

Identifying dynamic coupling between interacting populations using Granger causality and alternative dynamical approaches

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Abstract

Finding who interacts with whom based on time series data is a key endeavour of statistical ecology. Here, we show that multivariate autoregressive (MAR) modelling of finite but arbitrary order can be used, with appropriate log transformation and model selection based on information criteria, in order to infer causal links between interacting populations. Causality is here understood in the sense of Granger, i.e. time series x Granger causes y if information on present and past values of x helps predicting future values of y . Recent nonlinear approaches such as convergent cross-mapping (CCM) have been put forward to alleviate potential issues of Granger causality (GC), notably due to the assumption of linearity in most implementations of GC. This has led to a relative skepticism about the ability of (log)-linear parametric methods to infer causal links in nonlinear dynamical systems. The merits of nonlinear and nonparametric models notwithstanding, the present results show that the demise of parametric and linear modelling has been somewhat exaggerated. Not only parametric MAR(p) models are able to infer causal links for a number of nonlinear (stochastic) systems, but they can even do so for datasets with highly nonlinear dynamical behaviour (e.g., limit cycles in real data, simulated chaotic dynamics). GC demonstrates, surprisingly, similar performances to CCM in a number of highly nonlinear cases. We further show that the (log)-linear framework can be extended to large interaction networks, provided some assumptions about the interaction structure. Finally, we discuss nonparametric, spectral and nonlinear extensions of Granger causality approaches.

Keywords: time series, interaction network, interaction strength, causal inference, feedback, food web, community dynamics.

Introduction

There is a diversity of viewpoints regarding the importance of interactions between species for predicting their joint dynamics; a division that can be traced back at least to the Clementsian (integrated) vs Gleasonian (stochastically dominated) views of plant communities (Chase, 2003). Today, whether one should predict population dynamics as nearly isolated populations or integrated communities merges with management concerns, as exemplified by debates on ecosystem-based fisheries management in fisheries science (Link, 2002; Pikitch *et al.*, 2004). One reason for this continued tension within ecology is that most attempts to infer interaction strengths rely on relatively strong assumptions (Berlow *et al.*, 2004; Wootton & Emmerson, 2005). Reliably inferring how populations of different species are able to influence one another’s dynamics is therefore a longstanding quest of ecology.

At one end of the spectrum of beliefs on interaction networks roles in determining community dynamics, a large part of theoretical ecology models communities as variations of the generalized Lotka-Volterra equations (e.g., May, 1973; Yodzis, 1998; Coyte *et al.*, 2015; eq. 1), where the dynamics of food webs or competitive systems are modelled as fairly coupled deterministic dynamical systems, in discrete or continuous time. This implicitly assumes that interactions between populations of different species are many and strong enough (even if interaction strength is asymmetrically distributed) to deserve to be modelled explicitly, and such that interactions rates can be weighted by body mass or metabolic rates (Yodzis & Innes, 1992; Brose *et al.*, 2006; Weitz & Levin, 2006; Rall *et al.*, 2008; Brose, 2010).

$$\frac{dN_i}{dt} = r_i N_i + \sum_{j=1}^S g_{ij}(N_i, N_j) N_j \quad (1)$$

At the other end of the spectrum, other branches of theoretical ecology have highlighted that many species may have weak dynamical coupling to their competitors, enemies and resources. One reason for this is that intraspecific density-dependence dominates the dynamics (Barabás *et al.*, 2017) and even more so as community size increases. A variant being that as most consumers are generalists rather than specialists, their dynamics can be primarily determined by the intricacies of stage structure within populations (Murdoch *et al.*, 2002; Barraquand *et al.*, 2017). According to this view, a population’s dynamics may in effect be best modelled as isolated from the other species in the community. Recent statistical evidence seems to substantiate that view: most empirically-minded trials to infer interspecific interactions between species in large communities, using time series of counts, have yielded so far weak to null estimates of net species interactions (Mutshinda *et al.*, 2009, 2011; Barraquand *et al.*, 2018). In contrast to the statistical models though, experimental measures have shown that weak interactors can have strong impact within their communities (but experimental measures of interactions are not equivalent to the interaction concepts of dynamical models,

Berlow *et al.*, 2004).

Summarizing the evidence derived from theoretical and statistical models, ecologists are currently in the puzzling position where both theory and data have produced conflicting reports regarding the importance of species interactions for predicting community dynamics. To improve ecological modelling overall, a better statistical inference of dynamic coupling between species is therefore paramount - preferably one able to deal with the numerous nonlinearities present in ecological models.

