bootstrap is used to compute stochastic population growth and mean elasticities and their 95% confidence intervals.

e.g.: 10000

Standr Data: Use standardized data? YES or NO

e.g.: NO

StartYear: First year to be considered in the analysis.

e.g.: 1987

Variant. Using direct perturbations, two computational variants of the elasticity of interactions were explored. Variant 1 (equation 5) completely represents a direct perturbation process whereas variant 2 (equation 6) is a combination of vital rate elasticity and direct perturbation:

$$\varepsilon \left(x_{Chinook \to v_i} \right)_{DP, \text{variant 1}} = \frac{\Delta \lambda}{\Delta x_{Chinook}} = \frac{\left(\left(\lambda_{after} / \lambda_{before} \right) - 1 \right)}{\left(\left(x_{Chinook, after} / x_{Chinook, before} \right) - 1 \right)}$$

$$\varepsilon \left(x_{Chinook \to v_i} \right)_{DP, \text{ variant 2}} = \varepsilon \left(v_i \right) \frac{\Delta v_i}{\Delta x_{Chinook}} = \varepsilon \left(v_i \right) \frac{\left(\left(v_{i, after} / v_{i, before} \right) - 1 \right)}{\left(\left(x_{Chinook, after} / x_{Chinook, before} \right) - 1 \right)}$$

The term $x_{Chinook,before}$ is the Chinook abundance from a particular stock corresponding to the mean value of the interacting vital rate, $x_{Chinook,after}$ represents the simulated value of Chinook abundance that is used to explore the effect of changes in Chinook abundance (e.g. through changes in harvest rates) on RKW population growth rates. Thus, λ_{before} and λ_{after} represent the population growth rate before and after a perturbation on the vital rate(s) corresponding to a given change in Chinook abundance as per beta regressions, where $(v_{i,after})$ is the vital rate value after the perturbation. For more information see Velez-Espino et al. (Aquatic Conservation: Marine and Freshwater Ecosystems, *In press*)

e.g.: 2

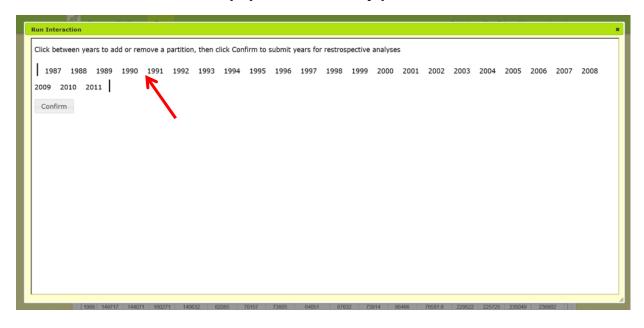
After the user has filled out the input ports and has clicked the **Start Run**, the workflow performs the analysis. To complete all the analysis may take few minutes, depends on the number of **Sims** and **NREPS** to carry out the analyses.

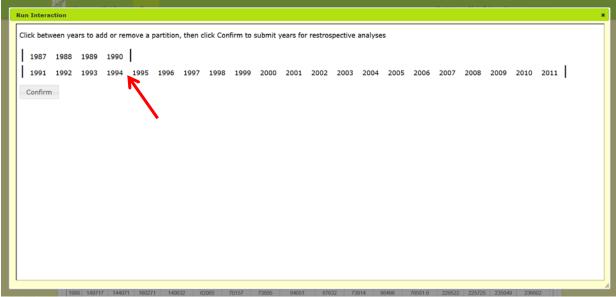
3.2. Dialogue

<u>Years for retrospective analysis:</u> Set the sets for the study period manually. Click after the desired year.

In this example 6 time periods are used for the retrospective analysis (i.e., five 4-year periods and one 5-year period). In practice, the decision about an appropriate number of time periods should be based on two criteria: (i) the more time periods the better for the resolution of IID dynamics, and (ii) there needs to be a minimum number of years in each time period to reduce the influence of outlier demographic conditions the could produce population matrices that are not representative of long-term dynamics

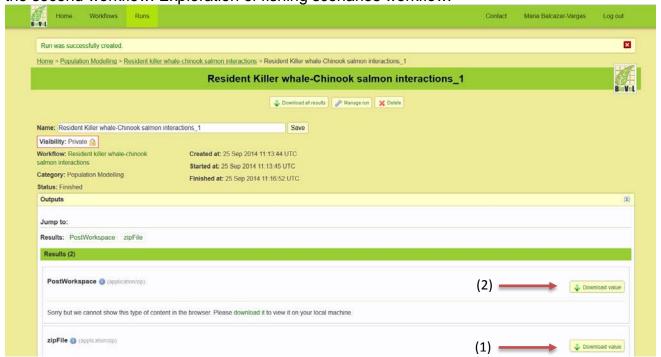
Click every 4 year, (e.g. 1987 1988 1989 1990, see red arrow). Click between 1990 and 1991, repeat the process. The last period will be for 5 years. Finally, click in confirm (red oval).





3.3 Outputs

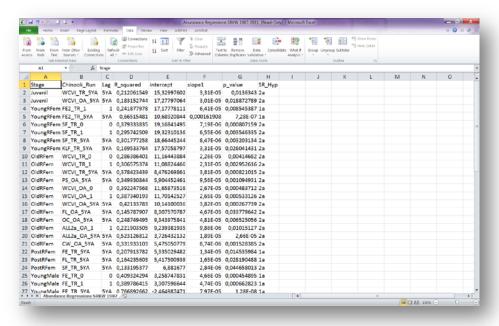
Once the analyses are finished, the user can download all the results by clicking Download value button (1). Numerical and graph results will be download as a zip file that can be save by the user. The numerical results are .csv files than can be opened with Excel and the plot files are .PDF files. A second result is the PostWorkspace, a zip file that is needed to run the second workflow: Exploration of fishing scenarios workflow.



3.3.1 Results

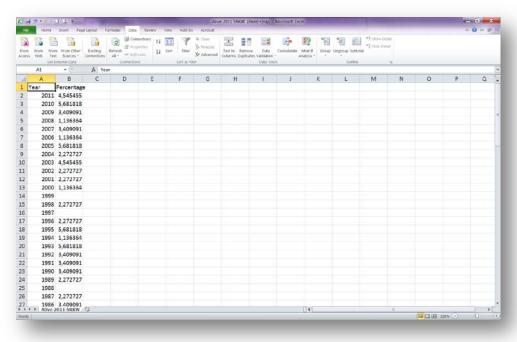
ZipFile

Abundance Regressions Population Start year-End year (csv): Statistics from beta regressions between Chinook abundance and killer whale vital rates.



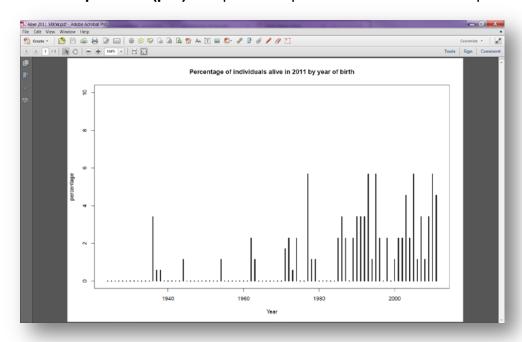
Abundance Regressions SRKW 1987-2011

Alive End Year Population (csv): Percentage of individuals alive in the last year of the study by year of birth. The sum of percentages for the selected time period indicates the number of individuals born during the study and alive the last year



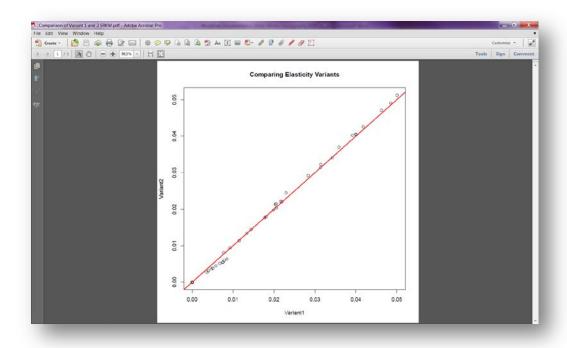
Alive 2011 SRKW.csv

Alive End Year Population (pdf): Graphical output for "Alive End Year Population"



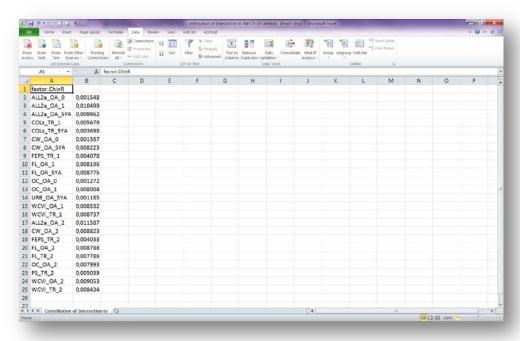
Alive 2011 SRKW.pdf

Comparison of Variant 1 and 2 Population (pdf): Plot showing the relationship between the two computational variants of the elasticity of interactions



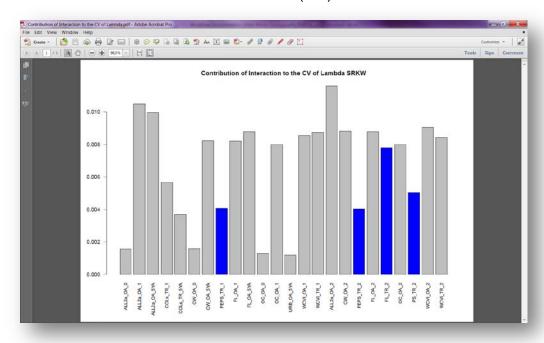
Comparison of Variant 1 and 2 SRKW

Contribution of Interaction to the CV of Lambda (csv): This file shows the proportion of the CV in population growth due to specific interactions between Chinook salmon stocks and abundance type and killer whale vital rates as explained by retrospective perturbation analysis.



