

Supporting Information for Ecological prophets: Quantifying metapopulation portfolio effects Methods in Ecology and Evolution

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R package to estimate metapopulation portfolio effects

In an R console, the `ecofolio` package can be installed either from the included source package (`.tar.gz` file) or via the web (instructions below). First, install dependencies if needed:

```
install.packages(c("plyr", "reshape", "MuMIn", "robustbase"))
```

Then, to install the included package:

```
install.packages("mee312093-sup-0001-Sourcepackage.tar.gz", type = "source")
```

or to install the current version from the web:

```
install.packages("devtools") # if needed  
devtools::install_github("ecofolio", username = "seananderson")
```

Current code and install details are available at
<https://github.com/seananderson/ecofolio>

You can load the package, read the vignette, and access the help pages with:

```
library(ecofolio)
vignette("ecofolio")
help(package = "ecofolio")
```

Data sources for the empirical portfolio effect analysis

We sought to include as many metapopulation time series from as diverse taxonomic groups as possible. However, due to availability, the included data primarily represent metapopulations in North America (salmon), the United Kingdom (moths), and Australia (reef fishes) (Fig. S2). We show a summary of the data included in our analysis of empirical ecological systems in Table S1 and the time series in Fig. S1.

Salmon

We obtained salmon data from a variety of sources, in particular Dorner *et al.* (2008). Most of the salmon populations are from the northwest coast of North America, but also: Kola Peninsula, Russia (Jensen *et al.* 1999), southern New England (Kocik & Sheehan 2006), and Central Valley, California (Carlson & Satterthwaite 2011) (Fig. S2). All data represent annual estimated returns — fisheries catch plus escape-ment to the spawning grounds. We divided pink salmon annual estimated returns into odd- and even-year time series due to their strongly distinct runs that do not interbreed (Quinn 2005). To maintain consistency with previous PE analyses involving sockeye salmon (Schindler *et al.* 2010) and analyses of time series of these data (Dorner *et al.* 2008), and due to the less distinct separate runs (Quinn 2005), we did not divide the sockeye salmon into separate runs.

Subsets of these salmon data have been used in numerous analyses relating diversity with stability. A particular feature of the salmon literature is a focus on the role of “biocomplexity” — a diversity of life-histories and local adaptations to the environment — in producing stability (Hilborn *et al.* 2003) and recent papers have focussed on measuring the portfolio effects we investigate in this paper (Schindler *et al.* 2010; Carlson & Satterthwaite 2011). In studying the mechanisms behind sub-population asynchrony, and hence portfolio effects, studies of Pacific salmon have generally focussed on drivers that fall into two categories: (1) landscape filtering of

the environment so that different subpopulations experience different environmental forces (e.g. local topology affecting stream flow) (e.g. Schindler *et al.* 2008), and (2) biologically-based response diversity to the environment (e.g. genetically-based variation in thermal tolerances) (e.g. Eliason *et al.* 2011). These patterns of asynchrony can play out not just at the decadal scale but also over centuries (Rogers *et al.* 2013).

Moths

We obtained moth abundance time series from the Rothamsted Insect Survey (RIS). L. R. Taylor started the trap network that forms the RIS in the early 1960s; the RIS is now one of the longest-running and largest-scale insect surveys in the world (Conrad *et al.* 2004). Details on the survey are available in Conrad *et al.* (2004) and Taylor (1986). The RIS captures moths by light traps (Williams 1948) placed 1–2 m above ground; these traps catch small but reliable samples of moth populations (Williams 1948; Taylor & French 1974; Conrad *et al.* 2004). Although different species may show different responses to the traps (Miurhead-Thomson 1991; Woiwod & Hanski 1992), we compare across sites within the same species so this should not affect our results.

Our moth data spanned from 1999–2010 for 13 species (Table S1) and 28 sites (Table S2). We included only moths with single broods per year (univoltine moths) and single annual flight episodes since we were aggregating the data annually to maintain consistency with data from other taxonomic groups that were available. We removed site-species combinations where there were eight or more years with zero moths caught in traps to avoid sites where a given species was exceptionally rare and not likely to be consistently censused. This removed 97 subpopulations leaving 280. Further culling of populations according to the criteria in the Methods section left us with 268 subpopulations. All the species included are common within Great Britain, although some have undergone declines in abundance since the RIS began (Conrad *et al.* 2004).

Earlier versions of these moth data featured heavily in the work of Taylor and colleagues on the property now known as Taylor’s power law (Taylor & Taylor 1977; Taylor & Woiwod 1980; Perry 1981). This early work focussed on behavioural properties that might regulate the stability and variance of moth populations (Taylor & Woiwod 1980). Work has continued with these datasets and studies have shown a

number of mechanisms generating stability. For example, authors have shown spatial asynchrony (Gaston 1988), polyphagy (eating different kinds of food) (Redfearn & Pimm 1988), and density dependence to act as stabilizing forces (Hanski & Woiwod 1993).

Reef fishes

We obtained reef visual census fish counts within the Greater Barrier Reef (GBR) from the Australian Institute of Marine Science’s (AIMS) Long-term Monitoring Program (LTMP) (Sweatman *et al.* 2008). The AIMS survey data used here are from fixed transects at selected sites across 46 reefs from 1994–2010 (Table S3). Details of the sampling design are available from Halford & Thompson (1994). Briefly, AIMS surveys reef fish annually within six sectors of the GBR. AIMS identifies inner-, mid-, and outer-shelf positions and three reefs within each shelf position. Within each reef, AIMS chooses three sites of the same habitat and establishes five permanent 50m transects at 6–9m depth 10m apart and parallel to the reef crest. Divers count damselfishes (Pomacentrids) on 1m-wide transects and all other families on 5m-wide transects. AIMS only censuses fish one year or older since recruitment can be highly spatially and temporally variable. AIMS conducts annual standardization exercises to avoid temporal bias in counts within and across divers (Halford & Thompson 1994).

A number of recent studies have used these reef-fish data to investigate stability-diversity relationships, often focusing on functional diversity or reef size and isolation. For example, Thibaut *et al.* (2012) found strong asynchrony of response to the environment between three functional groups of herbivorous reef fishes, which lead to greater stability. Another benefit to this functional diversity may be increased disease resistance (Raymundo *et al.* 2009), presumably enhancing stability. Independent of functional roles, Mellin *et al.* (2010) found that small, isolated reefs have higher population variability and therefore higher probability of local extinction.

Diagnosing the ecological properties of empirical portfolio effects

We overlaid the empirical PEs in their respective theoretical parameter space to investigate the ecological properties of real-world metapopulations (subpopulation correlation, mean-variance scaling, subpopulation number richness, and evenness). Specifically, we matched the empirical linear-regression z values and the number of subpopulations with their theoretical counterparts.