To quantify dynamic coupling between species, ecologists have used a number of statistical models ranging from mechanistic to purely phenomenological. They include most notably multivariate autoregressive models or order one, or MAR(1) models (also called VAR(1) - vector autoregressive models). These are statistical multispecies generalizations of the Gompertz discrete-time single-species models (Ives *et al.*, 2003; Mutshinda *et al.*, 2009). MAR(1) can to a large extent infer linkages between species population dynamics (Certain *et al.*, 2018). MAR(p) models, with a maximum time lag of order $p \geq 1$, generalize the MAR(1) framework familiar to ecologists and are interestingly linked to one of the most celebrated causality concept, the so-called Granger-Wiener causality (Granger, 1969; Sims, 1980; Ding *et al.*, 2006; Chen *et al.*, 2006; Barnett *et al.*, 2009; Detto *et al.*, 2012; Sugihara *et al.*, 2012; Barnett & Seth, 2014).

Granger-Wiener causality (Granger causality or GC for short) is a causality concept that is strongly tied to the idea that the cause must precede in time the effect. There are other ways to define causality, through interventions notably (e.g. Pearl, 2009) but these are usually less practical in a dynamical setting. Therefore, if a dynamical model for time series y can see its in-sample predictive power improve by inclusion of time series x , we say that x Granger-causes y . This definition is rather general and does not specify, in general, any sort of model framework. It can in principle be applied to phenomenological and mechanistic frameworks alike, as well as in nonparametric settings (Detto *et al.*, 2012). However, GC testing is often used in contexts where the a priori information on community dynamics is limited, so that one needs to reduce the universe of possible model formulations to a handful of contrasted scenarios. In this context, GC is usually tested within the context of statistically friendly MAR(p) models for whom confidence intervals for coefficients, model selection, and other inferential tools are well understood. In an ecological setting, we use mainly log-linear models because the MAR framework applies to log-abundances (Ives *et al.*, 2003).

In the last decade, other methods such as Convergent Cross-Mapping (CCM; Sugihara *et al.*, 2012) have been put forward as a new way to infer interactions between species, and alleviate problems due to the limitation of linear autoregressive models (although, as we say above and shall show later, MAR(p) models are log-linear, which makes them essentially power-law models).

In this article, we first evaluate the performance of MAR(p) models and compare it to CCM on a number of ecological examples for which CCM is currently thought to be more appropriate. We demonstrate that

somewhat harsh criticism of the Granger causality concept by Sugihara *et al.* (2012) may have been induced by nonstandard model selection and evaluation techniques. Using simpler model selection techniques, routinely used by statisticians (Lütkepohl, 2005), in order to infer lag order p of MAR(p) models as well as their parametric structure, we show that Granger causality techniques can in fact infer interactions surprisingly well in nonlinear cases. We then highlight intriguing parameter configurations and empirical case studies where Granger causality and Sugihara *et al.*’s convergent cross-mapping (CCM) either both fail or both work, which suggests that seemingly foreign causality concepts might in fact share some underlying mathematical similarities. We finally demonstrate that Granger causality / MAR(p) modelling can be scaled up to large interaction networks using appropriate model regularization techniques (LASSO-based).

Methods and models

In the following, we recall the basics of Granger causality concepts and MAR(p) modelling, which is the most common way (not the only one) to assess Granger causality. For completeness, we also present some common nonlinear alternatives to MAR(p) modelling which stays within the Granger causality purview in Appendix XX. We describe shortly thereafter convergent-cross mapping, which is implemented as well but takes a different approach to causal inference, based on dynamical systems theory and state-space reconstruction. We then describe the real datasets and numerical simulations that will be used for evaluating causal inference methods.

Causality concepts

Granger causality and MAR(p) implementation

$\mathbf{x} = (x_t)_{t \in [1:T]}$ Granger-causes $\mathbf{y} = (y_t)_{t \in [1:T]}$ \iff including x in a time series model for y improves in-sample prediction of y . In the MAR(p) framework, this translates into performing two time series autoregressions to explain time series y , one with only y and one with y and x :

$$y_t = \sum_{i=1}^L a_i y_{t-i} + \eta_t \quad (2)$$

$$y_t = \sum_{i=1}^L a_{1i} x_{t-i} + \sum_{i=1}^L a_{2i} y_{t-i} + \epsilon_t \quad (3)$$

Granger causality then occurs if $\sigma_\epsilon^2 < \sigma_\eta^2$. When more than two variables are considered, simple GC has to be differentiated from conditional GC. Conditional GC occurs whenever a third variable z is considered

and corrected for.

