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*, which is in preparation 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.

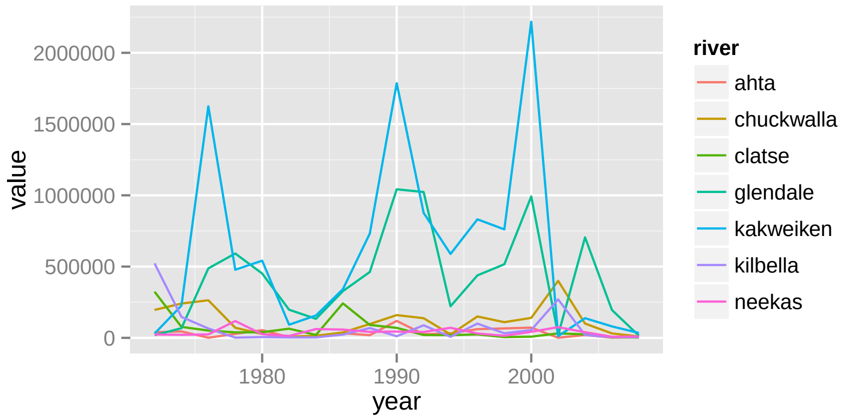
First, let's load the package and load the sample dataset. These data represent pink salmon recruits in the Broughton Archipelago for even years. Each column represents abundance for a different river through time. You can find these data in the supplementary materials of Krkošek et al. (2011) and they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

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

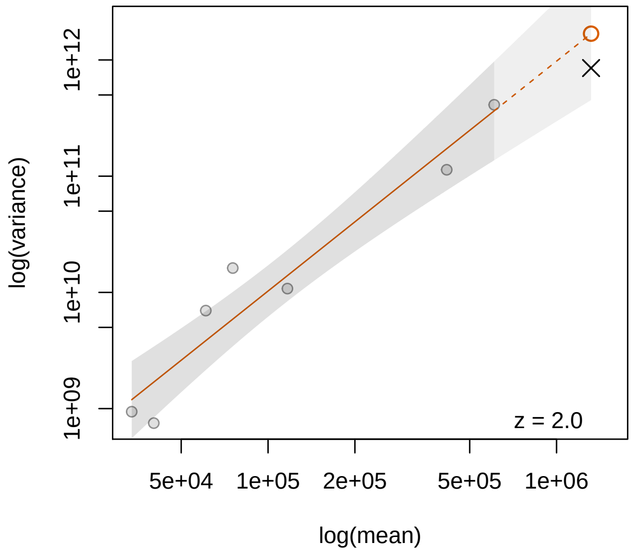
where σ^2 is the temporal variance and μ is the temporal mean. The parameter c does not affect the portfolio effect. The parameter z is often referred to as Taylor's power law exponent. Specifically, `fit_taylor` and the function `pe_mv` fit the mean-variance relationship on a log-log scale:

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

where i represents an individual subpopulation, and ϵ_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] 1.062932 2.168973
```

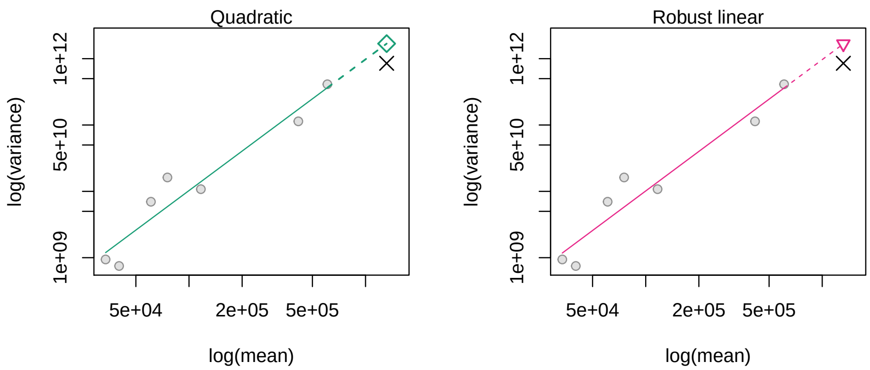
The `pe_avg_cv` function uses (bias-adjusted) bootstrap confidence intervals (`BCa` in the `boot` package). These confidence intervals are obtained by re-sampling the subpopulations with replacement and re-calculating the portfolio effect. If there aren't many subpopulations, these confidence intervals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

Krkošek, 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.