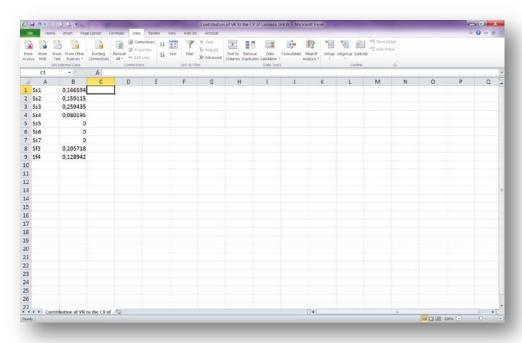
Contribution of Interaction to the CV of Lambda (csv)

Contribution of Interaction to the CV of Lambda (pdf): Graphical representation of Contribution of Interaction to the CV of Lambda (csv)



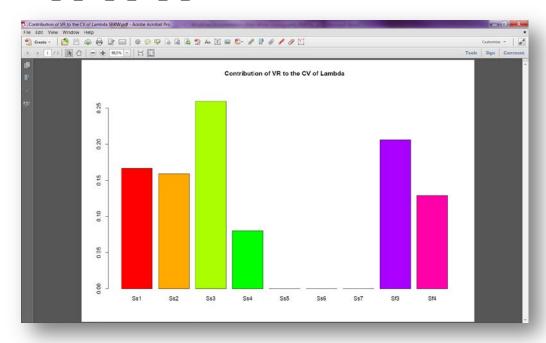
Contribution of Interaction to the CV of Lambda (pdf)

Contribution of VR to the CV of Lambda Population (.cvs): Results of retrospective perturbation analysis showing the contribution of past (observed) vital rate variation to the coefficient of variation of population growth rate (details in Vélez-Espino et al. 2013) e.g.: Contribution of VR to the CV of Lambda SRKW



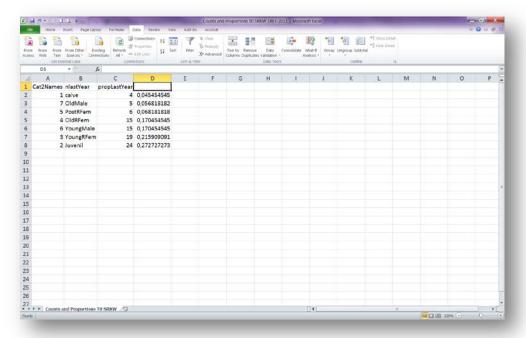
Contribution of VR to the CV of Lambda Population (cvs)

Contribution of VR to the CV of Lambda Population (pdf): Graphical representation of "Contribution_of_VR_to_CV_of_Lambda.csv".



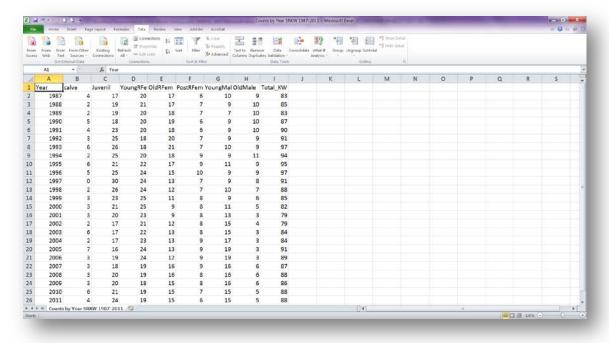
Contribution of VR to the CV of Lambda Population (pdf)

Counts and Proportions T0 Population Start year-End year (csv): Number of individuals and relative proportion by stage in the last year of the selected time period. These proportions are used to represent initial conditions for projections



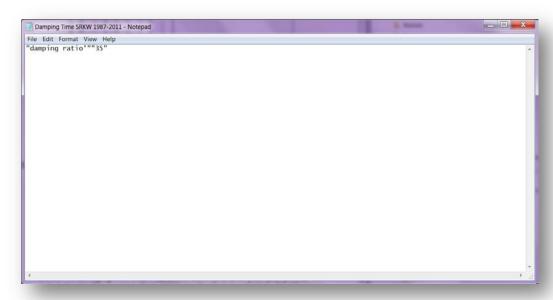
Counts and Proportions T0 Population Start year-End year (csv)

Counts by Year Population Start year-End year (csv): Number of individuals by life stage (calves, juveniles, young reproductive females, old reproductive females, post-reproductive females, young mature males, and old mature males) and year through the selected time period. Last column represents total population size



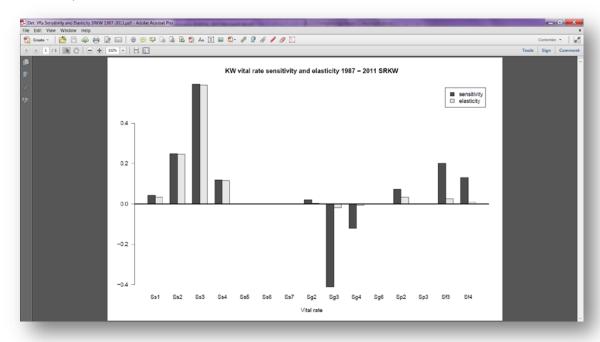
Counts by Year SRKW 1987-2011

Damping Time Population Start year-End year (txt): Damping time (τ) is defined as $\tau = \ln(z)/\ln(\rho)$, where ρ is the damping ratio and z is the number of times the contribution of λ_1 (dominant eigenvalue) becomes as great as that of λ_2 (subdominant eigenvalue). Damping times at z = 10 were used to define minimum time horizons for projections of population size.



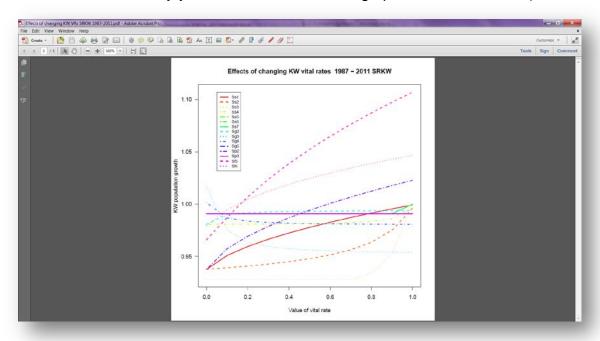
Damping Time SRKW 1987-2011

Det. VRs Sensitivity and Elasticity Population Start year-End year (pdf): Graphical output for sensitivities and elasticities of vital rates (survival, fecundity and stage transition probabilities)



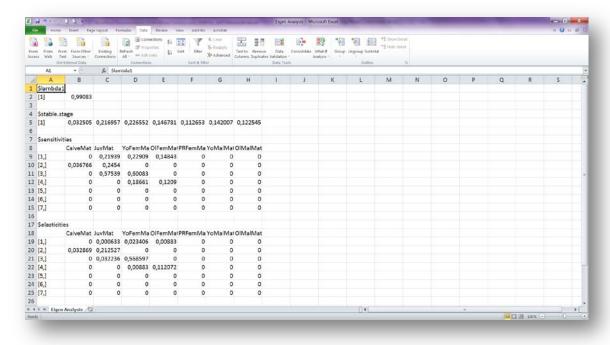
Det. VRs Sensitivity and Elasticity SRKW 1987-2011

Effects of changing KW VRs Population Start year-End year (pdf): Graphical output showing the response of population growth rate to hypothetical vital rate values ranging from 0.0 to 1.0. Some of these values could be biologically unfeasible (e.g., a fecundity rate of 1.0 would indicate every year all females in the stage produce a viable calf)



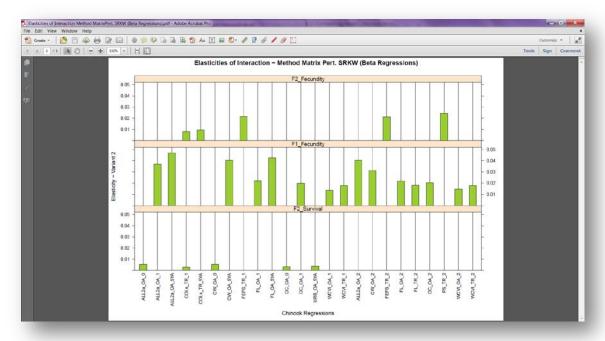
Effects of changing KW VRs SRKW 1987-2011

Eigen Analysis (txt): Dominant eigenvalue (asymptotic population growth rate), stable stage distribution, sensitivities, elasticities, reproductive value, and damping ratio based on mean matrix of selected population.