To present our results graphically in Fig. 5, we categorized the mean correlation of the empirical subpopulations ($\bar{\rho}$) into bins of $0 \leq \bar{\rho} < 0.25$, $0.25 \leq \bar{\rho} < 0.5$, and $0.50 \leq \bar{\rho} < 0.75$ and matched these with the theoretical PE estimated at the midpoints of these bins (i.e. 0.125, 0.375, and 0.625). We matched the disparity in subpopulation size by: (1) calculating the CV of the log of the subpopulation time series' means, $CV(\log \mu)$; (2) categorizing the empirical metapopulations into bins of $0 \leq CV(\log \mu) < 0.3$, $0.3 \leq CV(\log \mu) < 0.6$, and $0.6 \leq CV(\log \mu) < 0.9$; (3) estimating the theoretical PE using evenly-spaced values from a log-normal distribution with a mean of two and standard deviation of the midpoints of these bins (i.e. 0.15, 0.45, and 0.75). Here and in Fig. 2, we derived these evenly-spaced values as follows. We drew subpopulation (i) quantiles q_i from the evenly-spaced sequence: a_1, a_2, \dots, a_n , where $a_1 = 1/(n+1)$ and $a_n = 1 - (1/(n+1))$. We then calculated the subpopulation means at each q_i from a log-normal distribution with log-mean of two and a log-standard deviation of the “unevenness value” times the log-mean.

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Table S1. Metapopulations used in the empirical PE analyses. ID column numbers correspond to ID numbers in the figures.

ID	Species	Common	Location	Subpopulations	Years	Reference
1	<i>Oncorhynchus kisutch</i>	Coho salmon	Broughton archipelago, BC, Canada	6	16	(Krkošek <i>et al.</i> 2011)
2	<i>Oncorhynchus gorbuscha</i>	Pink salmon, odd years	Puget Sound, WA, United States	4	19	(Dorner <i>et al.</i> 2008)
3	<i>Oncorhynchus nerka</i>	Sockeye salmon	Bristol Bay, AK, United States	8	43	(West & Fair 2006)
4	<i>Oncorhynchus nerka</i>	Sockeye salmon	Kodiak, AK, United States	4	24	(Dorner <i>et al.</i> 2008)
5	<i>Oncorhynchus gorbuscha</i>	Pink salmon, odd years	Broughton archipelago, BC, Canada	7	19	(Krkošek <i>et al.</i> 2011)
6	<i>Oncorhynchus nerka</i>	Sockeye salmon	Fraser River, BC, Canada	16	44	(Dorner <i>et al.</i> 2008)
7	<i>Oncorhynchus gorbuscha</i>	Pink salmon, odd years	Kodiak, AK, United States	5	8	(Dorner <i>et al.</i> 2008)
8	<i>Oncorhynchus gorbuscha</i>	Pink salmon, even years	Chignik, AK, United States	5	16	(Dorner <i>et al.</i> 2008)
9	<i>Oncorhynchus nerka</i>	Sockeye salmon	Upper Cook Inlet, AK, United States	4	29	(Fair <i>et al.</i> 2011)
10	<i>Oncorhynchus gorbuscha</i>	Pink salmon, even years	Broughton archipelago, BC, Canada	7	19	(Krkošek <i>et al.</i> 2011)
11	<i>Salmo salar</i>	Atlantic salmon	Kola Peninsula, Russia	4	15	(Jensen <i>et al.</i> 1999)
12	<i>Oncorhynchus keta</i>	Chum salmon	Puget Sound, WA, United States	7	26	(Dorner <i>et al.</i> 2008)
13	<i>Oncorhynchus tshawytscha</i>	Chinook salmon	Columbia Estuary, OR/WA, United States	9	23	(StreamNet 2011)
14	<i>Oncorhynchus tshawytscha</i>	Chinook salmon	Elochoman River, WA, United States	5	27	(StreamNet 2011)
15	<i>Oncorhynchus keta</i>	Chum salmon	Arctic, Yukon, Kuskokwim, US and Canada	5	18	(Dorner <i>et al.</i> 2008)
16	<i>Oncorhynchus gorbuscha</i>	Pink salmon, odd years	Chignik, AK, United States	5	15	(Dorner <i>et al.</i> 2008)
17	<i>Oncorhynchus gorbuscha</i>	Pink salmon, even years	Kodiak, AK, United States	5	9	(Dorner <i>et al.</i> 2008)
18	<i>Salmo salar</i>	Atlantic salmon	Southern New England, United States	6	39	(Kocik & Sheehan 2006)
19	<i>Oncorhynchus tshawytscha</i>	Chinook salmon	Central Valley, California	9	54	(Dorner <i>et al.</i> 2008)
20	<i>Oncorhynchus keta</i>	Chum salmon	Alaska Peninsula, AK, United States	4	32	(Conrad <i>et al.</i> 2004)
21	<i>Abaxas grossulariata</i>	The magpie moth	UK	15	12	(Conrad <i>et al.</i> 2004)
22	<i>Orthosia cerasi</i>	Common quaker moth	UK	27	12	(Conrad <i>et al.</i> 2004)
23	<i>Hemithea aestivaria</i>	Common emerald moth	UK	16	12	(Conrad <i>et al.</i> 2004)
24	<i>Xestia xanthographa</i>	Square-spot rustic moth	UK	28	12	(Conrad <i>et al.</i> 2004)
25	<i>Petrophora chlorosata</i>	Brown silver-lines moth	UK	18	12	(Conrad <i>et al.</i> 2004)
26	<i>Erannis defoliaria</i>	Mottled umber moth	UK	19	12	(Conrad <i>et al.</i> 2004)
27	<i>Diarsia mendica</i>	Ingrailed clay moth	UK	24	12	(Conrad <i>et al.</i> 2004)
28	<i>Agrochola (Leptologia) macilenta</i>	Yellow-line quaker moth	UK	23	12	(Conrad <i>et al.</i> 2004)
29	<i>Pharmacis lupulina</i>	Common swift moth	UK	16	12	(Conrad <i>et al.</i> 2004)
30	<i>Poecilocampa populi</i>	December moth	UK	25	12	(Conrad <i>et al.</i> 2004)
31	<i>Eilema lurideola</i>	Common footman moth	UK	20	12	(Conrad <i>et al.</i> 2004)
32	<i>Agrotis exclamatoris</i>	Heart and dart moth	UK	23	12	(Conrad <i>et al.</i> 2004)
33	<i>Colotois pennaria</i>	Feathered thorn moth	UK	26	12	(Conrad <i>et al.</i> 2004)
34	<i>Scarus psittacus</i>	Scarus psittacus	GBR, Australia	37	14	(Sweatman <i>et al.</i> 2008)
35	<i>Pomacentrus moluccensis</i>	Pomacentrus moluccensis	GBR, Australia	35	14	(Sweatman <i>et al.</i> 2008)
36	<i>Acanthochromis polyacanthus</i>	Acanthochromis polyacanthus	GBR, Australia	40	14	(Sweatman <i>et al.</i> 2008)
37	<i>Neopomacentrus azysron</i>	Neopomacentrus azysron	GBR, Australia	39	14	(Sweatman <i>et al.</i> 2008)
38	<i>Chlorurus sordidus</i>	Chlorurus sordidus	GBR, Australia	37	14	(Sweatman <i>et al.</i> 2008)
39	<i>Ctenochaetus spp</i>	Ctenochaetus spp	GBR, Australia	36	14	(Sweatman <i>et al.</i> 2008)
40	<i>Pomacentrus lepidogenys</i>	Pomacentrus lepidogenys	GBR, Australia	39	14	(Sweatman <i>et al.</i> 2008)
41	<i>Plectropomus leopardus</i>	Plectropomus leopardus	GBR, Australia	37	14	(Sweatman <i>et al.</i> 2008)
42	<i>Scarus chameleon</i>	Scarus chameleon	GBR, Australia	37	14	(Sweatman <i>et al.</i> 2008)
43	<i>Chlorurus microrhinos</i>	Chlorurus microrhinos	GBR, Australia	37	14	(Sweatman <i>et al.</i> 2008)
44	<i>Scarus frenatus</i>	Scarus frenatus	GBR, Australia	36	14	(Sweatman <i>et al.</i> 2008)
45	<i>Hemigymmus melapterus</i>	Hemigymmus melapterus	GBR, Australia	37	14	(Sweatman <i>et al.</i> 2008)
46	<i>Hemigymmus fasciatus</i>	Hemigymmus fasciatus	GBR, Australia	37	14	(Sweatman <i>et al.</i> 2008)
47	<i>Scarus niger</i>	Scarus niger	GBR, Australia	37	14	(Sweatman <i>et al.</i> 2008)
48	<i>Epibulus insidiator</i>	Epibulus insidiator	GBR, Australia	37	14	(Sweatman <i>et al.</i> 2008)
49	<i>Chaetodon plebeius</i>	Chaetodon plebeius	GBR, Australia	35	14	(Sweatman <i>et al.</i> 2008)
50	<i>Gomphosus varius</i>	Gomphosus varius	GBR, Australia	36	14	(Sweatman <i>et al.</i> 2008)
51	<i>Chaetodon trifasciatus</i>	Chaetodon trifasciatus	GBR, Australia	36	14	(Sweatman <i>et al.</i> 2008)