When fitting a MAR(p) model, we typically estimate conditional GC. For instance, let us consider a MAR(1) model (eq. 4) with 3 species

$$\mathbf{x}_t = \ln(\mathbf{N}_t), \quad \mathbf{x}_{t+1} = \mathbf{a} + \mathbf{B}\mathbf{x}_t + \mathbf{C}\mathbf{u}_t + \mathbf{e}_t, \mathbf{e}_t \sim \mathcal{N}_3(\mathbf{0}, \mathbf{\Sigma}) \quad (4)$$

so that its B (interaction) matrix is defined by

$$\mathbf{B} = \begin{pmatrix} b_{11} & b_{12} & b_{13} \\ b_{21} & b_{22} & b_{23} \\ b_{31} & b_{32} & b_{33} \end{pmatrix} \quad (5)$$

Here, whenever b_{12} is significantly different from zero, we have a causal influence $x_2 \rightarrow x_1|x_3$. The condition then becomes, in a general MAR(p) setting (according to eq. 7):

$$\exists b_{ij}^{(q)} \neq 0 \Leftrightarrow x_j \rightarrow x_i | (x_1, \dots, x_{j-1}, x_{j+1}, \dots, x_d) \quad (6)$$

Using centered data so that the intercept disappears, the MAR(p) model is defined as

$$\mathbf{x}_{t+1} = \sum_{q=1}^p \mathbf{B}^{(q)} \mathbf{x}_t + \mathbf{e}_t, \quad \mathbf{e}_t \sim \mathcal{N}_d(\mathbf{0}, \mathbf{\Sigma}) \quad (7)$$

where each time lag is indexed by q . This highlights immediately the high model dimensionality than be attained with high p order and high number of species. Conversely, direct GC between x_i and x_j is assessed through a bivariate autoregressive model for each (i, j) pair; and therefore considerably lower-dimensional model. Direct GC testing requires, however, some false discovery correction to attain meaningful statistical significance (REF). In the following, we use a Benjamini-Hochberg correction (REF).

We finish this overview of Granger causality in parametric MAR(p) model by a note to ecological modellers already familiar with the MAR(1) framework. In ecology, a popular formulation of the MAR(1) model (Ives *et al.*, 2003; Hampton *et al.*, 2013) assumes

$$\mathbf{x}_{t+1} = \mathbf{a} + \mathbf{B}\mathbf{x}_t + \mathbf{C}\mathbf{u}_t + \mathbf{e}_t, \mathbf{e}_t \sim \mathcal{N}(0, \mathbf{\Sigma}) \quad (8)$$

where \mathbf{x}_t is the log-abundance vector and \mathbf{u}_t is some abiotic forcing or control variable on which the log-abundance vector does not exert feedback. In these models, causality is *always* conditional to \mathbf{u}_t .

MAR(p) model fitting has been performed using the package **vars** in **R**. The presence of Granger causality was assessed by the statistical significance of the interaction matrix coefficients, and more directly using parametric significance tests for nested models. For pairwise Granger causality testing, we used the function **grangertest** in the R package **lmtest** which performs a Wald test for nested models. For conditional Granger causality testing, we use the function **causality** in package **vars** which provides F-tests for the nested models. Both tests and implementation provided similar answers when compared.

Convergent-cross mapping

Convergent cross-mapping (Sugihara *et al.*, 2012) relies on state-space reconstruction. We assume two time series $\mathbf{x} = (x_t)_{t \in [1:T]}$ and $\mathbf{y} = (y_t)_{t \in [1:T]}$. The presentation is adapted from Sugihara *et al.*'s articles and also Palus (2018). The attractor manifold M_X is constructed as a set of E -dimensional vectors $\tilde{\mathbf{x}}(t) = (x(t), x(t-\tau), x(t-2\tau), \dots, x(t-(E-1)\tau), \dots)$ for $t = 1 + (E-1)\tau$ to $t = T$. E is the embedding dimension. This set of vectors constitutes the reconstructed manifold. We now find the $E+1$ nearest neighbours of $\tilde{\mathbf{x}}(t)$ in M_X . Their time indices are denoted t_1, \dots, t_{E+1} . The reconstruction of y_t from M_X proceeds as follows:

$$\hat{y}(t)|M_X = \sum_{i=1}^{E+1} w_i y(t_i)$$

with $w_i = u_i / \sum_{j=1}^{E+1} u_j$, and $u_j = \exp\left(\frac{-d(\tilde{\mathbf{x}}(t), \tilde{\mathbf{x}}(t_i))}{d(\tilde{\mathbf{x}}(t), \tilde{\mathbf{x}}(t_1))}\right)$. The cross-map skill from X to Y is then measured by the correlation coefficient $\rho(\mathbf{x}, \hat{\mathbf{y}}|M_X) > 0$, which increases with the library size L if Y causes X . The surprising thing here being that prediction of Y by M_X is equivalent to Y causing X and not the other way around. Hence, to know if X causes Y , we look at $\rho(\mathbf{x}, \hat{\mathbf{x}}|M_Y)$.

The analyses have been performed in R [3.4.4 for me [CP]] using the package **rEDM** [version **XXX**][0.7.1 for me [CP]].