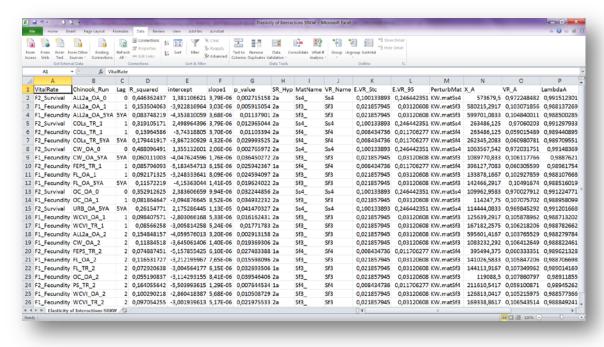
Eigen Analysis (open in Excel)

Elasticities of Interaction Method MatrixPert. Population (Type of Regressions) (pdf): This plot shows the elasticities (as determined by variant 2) of all significant interactions (as determined by beta regressions) between Chinook stock/abundance type/lag and killer whale vital rates



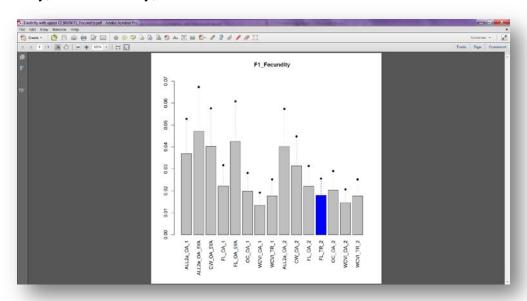
Elasticities of Interaction Method MatrixPert. SRKW (Beta Regressions)

Elasticity of Interactions Population (csv): This file shows the beta regression statistics and the value of variables involved in the direct perturbations used to compute the elasticities of all significant interactions.



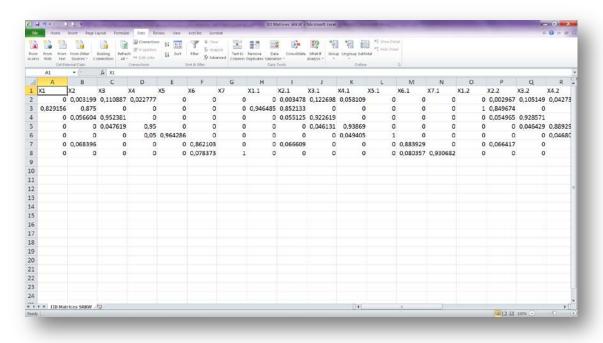
Elasticity of Interactions SRKW

Elasticity with upper CI Population Stage_Vital rate (pdf): These plots show the mean upper 95% confidence limit of elasticities of interactions by population (SRKW or NRKW) and vital rate. Interactions characterizing strong hypotheses 1a or 1b are highlighted in blue for SRKW and in green for NRKW. For example, using the 1987-2011 killer whale data, three vital rates exhibited significant interactions with Chinook salmon stocks: F1_Fecundity, F2_Fecundity, and F2_Survival.



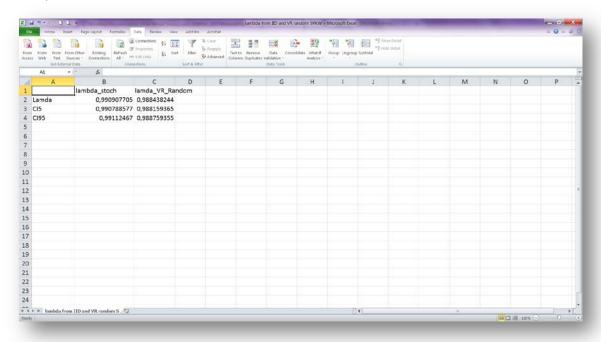
Elasticity with upper CI SRKW F1_Fecundity

IID Matrices Population (csv): Projection matrices produced by discrete time periods within the study period (see Input Port "ENVIR"). Each of these matrices represents population dynamics for discrete temporal strata. Default is six time periods (see Input Ports "Study_period_year_x"). These matrices are used for projections of population size if ENVIR is set to "IID"



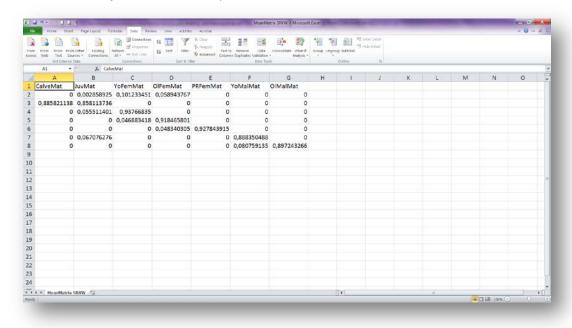
IID Matrices SRK

lambda from IID and VR random Population (csv): Stochastic population growth rate computed from IID matrices and from vital rates as random variables (see Input Port "ENVIR")



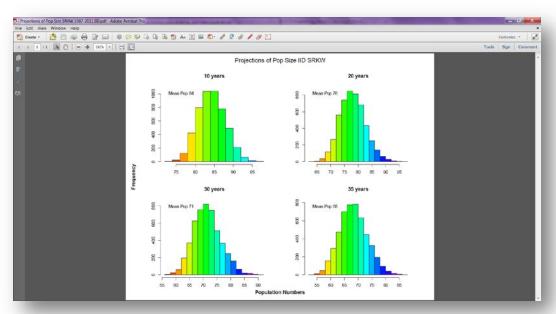
Lambda from IID and VR random SRKW

MeanMatrix Population (csv): Two-sex, stage structured matrix based on mean vital rate (survival and fecundity) values for the selected time period. A birth-flow matrix model is used with seven life stages and fixed transition probabilities based on stage duration (details in Vélez-Espino et al. 2014).



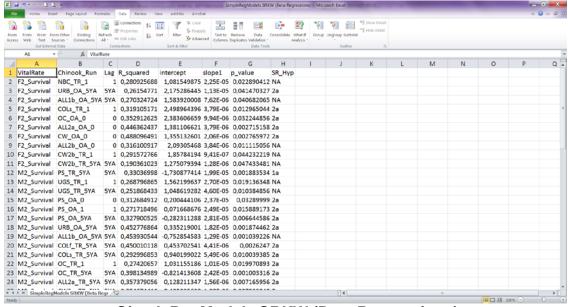
MeanMatrix SRKW

Projections of Pop Size Population Start year – End year IID (pdf): Graphical output showing frequency distributions for projections of population size at the four time horizons specified in Input Ports "Time_horizons_x". Along with stochastic population growth "Lambda_from_IID_and_VR_random", these outputs are the components of the analysis showing expected future population dynamics. Therefore, these two outputs can be seen as components of a PVA



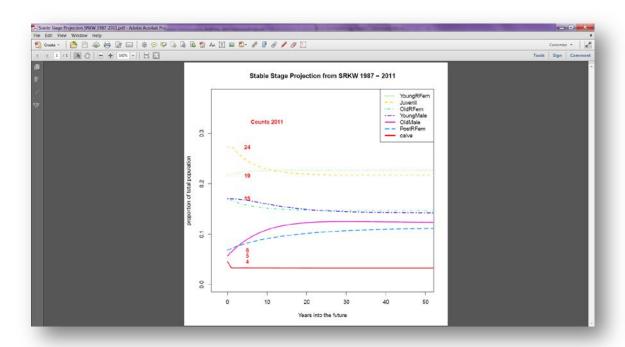
Projections of Pop Size SRKW 1987-2011 IID

SimpleRegModels Population (Type of Regressions) (csv): Statistics for all significant regressions (beta or linear) between killer whale vital rates and Chinook salmon stocks. The list of regressions includes vital rates not contributing directly to population growth such as survival of males and post-reproductive females.



SimpleRegModels SRKW (Beta Regressions)

Stable Stage Projection Population Start year – End year (pdf): Graphical output showing the change in stage composition with time towards stable stage distribution. Initial values correspond to counts and proportions in the last year of the study

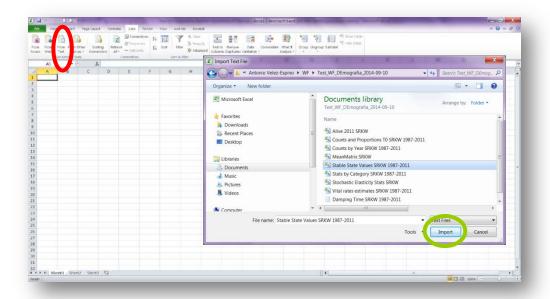


Stable Stage Projection SRKW 1987-2011

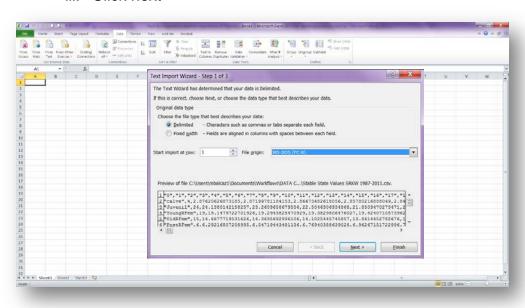
Stable State Values Population Start year – End year (csv): Long-term projections of population size by life stage based on transient dynamics.