Table S2. Moth sites used from the Rothamsted Insect Survey database. Sites are ordered from north to south. County refers to the British County. “Number of spp.” refers to the number of moth species remaining that matched our inclusion criteria.

Site name	County	Northing	Easting	Altitude (m)	Number of spp.
Starcross	South Devon	821	2972	9	12
Denny Lodge	South Hampshire	1056	4333	30	10
Bentley Wood	South Wiltshire	1324	4253	130	12
Winkworth	Surrey	1412	4991	130	12
Alice Holt	North Hampshire	1428	4803	122	12
Perry Wood	East Kent	1565	6040	80	13
Wisley II	Surrey	1579	5065	40	10
Westonbirt	West Gloucestershire	1898	3847	46	13
Geescroft I	Hertfordshire	2128	5132	130	12
Allotments	Hertfordshire	2134	5134	130	7
Barnfield	Hertfordshire	2135	5132	130	10
Hereford	Herefordshire	2476	3564	91	10
Cockayne Hatley	Bedfordshire	2494	5253	76	11
Llysdinam	Breconshire	2586	3009	197	11
Tregaron	Cardiganshire	2618	2687	198	10
Broom’s Barn	West Suffolk	2656	5752	73	9
Compton Park	Staffordshire	2988	3889	105	9
Preston Montford II	Shropshire	3143	3433	61	13
Malham Tarn	Mid-west Yorkshire	4672	3894	396	8
Sildon	County Durham	5262	4239	150	9
Forest-in-Teesdale	North-west Yorkshire	5306	3853	381	5
Castle Eden Dene I	County Durham	5394	4428	91	10
Auchincruive II	Ayrshire	6233	2377	52	10
Brodick	Clyde Islands	6380	2014	50	8
Rowardennan	Stirlingshire	6960	2378	15	8
Kindrogan	East Perthshire	7630	3055	259	7
Beinn Eighe I	West Ross & Cromarty	8629	2024	25	9
Cromarty	East Ross & Cromarty	8672	2785	30	10

Table S3. Reef locations used from the AIMS LTMP Great Barrier Reef database. Reefs are ordered from north to south. “Number of spp.” refers to the number of fish species remaining that matched our inclusion criteria.

Reef	Latitude (deg south)	Longitude (deg east)	Number of spp.
Carter Reef	14.52	145.58	17
Yonge Reef	14.57	145.62	16
No Name Reef	14.62	145.64	18
Macgillivray Reef	14.64	145.49	18
Lizard Island	14.69	145.46	18
North Direction Reef	14.74	145.51	18
Martin Reef(14123)	14.75	145.37	18
Linnet Reef	14.79	145.35	18
Agincourt Reefs (no 1)	16.04	145.87	17
St Crispin Reef	16.07	145.84	18
Opal (2)	16.20	145.90	18
Low Islands Reef	16.38	145.57	17
Hastings Reef	16.49	146.02	17
Michaelmas Reef	16.55	146.05	18
Green Island Reef	16.77	145.97	18
Fitzroy Island Reef	16.92	145.99	18
Myrmidon Reef	18.25	147.38	18
Dip Reef	18.39	147.45	17
Rib Reef	18.47	146.88	18
John Brewer Reef	18.62	147.08	18
Chicken Reef	18.66	147.72	18
Davies Reef	18.80	147.66	18
Pandora Reef	18.81	146.43	3
Slate Reef	19.66	149.91	18
Hyde Reef	19.73	150.09	18
19131s	19.77	149.38	18
Rebe Reef	19.80	150.16	18
19138s	19.80	149.43	18
Hayman Island Reef	20.05	148.89	4
Langford-bird Reef	20.07	148.87	4
Border Island Reef (no 1)	20.18	149.03	13
East Cay Reef	21.46	152.56	18
Turner Reef	21.70	152.56	18
21529s	21.87	152.18	18
Gannett Cay Reef	21.98	152.47	18
Horseshoe	22.02	152.62	18
Snake (22088)	22.02	152.19	18
Broomfield Reef	23.24	151.94	18
One Tree Reef	23.48	152.09	18
Lady Musgrave Reef	23.88	152.42	18