Conditional Granger causality in high-dimensional models

Full MAR(p) model fitting is highly impractical for high-dimensional models (e.g., $d > 5$ or $d > 10$ or even 100), unless very long time series are considered. This is because a $d \times d \times p$ dimensional model needs to be fitted to the data. For instance, let us imagine that a system involving 10 species with at least one cycling species is considered. To model it properly, we need $p = 2$ (long, regular cyclic behaviour in a one species AR(p) model requires $p > 1$). We then have 200 parameters in the interaction **B** matrix only. While it is possible to decrease this number by assuming some coefficients to be zero, even the MAR(1) model will have 100 elements, and therefore would be impossible to fit properly without a set of time series of length above 100. Preliminary simulations (Certain *et al.* 2017, Barraquand *et al.* Oikos 2018) suggest that a nonlinear,

stochastic ecological system of dimension 10 or 12 requires approximately times series of length 500 to 800 to be fitted properly without implementing additional constraints.

To deal with high-dimensionality for time series of long yet reasonable length (100 to 300 timesteps), we have considered two solutions:

- Pairwise Granger causality testing with false discovery rate correction (Benjamini-Hochberg).
- LASSO-penalized MAR(1) models with structured penalties, using the R package **simone**.

[description of both techniques here]

Simulated and real datasets of interacting species population dynamics

Real data: Veilleux's predator-prey cycles

The two first datasets that we consider are taken from Veilleux (1979) and have been analysed by other authors with mechanistic models which demonstrated two-way coupling (Jost & Ellner, 2000).

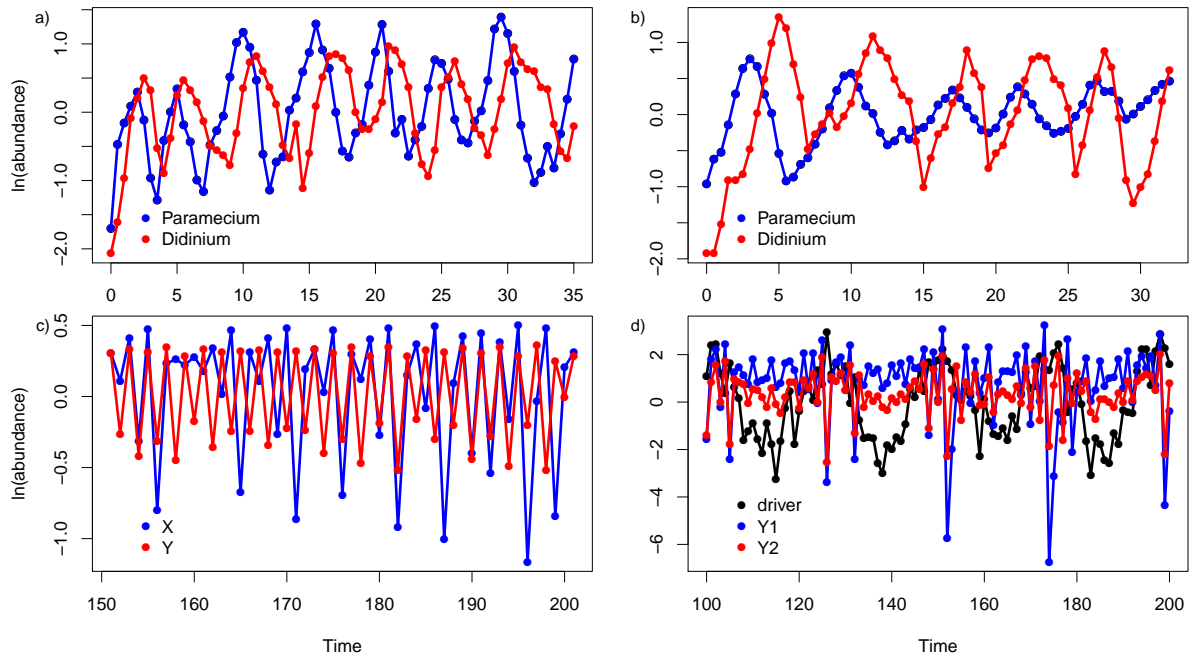


Figure 1: Time series of small-community models. The Veilleux's predator-prey data are shown in (a) (CC05) and (b) (CC0375); an example of the 2-species chaotic model is shown in (c) and an example of the model including a driver is shown in (d).

Deterministic chaos in two-species competition models

Here we use the same model as in Sugihara *et al.* (2012), a two-species discrete-time logistic competition model

$$x_{t+1} = x_t(3.8 - 3.8x_t - 0.02y_t) \quad (9)$$

$$y_{t+1} = y_t(3.5 - 3.5y_t - 0.1x_t) \quad (10)$$

The models are, as in Sugihara *et al.* (2012), in the chaotic regime, which constitutes a strong test of the log-linear MAR(p) framework. The only thing that is varied is the initial condition, which is taken at random 500 times. Although we acknowledge that “mirage correlations” can occur in some datasets, we aimed at reproducing a realistic sample of what this model can provide, as there are no justifications to take only specific initial conditions outside of illustration purposes. The sample size is taken to be $t_m = 300$ as in Sugihara *et al.* (2012).