Note: If the user used ≥ 1850 **Sims**, you need to open the file as follows:

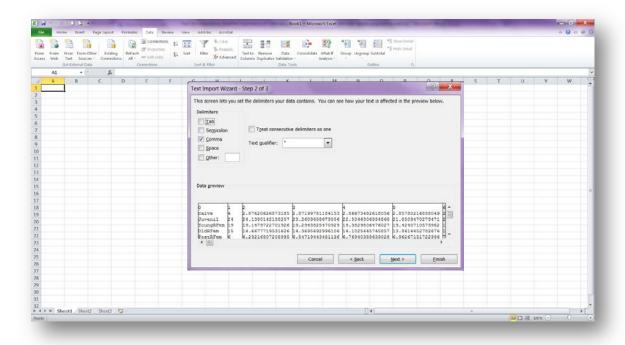
- 1. Open excel (versions 2007 onwards)
- 2. Go to Data tab
- 3. Click on From text (red oval)
- 4. Open the Folder where the file Stable State Values SRKW 1987-2011.csv is.
- 5. Import the file Stable State Values SRKW 1987-2011.csv (green oval).



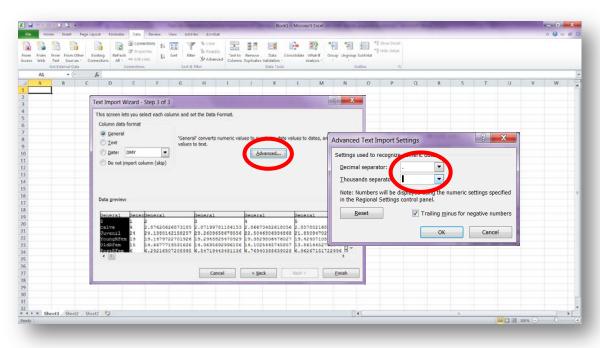
- 6. Follow three steps to open the file
 - a. Text import wizard: step 1:
 - i. Choose Delimited
 - ii. File origin: MS DOS (PC-8)
 - iii. Click next



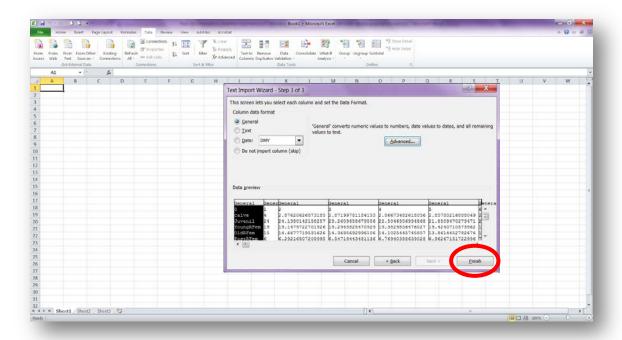
- b. Text import wizard: step 2:
 - i. Choose Coma delimited
 - ii. Click next



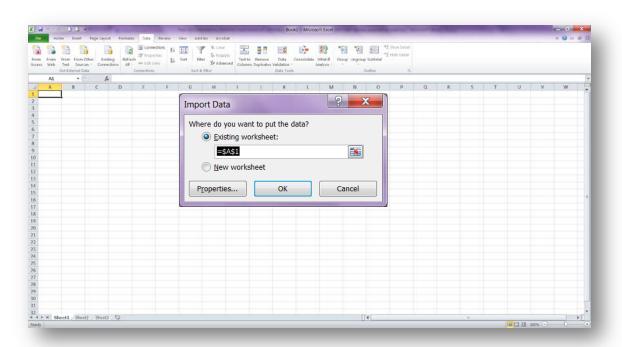
- c. Text import wizard: step 3:
 - i. Click in Advance (red oval) and the Advance Text Import Settings window appears.
 - ii. Decimal separator: decimal numbers must be separated by a period, red oval).
 - iii. Thousands separator: choose empty space (red oval).
 - iv. Click ok

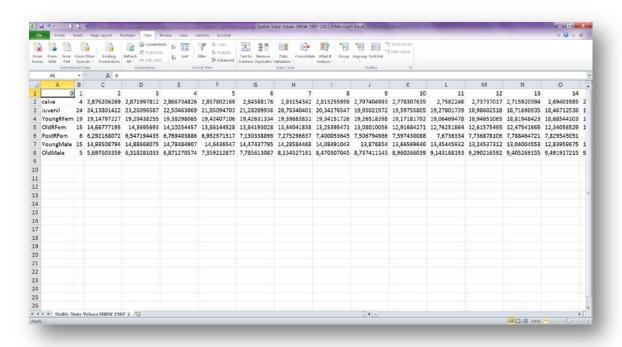


7. Click in Finish.



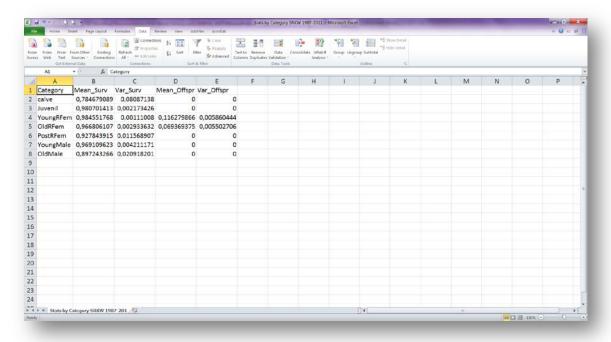
8. Import Data window appears, asking where do you want to put the data, choose Existing worksheet.





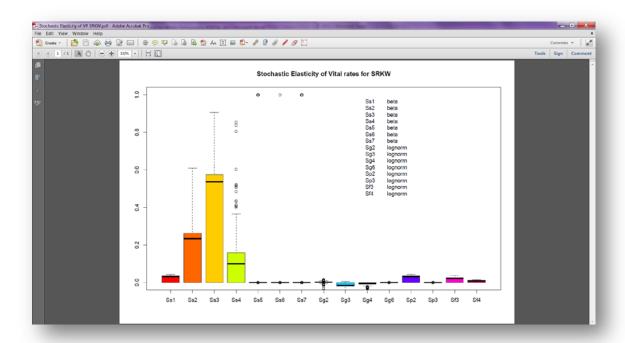
Stable State Values SRKW 1987-2011

Stats by Category Population Start year – End year (csv): Mean and variance of vital rates (survival and fecundity) by life stage. Mean and variance generated from annual values during the selected time period are used to generate vital rate probability distributions (see "Stochastic_Vital_rates").



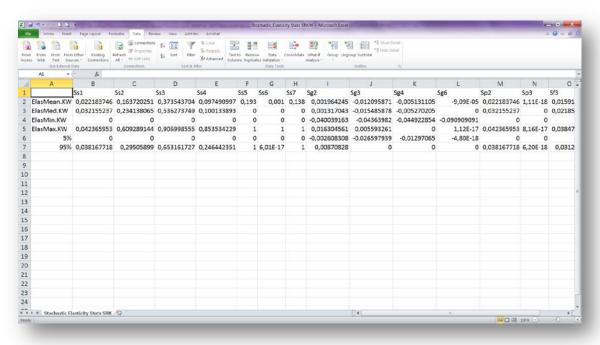
Stats by Category SRKW 1987-2011

Stochastic Elasticity of VR Population (pdf): Graphical output for stochastic elasticities of vital rates based on "Stochastic_Vital_rates"



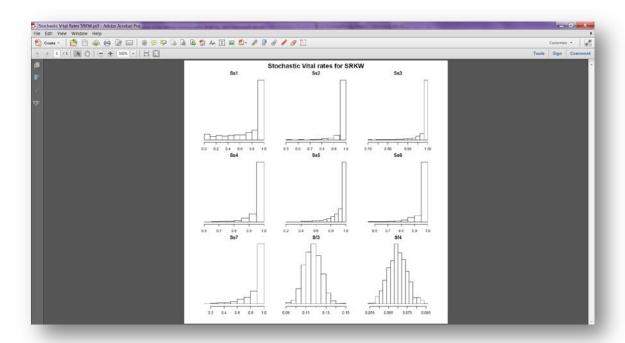
Stochastic Elasticity of VR SRKW

Stochastic Elasticity Stats Population (csv): Mean, median, minimum, maximum, and 95% confidence limits of stochastic elasticities of vital rates.



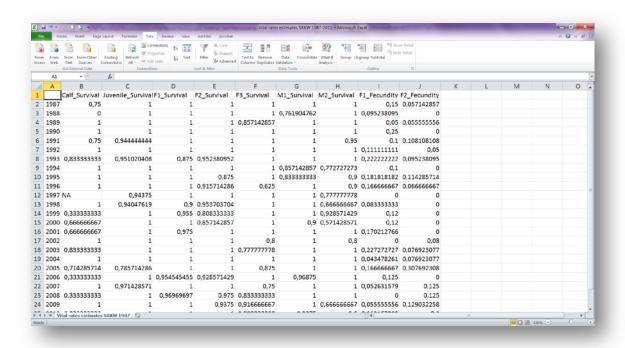
Stochastic Elasticity Stats SRKW

Stochastic Vital Rates Population (pdf): Graphical output for vital rate probability distributions. Beta distribution used for survival; lognormal distribution used for fecundity.



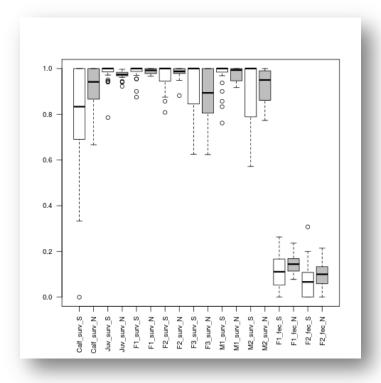
Stochastic Vital Rates SRKW

Vital rates estimates Population Start year – End year (csv): Vital rate (survival and fecundity) values by year and life stage through the selected time period



Vital rates estimates SRKW 1987-2011

VR_combined (.png): Box plot with the survival and fecundity probabilities of each stage.