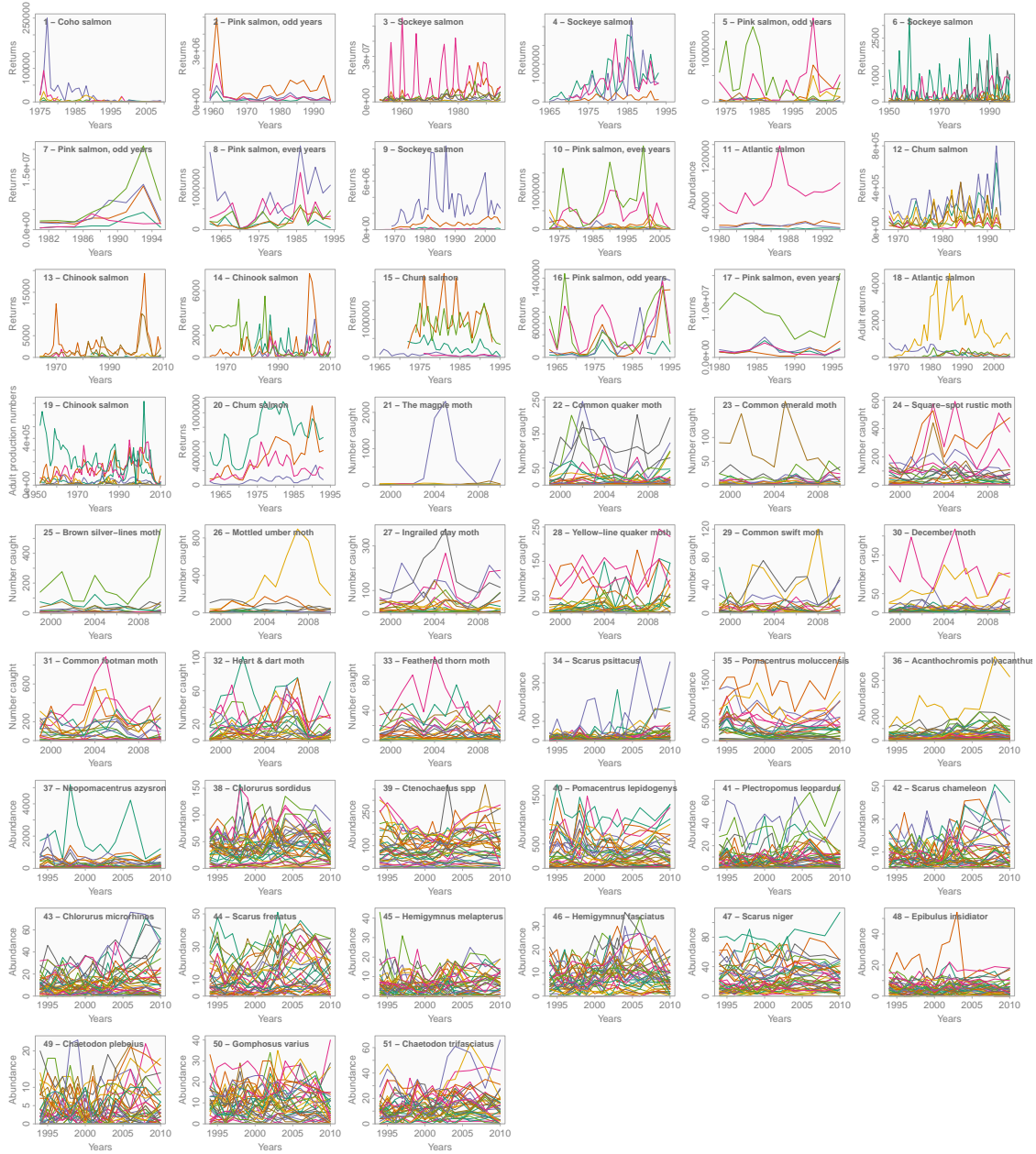


Fig. S1. Subpopulation time series. Each panel contains one metapopulation. Colours were randomly assigned to distinguish subpopulations. Numbers in top-left corners refer to metapopulation IDs (see Table S1).

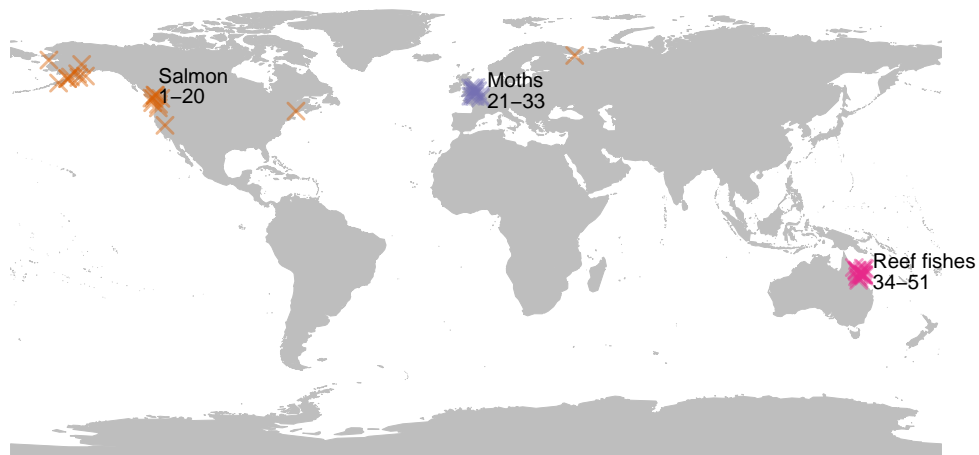


Fig. S2. Map of included metapopulations. We represented salmon metapopulations with orange symbols, moths with purple, and reef fishes with pink. Numbers refer to metapopulation IDs (Table S1). Points are jittered slightly for visual clarity.