Because a method that finds no interactions whenever absent is as important as one that finds interactions whenever they are present, we also consider the following deterministic “null competition” model:

$$x_{t+1} = x_t(3.8 - 3.8x_t - 0 \times y_t) \quad (11)$$

$$y_{t+1} = y_t(3.5 - 3.5y_t - 0 \times x_t) \quad (12)$$

We will evaluate both GC and CCM’s ability to find no interactions between these time series.

Two-species stochastic and nonlinear dynamics, including environmental drivers

First we consider a stochastic two-competition model, with Lotka-Volterra interactions in discrete time and a Ricker type of multispecies density-dependence.

$$N_{1,t+1} = N_{1,t} \exp(3 - 4N_{t,1} - 2N_{t,2} + \epsilon_{1,t}) \quad (13)$$

$$N_{2,t+1} = N_{2,t} \exp(2.1 - 0.31N_{t,1} - 3.1N_{t,2} + \epsilon_{2,t}) \quad (14)$$

This case was already investigated in Certain *et al.* (2018), but including an environmental driver on species 1. Then we consider a variant of this model adding an environmental driver u_t that has the same effect for

$$N_{1,t+1} = N_{1,t} \exp(3 + 0.5u_t - 4N_{t,1} - 2N_{t,2} + \epsilon_{1,t}) \quad (15)$$

$$N_{2,t+1} = N_{2,t} \exp(2.1 + 0.5u_t - 0.31N_{t,1} - 3.1N_{t,2} + \epsilon_{2,t}) \quad (16)$$

We consider, as in the deterministic case, the counterparts of the above models where the interspecific interactions are set to zero, i.e.

$$N_{1,t+1} = N_{1,t} \exp(3 + 0.5u_t - 4N_{t,1} - 0 \times N_{t,2} + \epsilon_{1,t}) \quad (17)$$

$$N_{2,t+1} = N_{2,t} \exp(2.1 + 0.5u_t - 0 \times N_{t,1} - 3.1N_{t,2} + \epsilon_{2,t}) \quad (18)$$

We run 500 simulations for each model.

Five- and ten-species interaction webs

[[We're not actually sure we're gonna do the 5-species model]]

We consider first the 5-species deterministic model considered by Sugihara *et al.* (2012), in a slightly modified Ricker-density-dependence version, which allowed to have non-negative equilibria for all initial conditions (unlike the initial logistic formulation whose trajectories frequently crossed zero, since this is an issue with the logistic map):

$$N_{t+1,1} = N_{t,1} \exp(4 - 4N_{t,1} - 2N_{t,2} - 0.4N_{t,3})$$

$$N_{t+1,2} = N_{t,2} \exp(3.1 - 0.31N_{t,1} - 3.1N_{t,2} - 0.93N_{t,3})$$

$$N_{t+1,3} = N_{t,3} \exp(0.12 + 0.636N_{t,1} + 0.636N_{t,2} - 2.12N_{t,3})$$

$$N_{t+1,4} = N_{t,4} \exp(3.8 - 0.111N_{t,1} - 0.111N_{t,2} + 0.131N_{t,3} - 3.8N_{t,4})$$

$$N_{t+1,5} = N_{t,5} \exp(4.1 - 0.082N_{t,1} - 0.111N_{t,2} - 0.125N_{t,3} - 4.1N_{t,5})$$

We consider a 10 species model which generalises the two-species Ricker competition to more species and more interaction types, with added stochasticity, and therefore represents a considerable challenge to interaction inference, due to the large quantity of potential false positives (many zero interactions) combined to both nonlinear dynamics and stochasticity. The dynamical equation can be written, in a logarithmic scale, as

$$\mathbf{n}_{t+1} = \mathbf{n}_t \circ \exp(\mathbf{r} + \mathbf{A}\mathbf{n}_t + \mathbf{e}_t), \mathbf{e}_t \sim \mathcal{N}(0, \sigma^2 \mathbf{I}) \quad (19)$$

where \mathbf{n} is the log-abundance, the error $\sigma^2 = 0.1$ and the interaction matrix is defined to be

$$A = \begin{pmatrix} -4 & -2 & -0.4 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ -0.31 & -3.1 & -0.93 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0.63 & 0.63 & -2.12 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ -0.11 & -0.11 & 0.13 & -3.8 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.5 & -2 & -2 & -0.4 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -0.31 & -3.1 & -0.93 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0.63 & 0.63 & -2.12 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -4 & -2 & -0.4 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -0.31 & -3.1 & -0.93 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.63 & 0.636 & -2.12 \end{pmatrix} \quad (20)$$

We use the same interaction matrix with Gompertz dynamics, and run 25 simulations over 500 time steps with different initial conditions.

