# Quantifying metapopulation portfolio effects with the `ecofolio` package

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This vignette accompanies the `ecofolio` `R` package and the manuscript *Ecological prophets: Quantifying metapopulation portfolio effects* by Sean C. Anderson, Andrew B. Cooper, and Nicholas K. Dulvy, for the journal *Methods in Ecology and Evolution*. Here, we briefly illustrate the use and interpretation of the functions in the `ecofolio` package with a sample dataset.

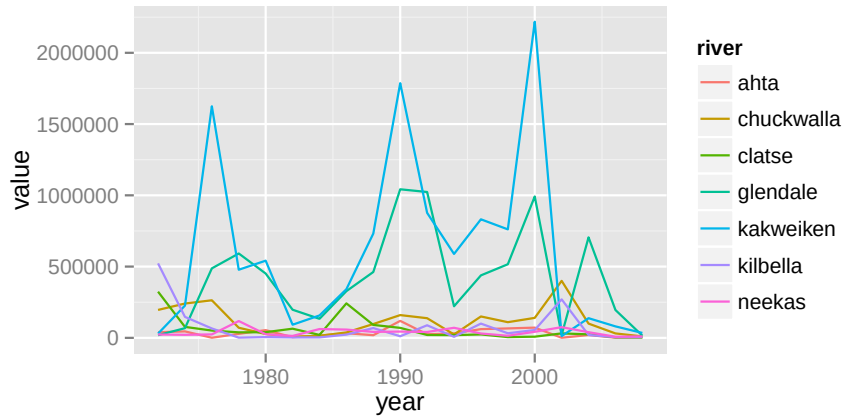
First, let's load the package and load the sample dataset. These data represent pink salmon recruits in the Broughton Archipelago for even years. Each column represents abundance for a different river through time. You can find these data in the supplementary materials of Krkoŝek et al. (2011) and they were originally collected by Fisheries and Oceans Canada.

```
> library(ecofolio)
> data(pinkbr)
> head(pinkbr)
```

```
  year  ahta chuckwalla clatse glendale kakweiken kilbella neekas
1 1972 39611     195937 324023    18815     29708   522499  23565
2 1974 45248     240733  76827    67873    226242   147115  21341
3 1976   812     263522  51206   487456   1624853    65881  24181
4 1978 27983      70752  38581   591956    477870     1415 117885
5 1980 54148      26999  39704   451232    541478     5400  25524
6 1982  4604       8156  64224   197308     92077     3058  13447
```

Let's plot the time series:

```
> library(reshape)
> library(ggplot2)
> x_long <- melt(pinkbr, id.vars = "year", variable_name = "river")
> ggplot(x_long, aes(year, value, colour = river)) + geom_line()
```




We can estimate Taylor's power law for this population:

```
> fit_taylor(pinkbr[,-1])

$c
[1] 0.2805908

$z
[1] 1.977981
```

These values reflect the equation:

$$\sigma^2 = c\mu^z \tag{1}$$

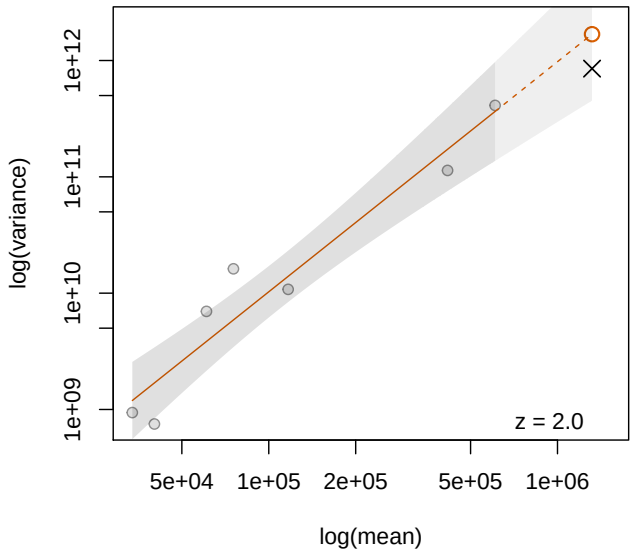
where $\sigma^2$ is the temporal variance and $\mu$ is the temporal mean. The parameter $c$ does not affect the portfolio effect. The parameter $z$ is often referred to as Taylor's power law exponent. Specifically, `fit_taylor` and the function `pe_mv` fit the mean-variance relationship on a log-log scale:

$$log(\sigma_i^2) = c + z \cdot log(\mu_i) + \epsilon_i \tag{2}$$

where $i$ represents an individual subpopulation, and $\epsilon_i$ represents independent and identically distributed residual error with mean zero and an estimated variance.