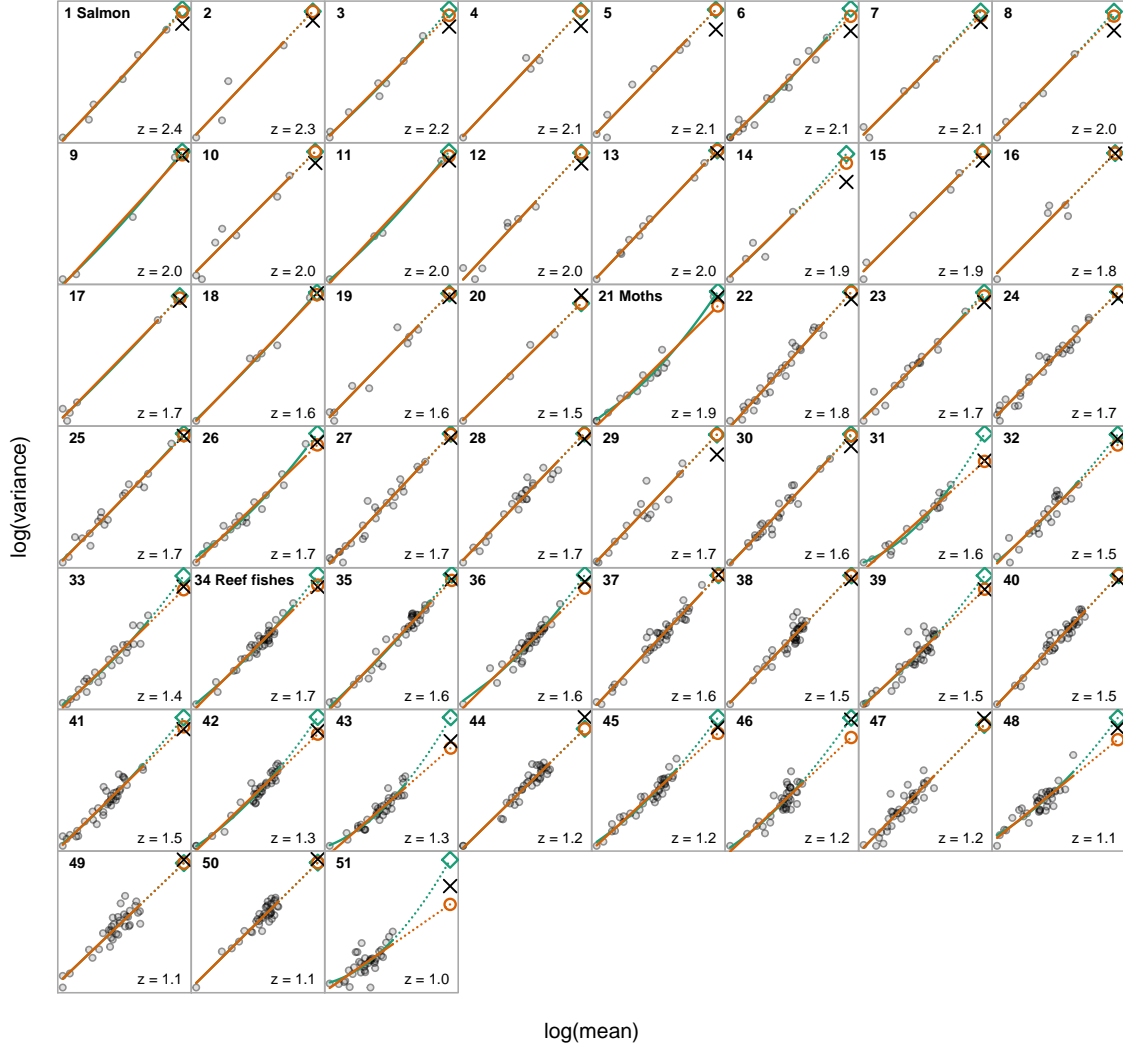


Fig. S3. Calculation of the mean-variance PE using Taylor's power law. Each dark-grey circle represents the $\log(\mu)$ and $\log(\sigma^2)$ of an individual subpopulation timeseries. The orange lines represent fitted linear regressions. The green lines represent fitted quadratic regressions. Black x symbols represent the observed meta-population or portfolio mean and variance. Dashed lines indicate the extrapolation of the model fit to the observed meta-population or portfolio mean and variance. Open-orange circles represent the predicted variance under the linear-fit assumption. Open-green diamonds represent the predicted variance under the quadratic-fit assumption. Metapopulations in which the predicted variance is greater than the observed variance represent variance-reducing PEs. We ordered the panels by decreasing Taylor's power law z -value (slope of the linear regression) within taxonomic groupings. Numbers in upper left of panels refer to metapopulation IDs (Supplementary Table 1)

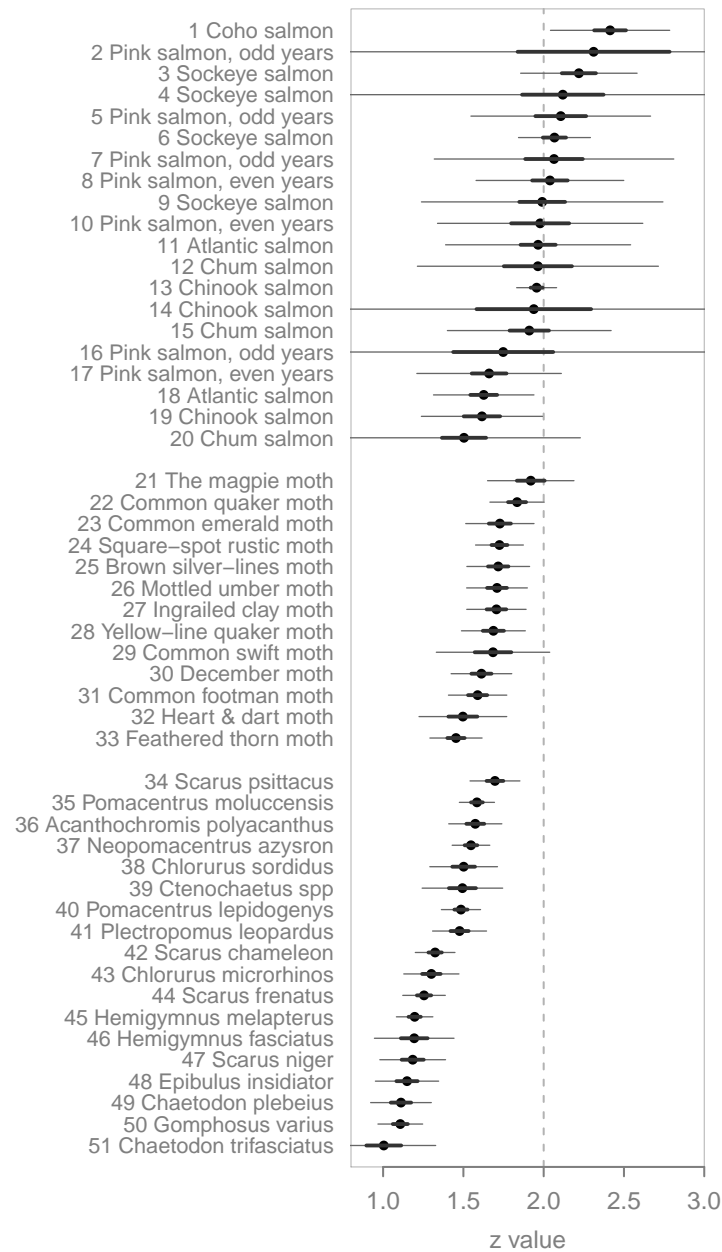


Fig. S4. Taylor's power law z values across metapopulations. Points represent maximum likelihood estimates, thick line segments represent 50% confidence intervals, and thin line segments represent 95% confidence intervals. The vertical dashed line at $z = 2$ represents the value assumed by the average-CV PE method.

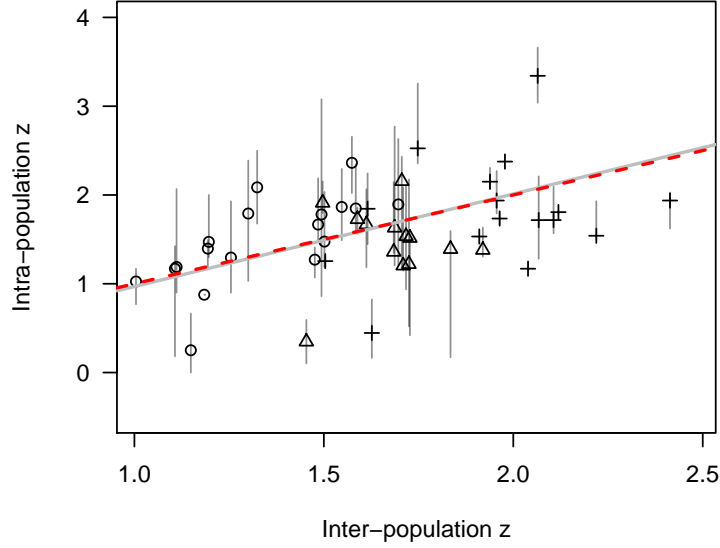


Fig. S5. Intra- vs. inter-subpopulation mean-variance scaling relationship (Taylor’s power law z -value). Our estimation of the empirical mean-variance PE assumes that the inter-subpopulation z -value can approximate the intra-subpopulation z -value. We use the inter-subpopulation z -value throughout our paper. Here, we have also calculated the intra-subpopulation z -value for subpopulation time series in which the mean abundance in the 1st or 2nd half of the time series is twice the magnitude of the other half. Points represent median intra-subpopulation z -values within each metapopulation and vertical line segments represent 1st and 3rd quartile values. The dashed-red line represents a one-to-one relationship and the solid-grey line (under the one-to-one line) represents a linear regression of the median intra-subpopulation z -values with inter-subpopulation z -values. Symbols represent salmon (crosses), moths (triangles), and reef fishes (circles).