VR_combined

PostWorkspace

PostWorkspace (zip file): An R Workspace that transfers values from the Resident killer whale-chinook salmon interactions (main) workflow to the Exploration of fishing scenario (post-processing) workflow. This file must be provided as an input to the post-processing workflow in order for it to have access to values generated in the main workflow.

Exploration of fishing scenarios.

This workflow cannot be run without running first the Resident killer whale-chinook salmon interactions workflow. The Exploration of fishing scenarios workflow needs the PostWorkspace, a zip file generated by the first workflow. See details page 39, PostWorkspace (zip file).

2. Input files for tutorial

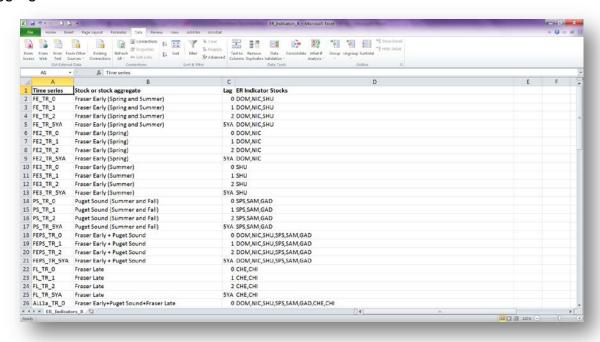
The workflow accepts input data in a .csv, coma delimited and a zip file. The examples input files for the tutorial are available and described below. In this tutorial, five input files are used.

2.1 Input data

To download click here on the file name or they can be downloaded at myExperiment (http://www.myexperiment.org/packs/667.html):

- ER Indicators R
- Term Run R
- TRE_HR_R
- TRE R
- PostWorkspace

ER Indicators R: This file shows the exploitation rate (ER) indicator stocks used to represent exploitation-rate time series with terminal-run time series of Chinook salmon aggregates.



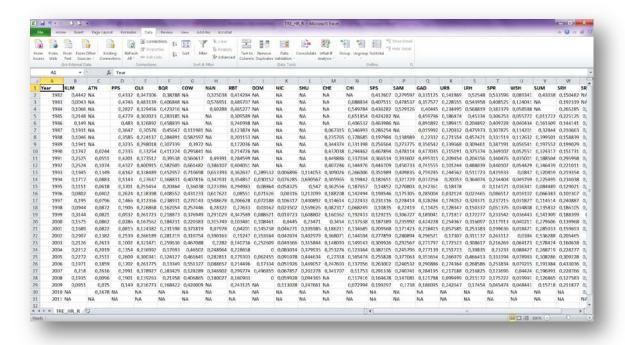
<u>Term_Run_R:</u> This file contains the time series of terminal run for each of the ER indicator stocks.

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	A	В	C	D	E	F	6	н	1	1	K	1.	М	N	0	р	Q	R	5	T	U	V	W
Ye	ar KLN	1 A	TN	PPS	QUI 8	QR C	ow N	AN	RBT D	MO	NIC	SHU	CHE	CHI	SPS	SAM	GAD	URB	LRH	SPR	WSH	SUM	SRH
	1982	3,6 N	IA.	174	466,2	310 N	IA.	348,1	1301,9 N	A	NA	NA	NA .	NA.	1075,3	2149,1	488,2	1121,7	1318,4	2125,8	3068,7	13,5	674,3
	1983	15,8 N	IA.	172	314	253,5 ₺	IA.	479,3	948,4 N	Δ,	NA	NA	NA.	1884,9	1796,8	3151,7	329,8	543,3	710,1	396,7	1793,3	NA	412,9
	1984	21,4 N	IA.	181	479	140 M	IA	193	960,3 N	Δ,	NA.	NA	NA:	1098,3	1621,9	174,5	484,8	1077	497	481,9	3637,3	NA	510,4
	1985	120,1 N	IA.	35	743,1	305,5 6	IA N	A	603,1 N	Д	NA .	NA	NA.	435,7	746,7	NA	187,6	2574,9	463,2	799,8	2408,9	67,7	514,7
	1986	164,3 N	IA.	47	719,1	361,9 ₺	IA N	A	390,3 N	Δ,	NA	NA	NA	594,5	215,7	NA.	2	3844,8		195,4	561,6	41,5	369,6
	1987	188,6 N	IA.	65	583,9	357,6	130,6 N	A	1077,1 N	Д	NA.	NA	14,4	893,6	236,1	NA	88,2	2598,2	3479,3	59,1	460,2	53,8	509,7
	1988	119,3 N	IA.	47	934,7	189,1	48,3 N	A.	1832,3 N	A	NA	NA	102,8	1206,7	1051,7	425,4				313,4	1638	70,3	965,2
		595,6 N		30		286,3	181 N		3090,9 N		NA	NA	553,6		2791,6	988		100000000000000000000000000000000000000		1120,7	2458,3	72,1	858
		473,3 N		60		283,9	248 N		3970,7 N		NA	NA	1259,3		2588,6	1092,9			F	1096,5	2329,4	156,7	968,7
	1991	194,3	651,3	39		312,5	702,9	303,7	5831,6 N		NA	NA	383,7	836,7	965,9	501,9			and the second	1638,1	2794	444,1	1494,4
	1992	477,7	786,2	33		186,5	572,5	683	4276,9 N		NA.	NA	560,3		636,5					1455	2290,3	154,1	2024,9
	1993	168,5	1065,6	23		158,9	808,1	444	3274,2	38,4	88,1		574		664,2	432,5				600,9	4600,4	132,2	1299,8
	1994	97,2	1459,4	8		137,5	500,5	229,7	1917,2	201,2	1606		237,5		1207,6	591,5	1,000,000	-		670,5	4662,5	22,1	2789,8
	1995	154,3	2147,8	17		146,8	839,5	961,5	842,2	422,7	1721,4		96,4		2809,4	484,8	-			823,4	4255,9	132,5	3531,4
		442,4	1973,7	28	0.000	141,8	565,2	282,7	615,4	339,1	69,4		681,3	25000	3679,5	958,8		-		766,1	3705,7	262,8	1768
		491,3	1058,1	21		156,7	566,2	101,5	1516,6	253,6	181,7		371,4		1923,2	995,2				462,7	2170,6	1007,1	2654,9
		424,7	937,5	1	375,6	142,8	295,7	136,6	2120,5	565,1	990,1		1027,3		1546,5	546,9	575,575	618,6	-	775,7	1506,7	1255	2266,8
		466,9	1272,2	40		182,2	237,5	173	794,9	14,8	2941,7		924,7		1821,5	161,9				1223,9	1667,4	476,3	1681,5
		258,7	945,7	54		162,6	533,2	116,4	206	58,8	2148,2		386	1000000	1728,6	221,5		662,8		682,6	6089,8	1105,3	2235,4
		432,2	630	192		325	358,8	257,1	830,1	227,7	2069,2		576		2722,6	1199,5			100000	5137,1	35071,4	3140,1	2911,9
	2002	647,9	613,3	82		209,6	438,1	455,2	1488,4	95,2	2025,8		176	Section 1985	2338,9	1063,9	-			2811	19189,2	3623,9	3524,8
		443,3	339,1	92		162	131,8	533,9	2200,2	114,2	2047,2		413,9		1355,6	507,8				4557,5	6337,2	2897,2	3630,4
		712,3	373,5 470.2	72	518,3 538,1	279,4 308,3	122,9	587,4 361	3610,4	4,1 206,8	401,6		291,3		1058,2	327,4				4553,7 1578,4	6332,1 2741,4	2487,7 6399,4	3413,1 2871.5
		218.1	1019.8	231 170.1	549,2	489.1	104.3	1189.4	2006.3	60,4	410,		461,4		2277.9	1027,9		1205.2		513.8	1823.3	2518.9	929
	2006	381.4	239.7	109,7	319,7	381.5	104,3	630.5	1366.8	8	125.4		199		2189.8	1393.5			CHICAGO CO.	513,8 853,5	1511.4	3564.6	1001,6
		377.6	120.5	73		264.9	93,4	212,8	1225,1	76.2	670.9			2056.5	1768.6	1393,3	901,1	653.3		1757.9	2176,5	1248,6	533.9
		497.3	423.1	193		381.4	146.2 N		905.6 N	A	254.7			2484.6	1909.4	1214.2				2321.8	1466,1	610,9	766.4
	2010 NA	457,3	509.8		NA N		IA N		NA N		NA 234,		NA NA	NA NA	NA 1909/4	NA.	980,4 NA	NA /95,4	NA NA	1000000000			NA NA
	2010 NA 2011 NA		309,8	NA AM	NA N		IA N		NA N		NA.		NA NA	NA.	NA NA	NA.	NA NA	NA	NA NA				NA NA
	SOLI IN											****		100				184			1303		
i	H Term R	un R	2											- 51	4								