We slightly modified this model to scale it up to 20 species. Its structure is still fairly modular (eq. 21)

$$B = \begin{pmatrix} b_{1,1} & b_{1,2} & b_{1,3} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ b_{2,1} & b_{2,2} & b_{2,3} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ b_{3,1} & b_{3,2} & b_{3,3} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ b_{4,1} & b_{4,2} & b_{4,3} & b_{4,4} & b_{4,5} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & b_{5,4} & b_{5,5} & b_{5,6} & b_{5,7} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & b_{6,5} & b_{6,6} & b_{6,7} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & b_{7,5} & b_{7,6} & b_{7,7} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{8,8} & b_{8,9} & b_{8,10} & b_{8,11} & b_{8,12} & b_{8,13} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{9,8} & b_{9,9} & b_{9,10} & b_{9,11} & b_{9,12} & b_{9,13} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{10,8} & b_{10,9} & b_{10,10} & b_{10,11} & b_{10,12} & b_{10,13} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{11,8} & b_{11,9} & b_{11,10} & b_{11,11} & b_{11,12} & b_{11,13} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{12,8} & b_{12,9} & b_{12,10} & b_{12,11} & b_{12,12} & b_{12,13} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{13,8} & b_{13,9} & b_{13,10} & b_{13,11} & b_{13,12} & b_{13,13} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{14,11} & b_{14,12} & b_{14,13} & b_{14,14} & b_{14,15} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{15,14} & b_{15,15} & b_{15,16} & b_{15,17} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{16,15} & b_{16,16} & b_{16,17} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{17,15} & b_{17,16} & b_{17,17} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{18,18} & b_{18,19} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{19,18} & b_{19,19} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{20,18} & b_{20,19} \end{pmatrix} \quad (21)$$

For the 20-species model, we also compare Ricker and Gompertz dynamics for 25 different simulations over 100 time steps, but in this case, coefficients are drawn from a random distribution (eq. 22 and eq. 23).

$$b_{i,j} = b_{min} + (b_{max} - b_{min})\beta(2, 2) \quad (22)$$

$$b_{min}, b_{max} = \begin{cases} [0.05, 0.1] & \forall i \neq j, B(1, 0.2) = 1 \\ [-0.2, -0.1] & \forall i \neq j, B(1, 0.2) = 0 \\ [-0.8, -0.3] & \forall i = j \end{cases} \quad (23)$$

For all datasets, real and simulated alike, the data are log-transformed before analysis.

Results

In each section, we apply both GC/MAR(p) modelling and CCM, except for high-dimensional datasets.

Real data: Veilleux's predator-prey cycles

Model selection of MAR(p) model by all information criteria selected a lag $p = 1$ for the CC05 dataset and a lag of 2 for the CCXXX dataset (Fig. 2). The p-values for the GC test (null hypothesis: “no GC”) demonstrate convincingly that the “no GC” hypothesis can be rejected, for both datasets (1).

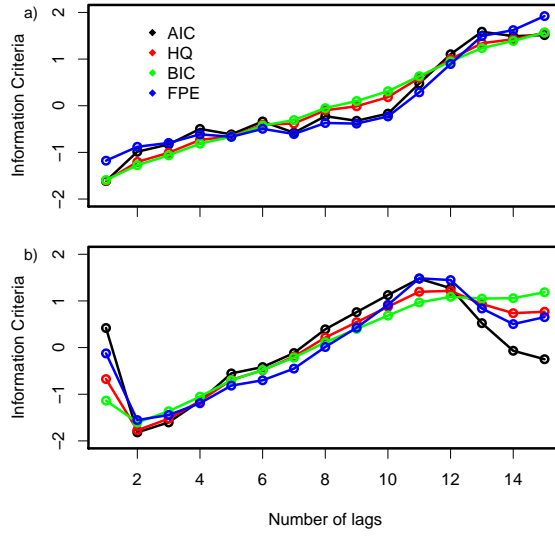


Figure 2: Results of model information criteria vs. lag order for the predator-prey data, for the two datasets.

Dataset	CC = 05	CC = 0.375
Lag p in VAR(p)	1	2
$1 \rightarrow 2$	2.79×10^{-11}	0.0409
$2 \rightarrow 1$	1.76×10^{-14}	0.0464

Table 1: P-values for H₀: No Granger causality between x and y .

CCM also demonstrate bi-directional causality, as demonstrated by the increase in $\rho(X, \hat{X}|M_Y)$ with library size L in both directions (Fig. 3).