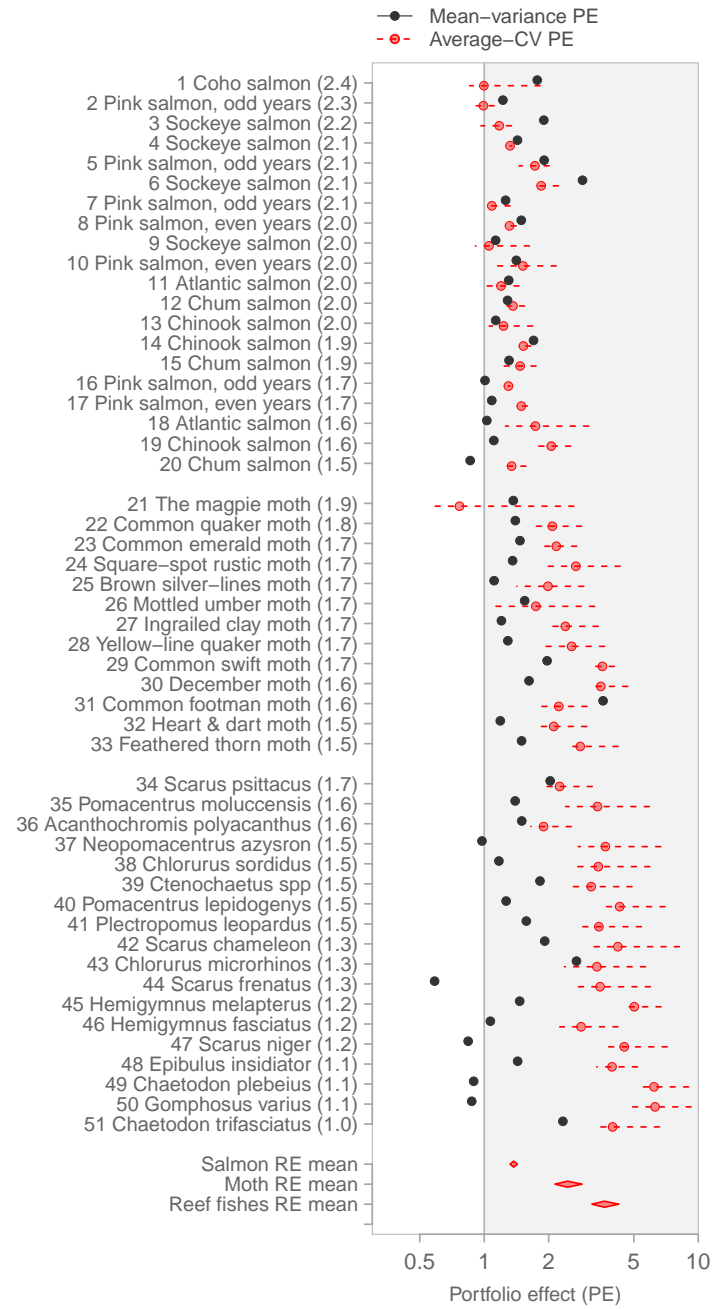


Fig. S6. PEs with the **mean-variance PEs** estimated from a quadratic model. See Fig. 3 for details.

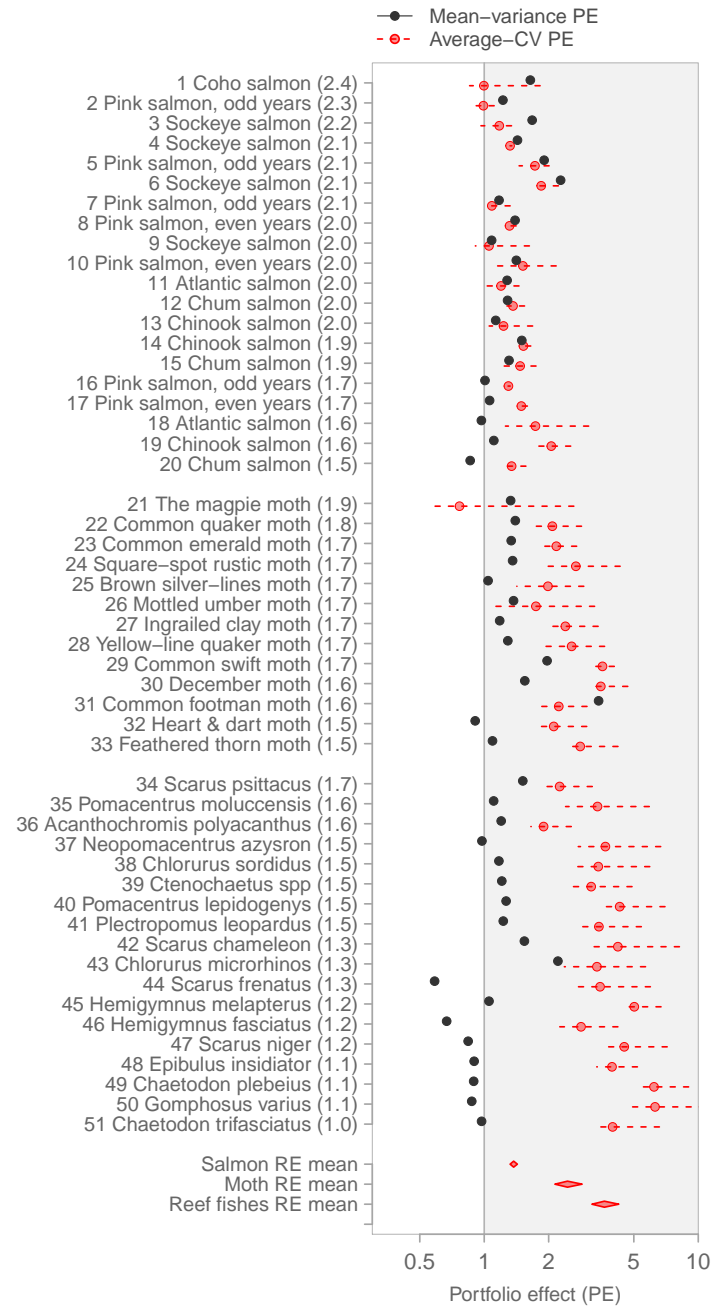


Fig. S7. PEs with the mean-variance PEs estimated from a linear-quadratic averaged model. See Fig. 3 for details.