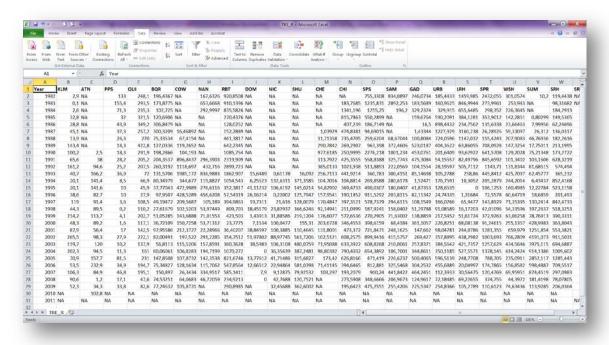
TRE HR_R: This file contains the time series of terminal run equivalent (TRE) ocean harvest rates of ER indicator stocks, where TRE is computed as:

$$\mathit{TRE}_{\mathit{indicator}, y} = \sum_{\mathsf{PreTerm \, Fishery}} \sum_{a=3}^{6} \mathit{Catch}_{a, y} * \mathit{MR}_{a, y}$$

Chinook salmon is an anadromous and semelparous species that spend 1-5 years in the ocean before returning to their natal streams to spawn. For the exploration of fishing scenarios where changes in terminal run size occur as a result of changes in ocean (i.e. pre-terminal) harvest rates, terminal run equivalents (*TRE*) were used to account for the fact that only a portion of the fish not caught in ocean fisheries in a given year is expected to become part of the terminal run according to their maturation rates (*MR*), which are time variant and stock specific. Age-2 Chinook were not included in this equation because RKW prey mostly on age-3 and older Chinook. *TRE*s were then used to compute both proportional increases in terminal run size in the absence of pre-terminal (i.e. ocean) fishing and the terminal run scalars resulting from a specified change in ocean harvest rates in exploitation rate indicator stocks. These scalars were then used to calculate changes in terminal run of a stock of interest (more details in Vélez-Espino et al. 2014).



TRE R: This file contains the time series of terminal run equivalents (TREs) of all ER indicator stocks.



Hypotheses addressed in this investigation regarding RKW-Chinook salmon interactions.

- 1. **Hypothesis 1a (based on current evidence):** there is a strong link between SRKW population growth and the terminal run size¹ of Fraser Early, Fraser Late, and Puget Sound Chinook stocks².
- 2. **Hypothesis 1b (based on current evidence)**: there is a strong link between NRKW population growth and the terminal run size¹ of Northern BC, Central BC, WCVI, Upper Georgia Strait, and Lower Georgia Strait Chinook salmon stocks as well as the ocean (pre-terminal) abundance of Fraser Early, Puget Sound, and Upper Columbia Chinook stocks².
- 3. Hypothesis 2a (assuming Chinook salmon remains an important diet component year-round and outside identified critical habitats): there is a strong link between SRKW population growth and the terminal run size of large stocks such as Sacramento Fall, Klamath Fall, Columbia Upriver Brights, Columbia Spring/Summer/Fall, Oregon Coastal, WCVI, or coastwide (excluding Northern BC, Central BC, and Southeast Alaska³), as well as the ocean (pre-terminal) abundance of ocean-type⁴ stocks with large contributions to ocean fisheries such as WCVI, Columbia Upriver Brights, Fraser Late, Oregon Coastal, Puget Sound, or coastwide (excluding Southeast Alaska⁵).
- 4. Hypothesis 2b (assuming Chinook salmon remains an important diet component year-round and outside identified critical habitats): there is a strong link between NRKW population growth and the terminal run size of Fraser Early and Puget Sound⁶, and large stocks such as Columbia Upriver Brights, Columbia Spring/Summer/Fall, Fraser Late, Oregon Coastal, or coastwide (excluding Sacramento Fall, Klamath Fall⁷ but including Southeast Alaska⁸), as well as the ocean (pre-terminal) abundance of ocean-type³ stocks with large contributions to ocean fisheries such as WCVI, Fraser Late, Oregon Coastal, or coastwide (excluding Southeast Alaska⁵).
- 1 The terminal run includes terminal catch, which occurs after fish are available for killer whales, and therefore represents the Chinook available for RKW in their summer ranges.
- 2 Based on diet composition studies.
- 3 Out of the known preferred geographic range of SRKW.
- **4** Ocean-type Chinook stocks spend most of their ocean life in coastal waters and are therefore within known RKW geographic range.
- 5 South East Alaska Chinook salmon stocks exhibit a stream-type life history and perform extensive offshore oceanic migrations, and it is unlikely they are available for RKW. These stocks contribute on average less than 1% to the Chinook salmon available for PST ocean (pre-terminal) fisheries
- **6** Although Fraser Early is not among the larger stocks, NRKW encounters with both Puget Sound and Fraser Early terminal runs could be greater than determined by current observations.
- 7 Out of the known preferred geographic range of NRKW.
- 8 Within the known geographic range of NRKW.

<u>PostWorkspace:</u> An R Workspace that transfers values from the Resident killer whale-chinook salmon interactions (main) workflow to the Exploration of fishing scenario (post-processing) workflow. The zip file must be provided as an input to the post-processing workflow in order for it to have access to values generated in the main workflow. Therefore, take in account the input values used to run the main workflow.

2.1 Related publications

- Vélez-Espino, L.A., John K.B. Ford, Eric Ward, Chuck K. Parken, Larrie LaVoy, Ken Balcomb, M. Bradley Hanson, Dawn. P. Noren, Graeme Ellis, Tom Cooney, and Rishi Sharma. 2013. Sensitivity of resident Killer Whale population dynamics to Chinook salmon abundance. Completion Report, Pacific Salmon Commission, Southern Boundary Restoration and Enhancement Fund, Vancouver BC. 191 p.
- Vélez-Espino, L.A., Ford, J.K.B., Araujo, H.A., Ellis, G., Parken, C.K, & Balcomb, K. 2014. Comparative demography and viability of northeast Pacific resident killer whale populations at risk. Can. Tech. Rep. Fish. Aquat. Sci. 3084: vi + 56 p.
- Vélez-Espino, L.A., John K.B. Ford, H. Andres Araujo, Graeme Ellis, Charles K. Parken and Rishi Sharma. In Press. Relative importance of Chinook salmon abundance on resident killer whale population growth and viability. Aquatic Conservation: Marine and Freshwater Ecosystems. Article first published online: 21 AUG 2014. DOI: 10.1002/aqc.2494

3. Tutorial:

This tutorial explains the type of input data needed to run the workflow. The corresponding analysis use data from two distinct *O. orca* populations in Canada, Southern Resident Killer Whales (SRKW) and the Northern Resident Killer Whales (NRKW).

Associations between RKW vital rates (fecundity and survival) and Chinook abundance were evaluated in light of the four hypotheses in Box 1 using beta regressions (see text above). Beta regressions were used because they incorporate features such as heteroscedasticity or skewness which are commonly observed in data taking values in the standard unit interval, such as rates or proportions. Abundance lags of 0-year and 1-year were used to examine relationships with survival rates whereas 0-year, 1-year, and 2-year abundance lags were used to examine relationships with fecundity. The rationale for the use of lag-1 models for survival is that the effects of nutritional stress could be capitalized on mortalities the next year after food shortage occurred. A recent study revealed that mortality indices were most highly correlated to changes in Chinook abundance after a lag of one year. Following the same rationale, lag-2 models were used for fecundity to account for malnutrition or starvation effects on pregnancy as well. Pregnancy lasts about a year in RKW. In addition, and in order to account for cumulative effects of Chinook abundance on RKW vital rates, a 5-year running average (Chinook abundance from t-4 to t) was also used for regression analyses. A total of 128 combinations of stock or stock aggregates. abundance type, and time lag were considered in the analysis of RKW-Chinook interactions. Since some of these stock-abundance type-time lag combinations were explored in relation to both NRKW and SRKW (see Hypotheses), a total of 196 RKW-Chinook linkages were analysed: 28 for hypothesis 1a, 60 for 2a, 40 for 1b, and 68 for 2b. Each one of these linkages encompasses relationships with the fecundity and survival of stages directly contributing to population growth, thus producing a total of 980 RKW-Chinook interactions

The relevance of interactions between Chinook abundance and killer whale population viability were based not only on statistical significance but also on their influence on expected population growth rates as quantified by perturbation analyses. The execution of demographic perturbation analyses involved prospective evaluations quantifying the relative effects on SRKW and NRKW population growth of interactions between RKW vital rates and Chinook salmon abundance within the hypothesis-driven framework. Prospective evaluations, based on elasticity analysis, were used to quantify the changes in λ that would result from any specified change in the vital rates. This information can be used to identify potential management targets because elasticities measure the relative influence of vital rates on λ .

