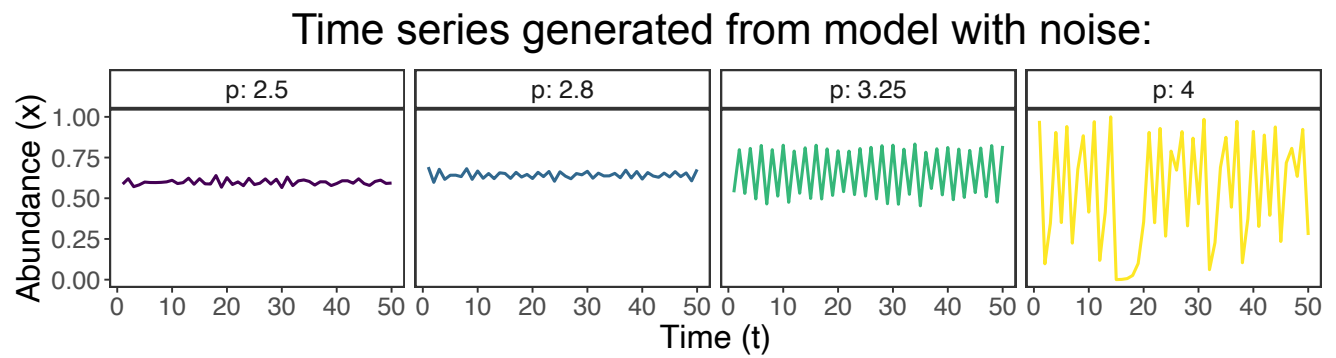
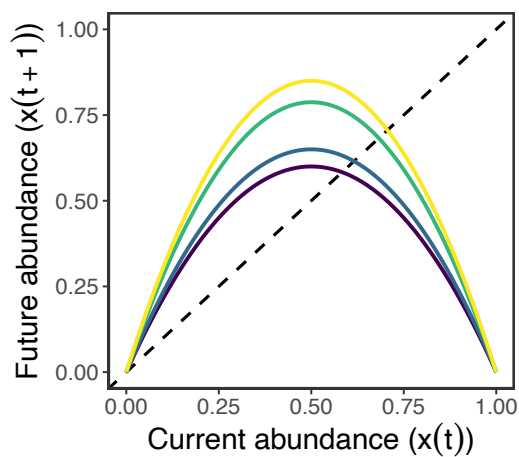


# Single-species model (logistic map): $x(t + 1) = px(t)[1 - x(t)]$



## Step 1

Fit a Gaussian Process regression model with lagged abundances and  $p$  as inputs (e.g., GPEDM package in R) to approximate  $x(t + 1) = G[x(t), \dots, x(t - E), p]$

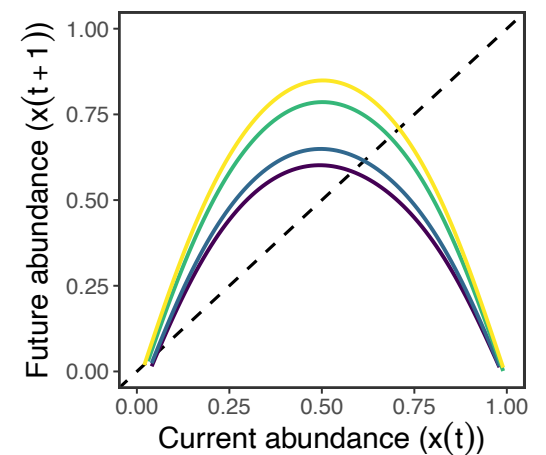
data

(50 points for each level of  $p$ , 200 points in total)

(In this example,  $E = 0$ )

t	x	x_1	p
1	0.587	NA	2.5
2	0.620	0.587	2.5
3	0.571	0.620	2.5
...	...	...	...
1	0.691	NA	2.8
2	0.598	0.691	2.8
3	0.678	0.598	2.8
...	...	...	...

$G[x(t), p]$



```
G <- fitGP(data = data, y = "x", x = c("x_1", "p"))
```

(See SI Appendix Section S3 for a mathematical description of the approximated function  $G$ )

## Step 2 Sequentially predict $x$ by extrapolating function $G$ to an unseen level of $p$ (e.g., $p = 3.52$ )

```
for (t in 1:100) {
```

newdata

x_1	p
0.524	3.52

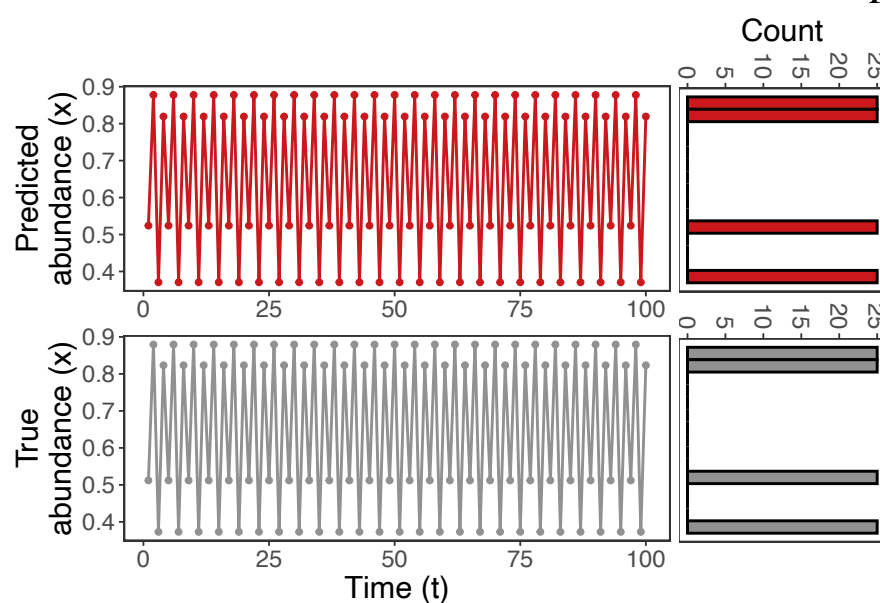
```
x[t] <- predict(object = G, newdata = newdata)$outsampresults$predmean
```

```
newdata <- c(x[t], newdata$p)
```

```
}
```

## Step 3

Compare true and predicted time series of  $x$  (e.g., Jensen-Shannon divergence) for each level of  $p$



(In this example,  $p = 3.52$ )

(Jensen-Shannon divergence is computed by comparing these two histograms of  $x$ )