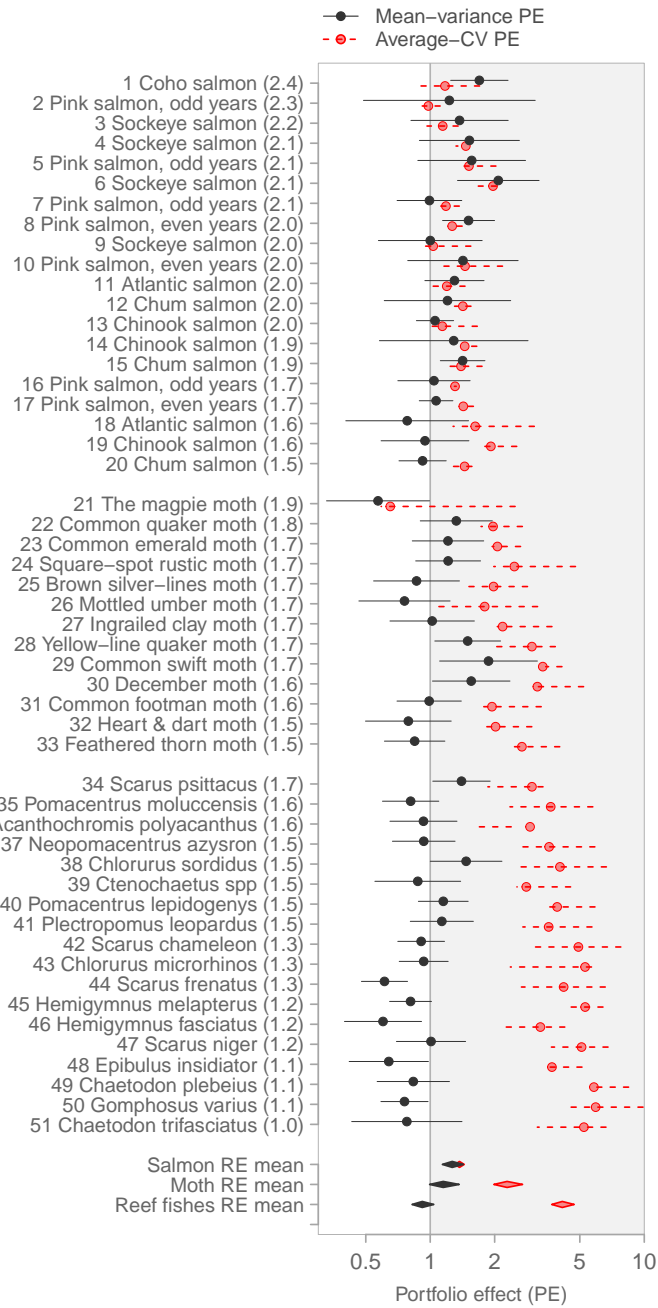


Fig. S8. PEs from **linear detrended** time series. See Fig. 3 for details.

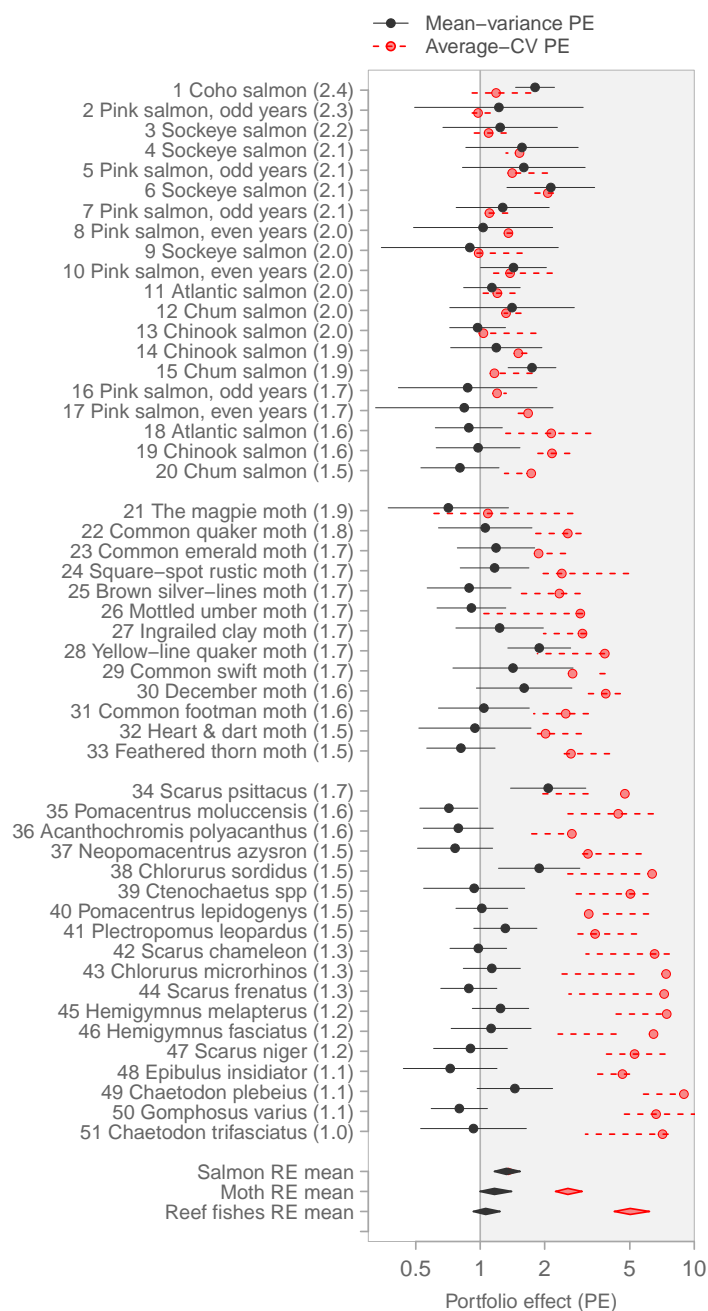


Fig. S9. PEs from **loess detrended** time series. See Fig. 3 for details.

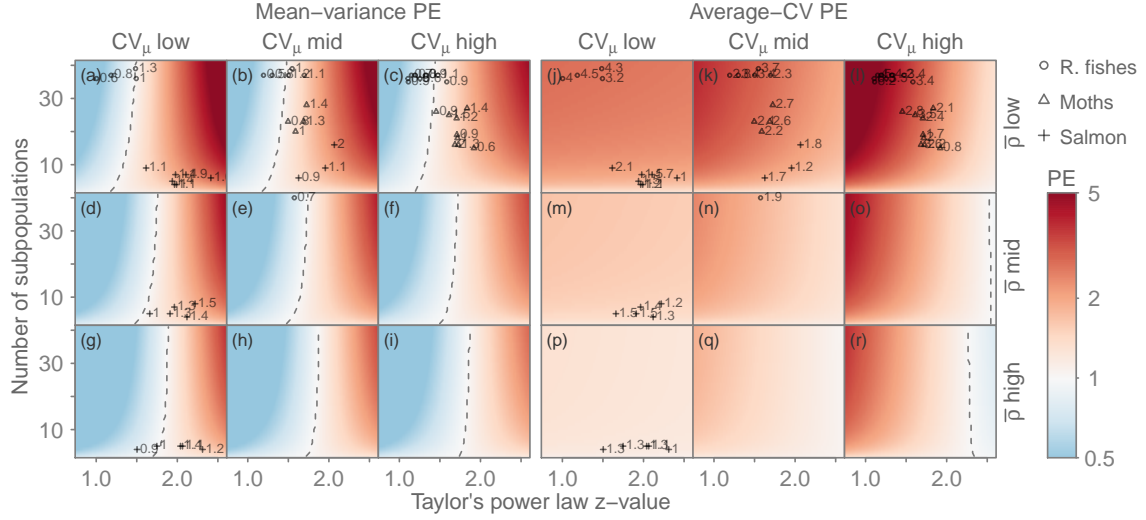


Fig. S10. Empirical ecological PEs (points) overlaid in theoretical PE parameter space (colour shading). **This is the same as Fig. 5 except that here we indicate the empirical PE values beside the points.** The colour shading indicates the stabilizing-effect of the theoretical mean-variance PEs (a–i) and average-CV PEs (j–r): red indicates a stabilizing effect and blue indicates a destabilizing effect. The dashed lines indicate neutral PEs. Columns from left to right show systems with increasingly uneven subpopulation sizes, and rows from top to bottom show systems with increasingly strong mean correlation between subpopulation