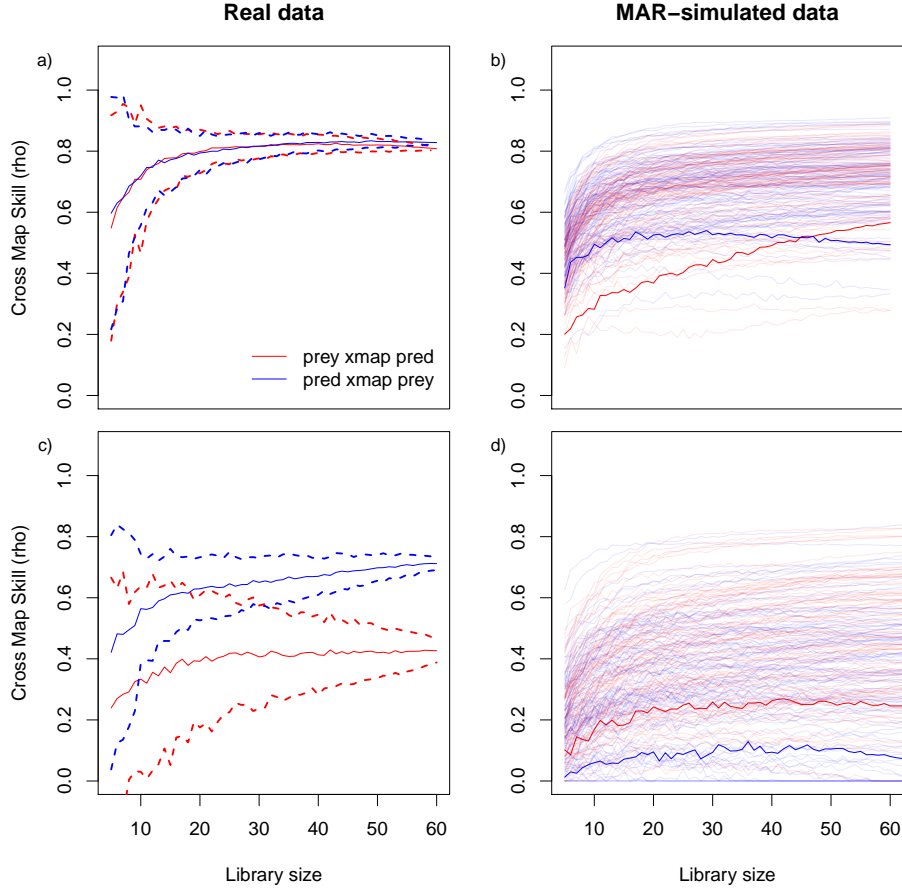


Figure 3: Convergent cross-mapping for Veilleux's CC05 dataset (a and b) and CC0.375 dataset (c and d). Dotted lines represent the confidence interval.

Deterministic chaos in two-species competition models

In the 2-species chaotic competition model high-order lags tend to be selected (Fig. 12) despite the single timelag considered in the simulation model (i.e., higher nonlinearity is identified as high-order lags). Despite this potential overparameterization, the GC tests show that causality is detected for most timelags (including the optimal one, $p=7$) whenever causality is present. Further, the tests are not able to reject the null hypothesis of no GC when GC is not present (Fig. 4).

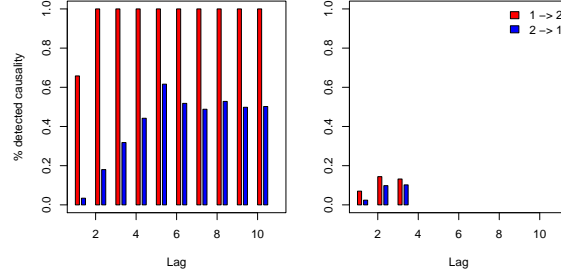


Figure 4: Proportion of detected Granger-causality, at the 10% significance threshold, over 500 chaotic simulations with (left) and without (right) actual interactions between species, depending on the number of lags taken into account. For the simulations without competition, time series tended to be too correlated for lags over 3 to allow estimates.

	With interactions	Without interactions
	GC/CCM	GC/CCM
$1 \rightarrow 2$	100%/100% ($\phi = 1$)	14%/0% ($\phi = 0.74$)
$2 \rightarrow 1$	51%/41% ($\phi = 0.35$)	15%/5% ($\phi = 0.02$)

Table 2: Proportion of simulations with significant Granger-causality or CCM between x and y, at the 10% threshold [**We need to talk about ϕ**]