Elasticities (ϵ) are partial derivatives of λ that can be computed in reference to small changes to matrix **M** elements (a_{kl} , equation 2) or lower-level parameters such as vital rates

 $\binom{v_i}{i}$, which usually contribute to more than one matrix element, by applying the chain rule of differentiation (equation 3). Similarly, mean elasticities of interactions between individual vital rates and Chinook salmon abundance can be computed by extending the chain rule of differentiation to factors influencing the vital rates. Equation 4 transfers the effect of a change in Chinook abundance on a given vital rate (as determined by significant and filtered beta regressions) to effects on population growth (λ).

$$\varepsilon(a_{kl}) = \partial \log \lambda / \partial \log a_{kl} \tag{2}$$

$$\varepsilon(v_i) = \frac{v_i}{\lambda} \frac{\partial \lambda}{\partial v_i} = \frac{v_i}{\lambda} \sum_{i} \frac{\partial \lambda}{\partial a_{kl}} \frac{\partial a_{kl}}{\partial v_i}$$
(3)

$$\varepsilon \left(x_{Chinook \to v_i} \right) = \sum_{i} \frac{\partial \log \lambda}{\partial \log a_{kl}} \frac{\partial \log a_{kl}}{\partial v_i} \frac{\partial v_i}{\partial x_{Chinook \to v_i}}$$
(4)

The term $^{\mathcal{X}_{Chinook} \to v_i}$ denotes Chinook abundance from specific stocks or stock aggregates interacting with vital rate v_i , and $^{\varepsilon\left(\mathcal{X}_{Chinook} \to v_i\right)}$ denotes the proportional change in $^{\lambda}$ resulting from a small change in $^{\mathcal{X}_{Chinook} \to v_i}$ through its interaction with v_i . The effects of $^{\mathcal{X}_{Chinook} \to v_i}$ on more than one vital rate are additive.

These analytical solutions are robust for perturbations up to 30% and occasionally up to 50%. However, nonlinearities often exhibited between vital rates and λ , reduce the accuracy of projections using elasticities for larger perturbations. Hence, we also conducted prospective perturbation analysis by directly perturbing the projection matrices Direct perturbations involve an iterative process, altering the magnitude of the vital rate in question while keeping all other matrix elements unchanged. Using direct perturbations, two computational variants of the elasticity of interactions were explored. Variant 1 (equation 5) completely represents a direct perturbation process whereas variant 2 (equation 6) is a combination of vital rate elasticity and direct perturbation:

$$\varepsilon \left(x_{Chinook \to v_i} \right)_{DP, \text{variant 1}} = \frac{\Delta \lambda}{\Delta x_{Chinook}} = \frac{\left(\left(\lambda_{after} / \lambda_{before} \right) - 1 \right)}{\left(\left(x_{Chinook, after} / x_{Chinook, before} \right) - 1 \right)}$$
(5)

$$\varepsilon \left(x_{Chinook \to v_i} \right)_{DP, \text{ variant 2}} = \varepsilon \left(v_i \right) \frac{\Delta v_i}{\Delta x_{Chinook}} = \varepsilon \left(v_i \right) \frac{\left(\left(v_{i, after} / v_{i, before} \right) - 1 \right)}{\left(\left(x_{Chinook, after} / x_{Chinook, before} \right) - 1 \right)}$$
(6)

The term $x_{Chinook,before}$ is the Chinook abundance from a particular stock corresponding to the mean value of the interacting vital rate, $x_{Chinook,after}$ represents the simulated value of Chinook abundance that is used to explore the effect of changes in Chinook abundance (e.g. through changes in harvest rates) on RKW population growth rates. Thus, λ_{before} and λ_{after} represent the population growth rate before and after a perturbation on the vital rate(s) corresponding to a given change in Chinook abundance as per beta regressions, where $(v_{i,after})$ is the vital rate value after the perturbation. Across all significant beta regressions, the two variants generated similar elasticities of the interactions for SRKW and a slight divergence at higher elasticity values for NRKW. Variant 2 was used for subsequent analysis because it is better suited to incorporate uncertainty in vital rate elasticities as described below.

Stochastic elasticities were generated through simulations with vital rates represented as random variables. Vital rate annual values from 1987 to 2011 were used to generate their mean and variances for each of the killer whale populations. Simulations generated 5000

random matrices with vital rates drawn from defined probability distributions following Vélez-Espino *et al.* (2014). The beta distribution was used to simulate variation in stage-specific survival (σ_i). This distribution is appropriate for binary events (such as survival) and produces random variables confined to the interval 0 to 1. The lognormal distribution was used to simulate fecundity values (μ_i). This distribution produces only positive random variables bounded by zero and infinity. Population growth rates and vital rate elasticities were calculated for each of the 5000 matrices, and a parametric bootstrap was used to estimate mean stochastic elasticities and their 95% confidence intervals.

In your browser (preferably Firefox or Chrome) navigate to the <u>BioVeL Portal</u> page (<u>http://portal.biovel.eu</u>/) and log in with your username and password (1). You will need to register if you have not already done so.

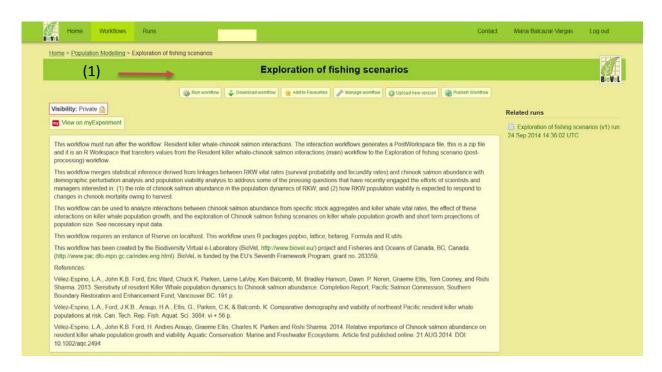
Choose the Population Modelling analysis and click, this will show you a list of relevant analysis:



On the resulting page choose the workflow: Exploration of fishing scenarios (1) you can also directly run the workflow using the 'Run workflow' button at the bottom-right (2).



On the resulting page click on the 'Run Workflow' button at the top (1).



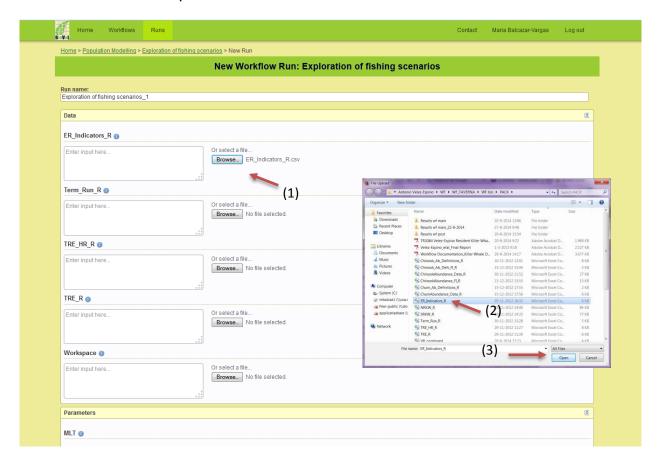
On the next page you can edit the name of the workflow run to make it easier for you to identify it later (e.g. *Exploration of fishing scenarios*_1).



3.1 Input Ports

3.1.1 Data

ER Indicators R: This file shows the exploitation rate (ER) indicator stocks used to represent exploitation-rate time series with terminal-run time series of Chinook salmon aggregates. To open the file. Click in Browse (1), a window dialog appears and the user selects the file ER_Indicators_R.csv, (2) and then clicks the Open button (3). Repeat this action for all the input DATA.



Term Run R: This file contains the time series of terminal run for each of the ER indicator stocks. To open the file. Click in choose file, a window dialog appears and the user selects the file e.g. Term_Run_R.csv and then clicks the Open button.

TRE HR R: This file contains the time series of terminal run equivalent (TRE) ocean harvest rates of ER indicator stocks. To open the file. Click in choose file, a window dialog appears and the user selects the file e.g. TRE_HR_R.csv and then clicks the Open button.

TRE R: This file contains the time series of terminal run equivalents (TREs) of all ER indicator stocks. To open the file. Click in choose file, a window dialog appears and the user selects the file e.g. TRE_R.csv and then clicks the Open button.

<u>Workspace:</u> The PostWorkspace is a zip file and it is an R Workspace that transfers values from the Resident killer whale-chinook salmon interactions (main) workflow to the Exploration of fishing scenario (post-processing) workflow. To open the file. Click in choose file, a window dialog appears and the user selects the file e.g. Workspace and then clicks the Open button.

3.1.2 Parameters

To determine the parameters, type in each box the value of the variable (1).



EndYear: Last year to be considered in the analysis.

e.g.: 2011

<u>MLT:</u> This is a user-defined inverse multiplier for the harvest rate (HR) that affects the stock aggregates directly. MLT is inversely proportional to HRs but directly proportional to killer whale vital rates. MLT = 0.0 is used to maximize HRs. MLT values between 1.0 and 2.0 are used to represent increments in ocean abundance proportional to percent reductions in HRs.

e.g.: 1.64

<u>Mult:</u> This is a user-defined multiplier of ocean harvest rates impacting terminal runs. Mult = 0.0 indicates the closure of ocean fisheries; Mult = 1.0 indicates no change in

base values; Mult = 1.5 indicates a 50% increase in ocean HRs.

e.g.: 1.5.