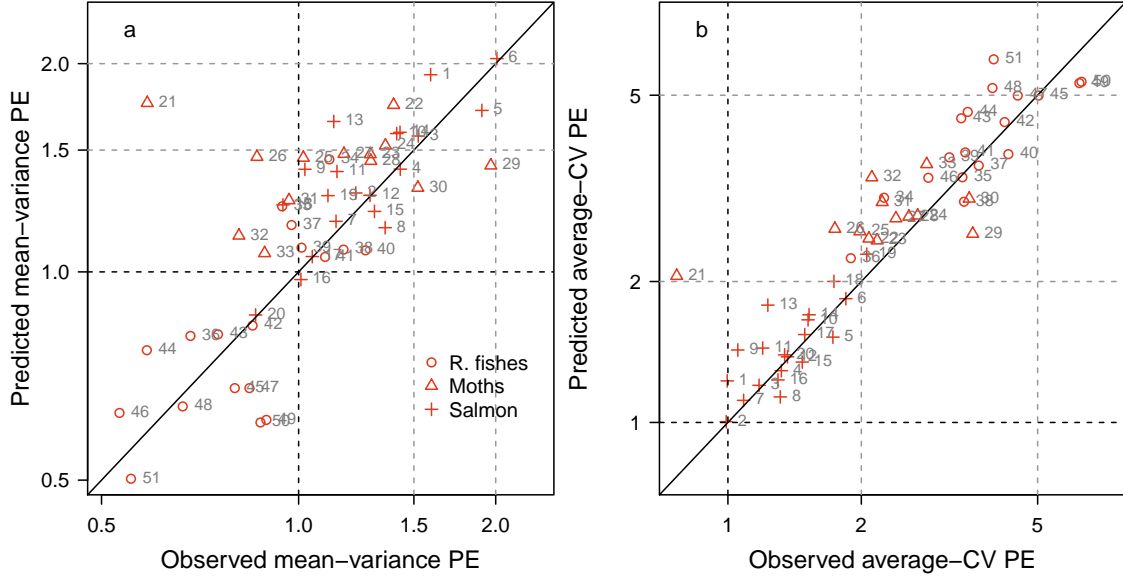


Fig. S11. Predicted vs. observed mean-variance (a) and average-CV PEs (b). Predicted PEs correspond to the colour underlying the metapopulations displayed in Fig. 5; observed PEs to the values calculated directly from the empirical data and shown in Fig. 3. The predicted PEs are approximate due to other statistical properties of the data beyond the four examined in Fig. 5, and due to grouping the CV_{mu} and correlation values from the metapopulations to match the displayed theoretical values in the bins. Numbers indicate the metapopulation IDs used throughout the paper (Table S1). The solid sloped lines indicate one-to-one relationships. Note that all axes have been log transformed and the two panels have separate axis limits.

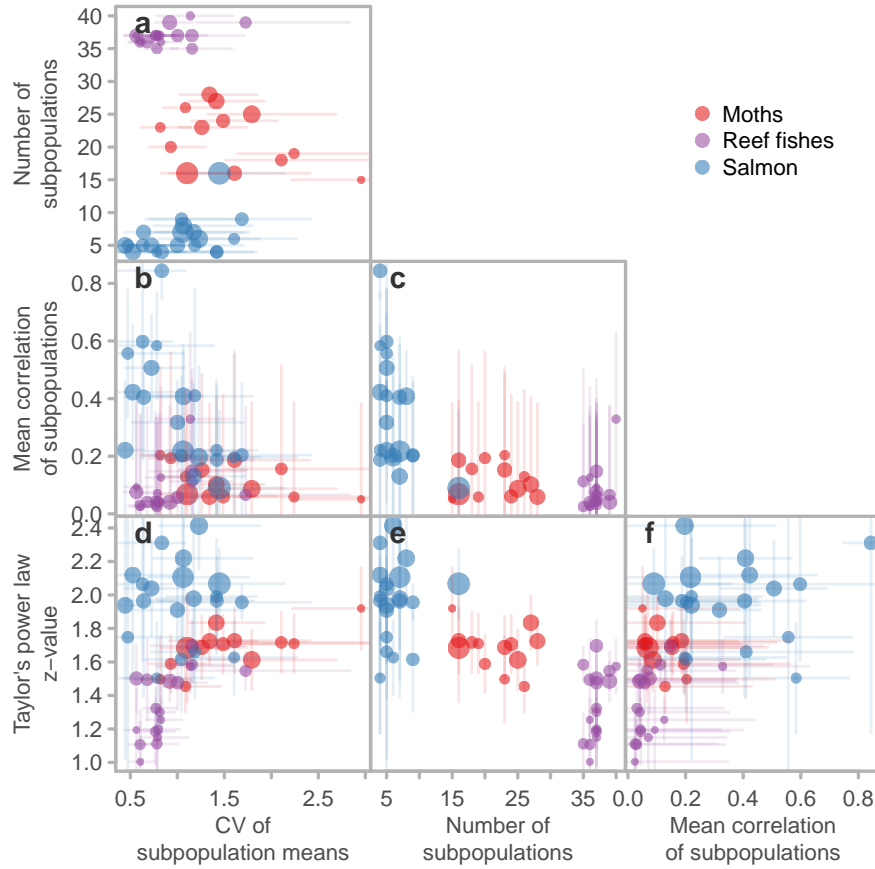


Fig. S12. Relationship between the drivers of the PE in empirical systems for moths (red), reef fishes (purple), and salmon (blue). The area of the filled circles corresponds to the strength of the mean-variance PE with larger circles corresponding to more stabilizing PEs. Line segments indicate 95% confidence intervals.

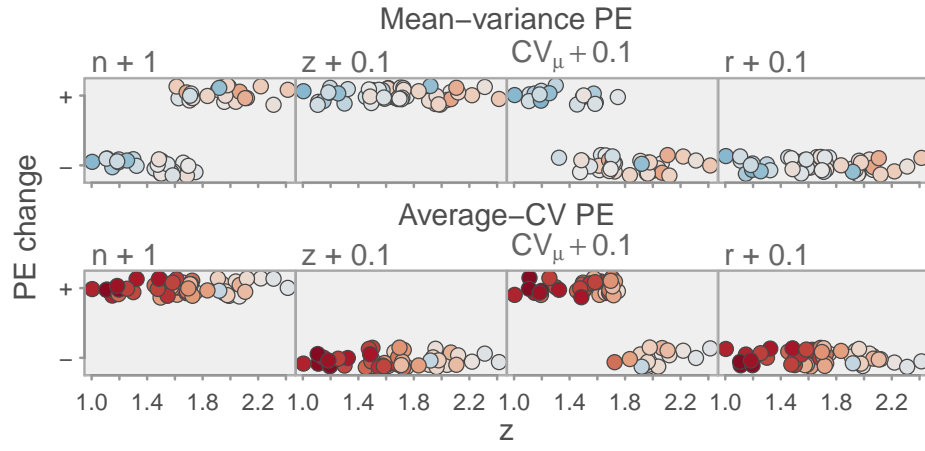


Fig. S13. The PE used as an index of ecosystem change. The upper panel shows the mean-variance PE and the lower panel the average-CV PE. The horizontal axis shows Taylor's power law z -value. The vertical axis shows the change in the PE (more stabilizing = +, less stabilizing = -). The panels from left to right indicate an increase in the number of subpopulations ($n+1$), Taylor's power law z -value ($z+1$), subpopulation unevenness ($CV_\mu+0.1$), or the correlation between subpopulations ($r+0.1$). The quantities added are arbitrary and the results would look the same for any quantity added greater than zero. Each dot represents an empirical metapopulation and the colour indicates the observed empirical PE using the same colour scale as Figs. 4 and 5. The dots are jittered vertically slightly for visual clarity.