The package also contains a function `plot_mv` to visualize the various mean-variance model fits to empirical data. Let's look at the linear model we just fit:

```
> plot_mv(pinkbr[,-1], show = "linear", ci = TRUE)
```




In this plot, we see the log(mean) and log(variance) values for each river as grey dots. The orange line shows the mean-variance fit. The $\times$ shows the observed metapopulation log(mean) and log(variance) values. The orange-open circle shows the expected log(variance) value at the observed log(mean) value for the metapopulation. The ratio of the y-value of the open-orange circle and the $\times$ represents the mean-variance portfolio effect. It's the ratio of the expected to the observed variability at the metapopulation size.

So, $z$ is around 2. Let's look at the default mean-variance portfolio effect, which uses the linear model we just fit:

```
> pe_mv(pinkbr[,-1], ci = TRUE)

$pe
[1] 1.412039

$ci
[1] 0.7269781 2.7426593
```

This tells us that the metapopulation is 1.4 times more stable than if it acted as a homogeneous population. These (frequentist) confidence intervals indicate that

under repeated conditions, we would expect 95% of these intervals to contain the true value of the mean-variance portfolio effect given that our model is correct.

We can compare this to the average-CV portfolio effect. In this case, we find that the average-CV portfolio effect is similar for this population. We would expect this given that Taylor's power law z-value is close to 2.

```
> pe_avg_cv(pinkbr[,-1], ci = TRUE, boot_reps = 500)

$pe
[1] 1.516637

$ci
[1] 1.086787 2.121533
```

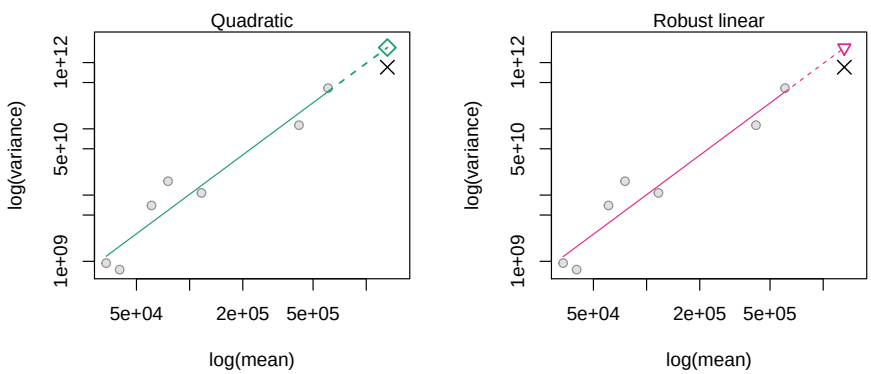
The `pe_avg_cv` function uses (bias-adjusted) bootstrap confidence intervals (`BCa` in the `boot` package). These confidence intervals are obtained by re-sampling the subpopulations with replacement and re-calculating the portfolio effect. If there aren't many subpopulations, these confidence intervals may not be an accurate reflection of the uncertainty in the average-CV portfolio effect.

Returning to the mean-variance portfolio effect, we can explore whether different kinds of mean-variance extrapolations would yield different results. Let's fit some different mean-variance extrapolations:

```
> pe_mv(pinkbr[,-1], type = "linear_robust")

[1] 1.405554

> pe_mv(pinkbr[,-1], type = "quadratic")

[1] 1.412039

> pe_mv(pinkbr[,-1], type = "linear_quad_avg")

[1] 1.412039
```

The `quadratic` and `linear_quad_avg` options give us the same value as the `linear` version because the quadratic model curvature has been bounded to only curve up. In this case, they simplify to the linear model. We could look at these using the `plot_mv` function:

```
> par(mfrow = c(1, 2))
> plot_mv(pinkbr[,-1], show = "quadratic", add_z = FALSE)
> mtext("Quadratic")
> plot_mv(pinkbr[,-1], show = "robust", add_z = FALSE)
> mtext("Robust linear")
```




We can also try detrending the time series with linear or loess models to see how that affects the mean-variance portfolio effect. Estimates of variability such as the variance and CV can be biased upward if the time series are non-stationary.

```
> pe_mv(pinkbr[,-1], type = "linear")
[1] 1.412039
> pe_mv(pinkbr[,-1], type = "linear_detrended")
[1] 1.421514
> pe_mv(pinkbr[,-1], type = "loess_detrended")
[1] 1.43015
```

We've suppressed the confidence intervals here for brevity, but we can see that for this population, the estimates are similar whether or not we detrend the data.

# References

Krkoŝek, M., Connors, B.M., Morton, A., Lewis, M.A., Dill, L.M. & Hilborn, R. (2011). Effects of parasites from salmon farms on productivity of wild salmon. Proceedings of the National Academy of Sciences of the United States of America, 108, 14700–14704.