<u>nreps:</u> Number of replications for projections of population size.

e.g.: 10000

population: It is the name of the analysed population.

e.g.: SRKW

StartYear: First year to be considered in the analysis.

e.g.: 1987

StockAggr: The stock aggregate, with abundance represented as terminal run (TR), is user defined from the list of significant stocks from the regression and elasticity analyses. The user needs to see "Elasticities of Interaction Method Matrix Pert._Population_(Beta Regressions).pdf" or "Elasticity of Interactions_Population.csv" to select relevant stock aggregates for further analysis.

e.g.: FEPS_TR_1

StockAggrOA: The stock aggregate, with abundance represented as ocean abundance (OA), is user defined from the list of significant stocks from the regression and elasticity analyses. The user needs to see "Elasticities of Interaction Method Matrix Pert._Population_(Beta Regressions).pdf" or "Elasticity of Interactions_Population.csv" to select relevant stock aggregates for further analysis.

e.g.: CW_OA_2

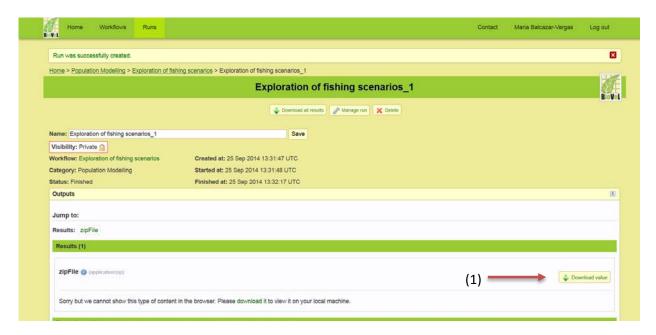
<u>UseFImpacts:</u> Instead of ocean abundance, the user can select time series of fishery impacts to run the analyses. In this case, the interaction would be between killer whale vital rates and fishing impacts rather than Chinook salmon ocean abundance. Choose "FALSE" to conduct analyses at the ocean abundance level.

e.g.: FALSE

After the user has filled out the input ports and has clicked the **Start Run**, the workflow performs the analysis. To complete all the analysis may take few minutes, depends on the number of **NREPS** to carry out the analyses.

3.3 Outputs

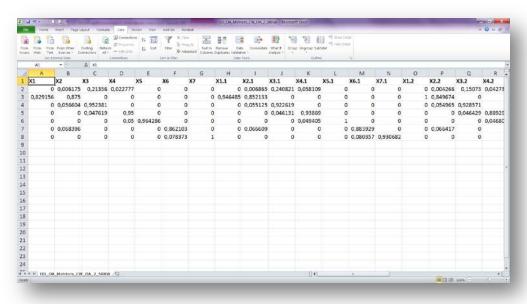
Once the analyses are finished, the user can download all the results by clicking Download value button (1). Numerical and graph results will be download as a zip file that can be save by the user. The numerical results are .csv files than can be opened with Excel and the plot files are .PDF files. A second result is PostWorkspace, a zip file that is needed to run the second workflow: Interaction between killer whale population dynamics and Chinook salmon abundance workflow.



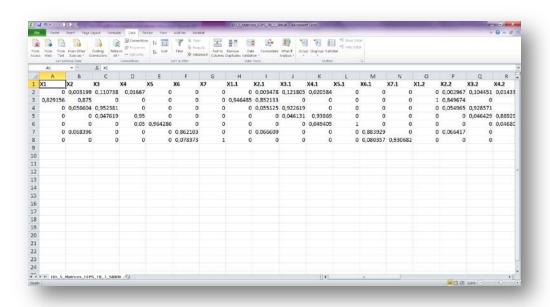
3.3.1 Results

Zip File

IID_Abundance type (OA or TR)_Stock aggregate_Abundance type_time series lag_Population/csv: This output file shows the matrices produced by the retrospective analysis. There will be as many matrices in this file as time periods specified by the user. Following, there are two examples for two different stock aggregates: the first one is for the interaction between coastwide Chinook ocean abundance, two years lagged, and SRKW vital rates; the second is for Fraser Early-Puget Sound Chinook ocean abundance, one year lagged, and SRKW vital rates

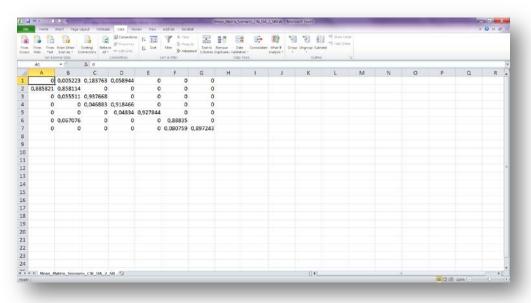


IID_OA_Matrices_CW_OA_2_SRKW.csv

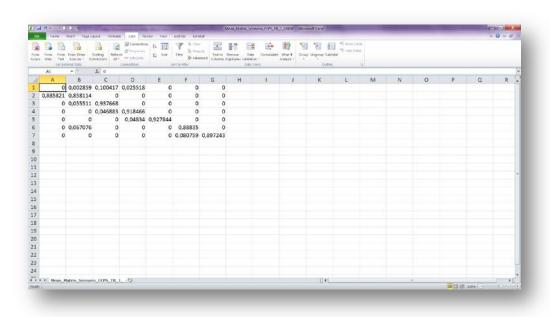


IID S Matrices FEPS TR 1 SRKW.csv

Mean_Matrix_Scenario_Stock Aggregate_Abundance type_time series lag_Population.csv: This output shows the mean killer whale matrix generated after the implementation of a fishing scenario (i.e., changes in ocean abundance or terminal run or fishing impacts), Following, there are two examples for two different stock aggregates: the first one is for the interaction between coastwide Chinook ocean abundance, two years lagged, and SRKW vital rates; the second is for Fraser Early-Puget Sound Chinook ocean abundance, one year lagged, and SRKW vital rates



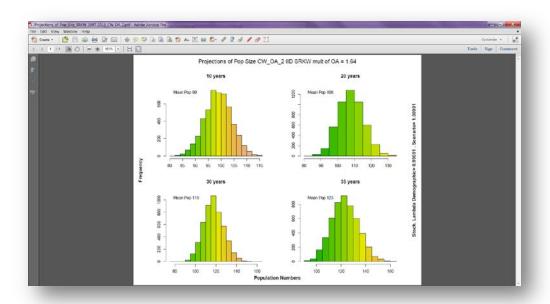
Mean_Matrix_Scenario_CW_OA_2_SRKW.cvs



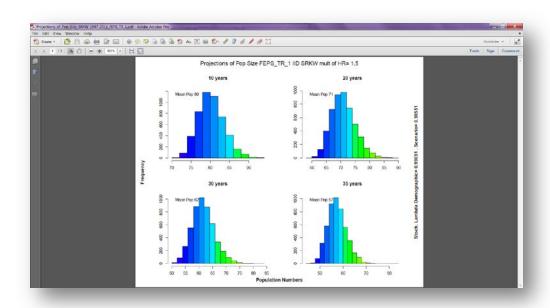
Mean_Matrix_Scenario_FEPS_TR_1_SRKW.csv

Projections_of_Pop_Size_Population_Start_year-

End_year_Stock_Aggregate_Abundance type_time series lag_Population. (pdf): This figure shows histograms of population size projections at four time horizons with the farthest one being the damping time. In addition, this figure shows the values of the population growth rate before and after the implementation of a particular fishing scenario. The attributes of the fishing scenario are shown at the top of the figure. Following, there are two examples for two different stock aggregates: the first one is for the interaction between coastwide Chinook ocean abundance, two years lagged, and SRKW vital rates; the second is for Fraser Early-Puget Sound Chinook ocean abundance, one year lagged, and SRKW vital rates

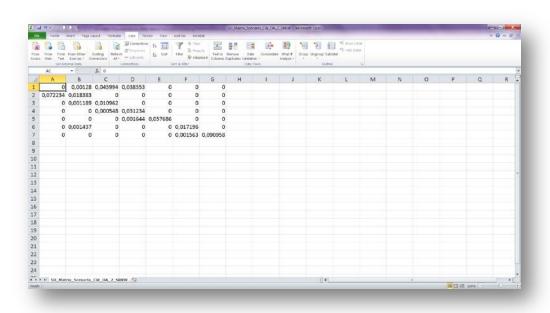


Projections_of_Pop_Size_SRKW_1987-2011_CW_OA_2.pdf

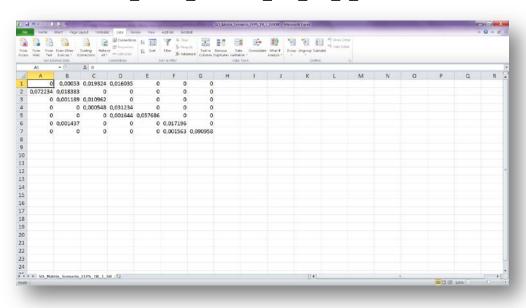


Projections of Pop Size SRKW 1987-2011 FEPS TR 1 (pdf)

SD_Matrix_Scenario_Stock Aggregate_Abundance type_time series lag_Population.csv: This output shows the standard-deviation killer whale matrix generated after the implementation of a fishing scenario (i.e., changes in ocean abundance or terminal run or fishing impacts), Following, there are two examples for two different stock aggregates: the first one is for the interaction between coastwide Chinook ocean abundance, two years lagged, and SRKW vital rates; the second is for Fraser Early-Puget Sound Chinook ocean abundance, one year lagged, and SRKW vital rates



SD_Matrix_Scenario_CW_OA_2_SRKW.csv



SD_Matrix_Scenario_FEPS_TR_1_SRKW.csv

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This workflow was created using and based on Packages 'popbio' in R. (Stubben & Milligan 2007; Stubben, Milligan & Nantel 2011), lattice and betareg.

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