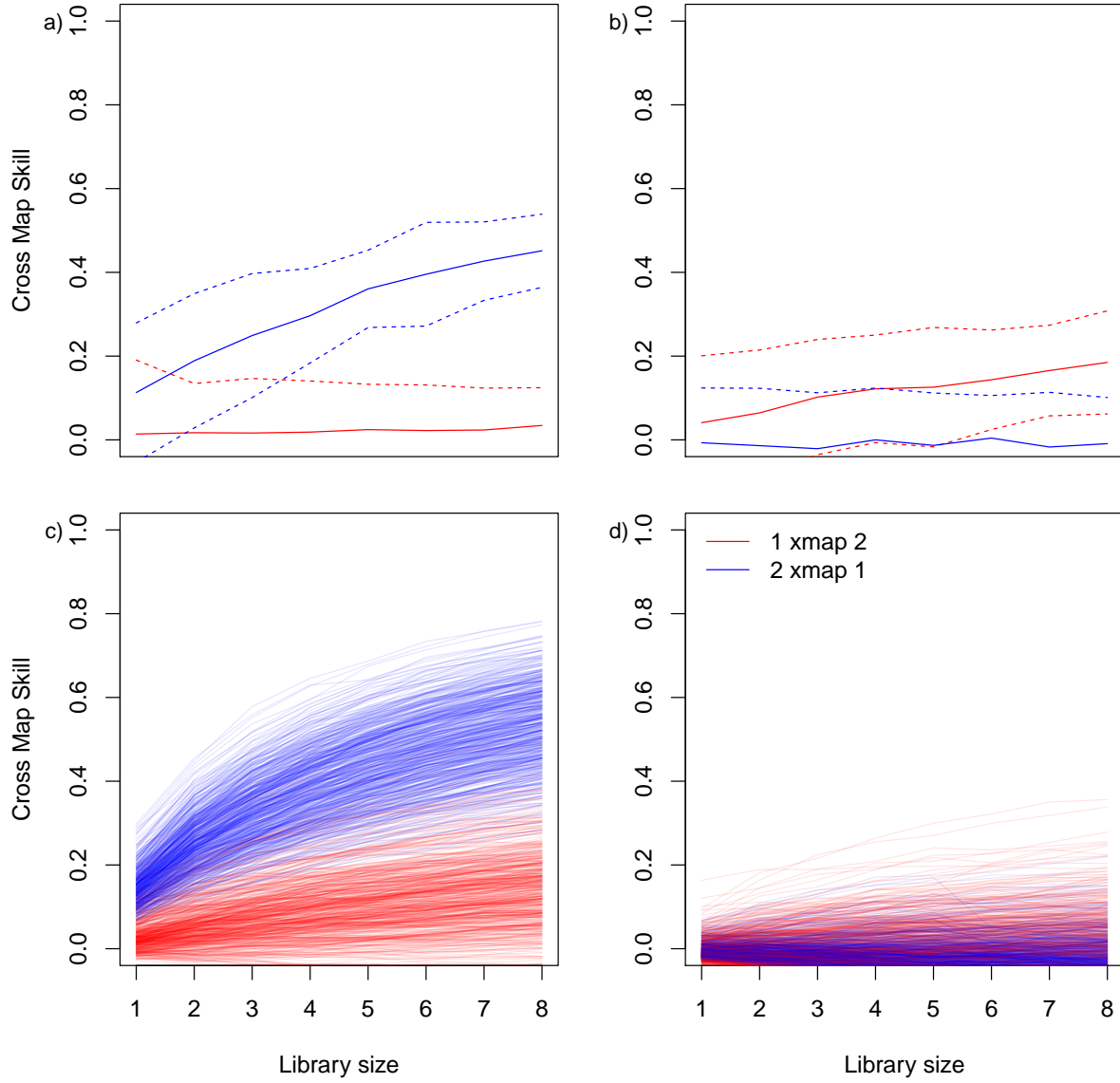


Figure 5: Convergent-cross mapping on simulated deterministic data, with (left) and without (right) competition between the two species[move to Appendix?]

Two-species stochastic and nonlinear dynamics forced by an environmental driver

	With interactions	Without interactions
	GC/CCM	GC/CCM
$1 \rightarrow 2$	97%/45% ($\phi = 0.07$)	0%/0% ($\phi = 1$)
$2 \rightarrow 1$	100%/100% ($\phi = 0.99$)	0%/0% ($\phi = 1$)

Table 3: Proportion of simulations with significant Granger-causality or CCM between x and y, at the 10% threshold, over 500 simulations, for a stochastic model without driver

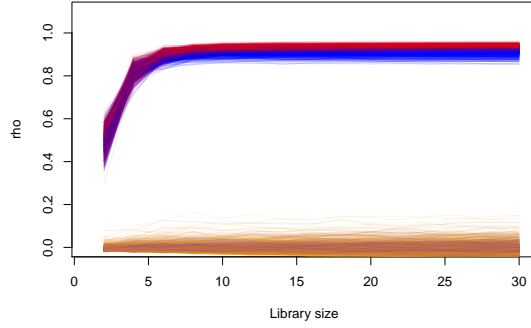


Figure 6: Convergent-cross mapping on simulated stochastic data, with (red, blue) and without (orange, purple) competition between the two species, over 500 simulations

Without driver The model selected by BIC had a lag of $p = 3$ timesteps.

Direction	P-values
$1 \rightarrow 2$	0.004054
$2 \rightarrow 1$	0.00000
Direction	P-values
$1 \rightarrow 2$	0.03859
$2 \rightarrow 1$	0.00067

Table 4: P-values for H_0 : No Granger causality between x and y . Top: when the simulated model has non-zero interspecific interaction coefficients; bottom when interspecific interactions are zero. The potential misleading p-values are highlighted in bold [need to consider more initial conditions and summarize that info] [Will do, I had forgotten this part. Wondering if we should use the surrogates with GC too. Seems fair.]

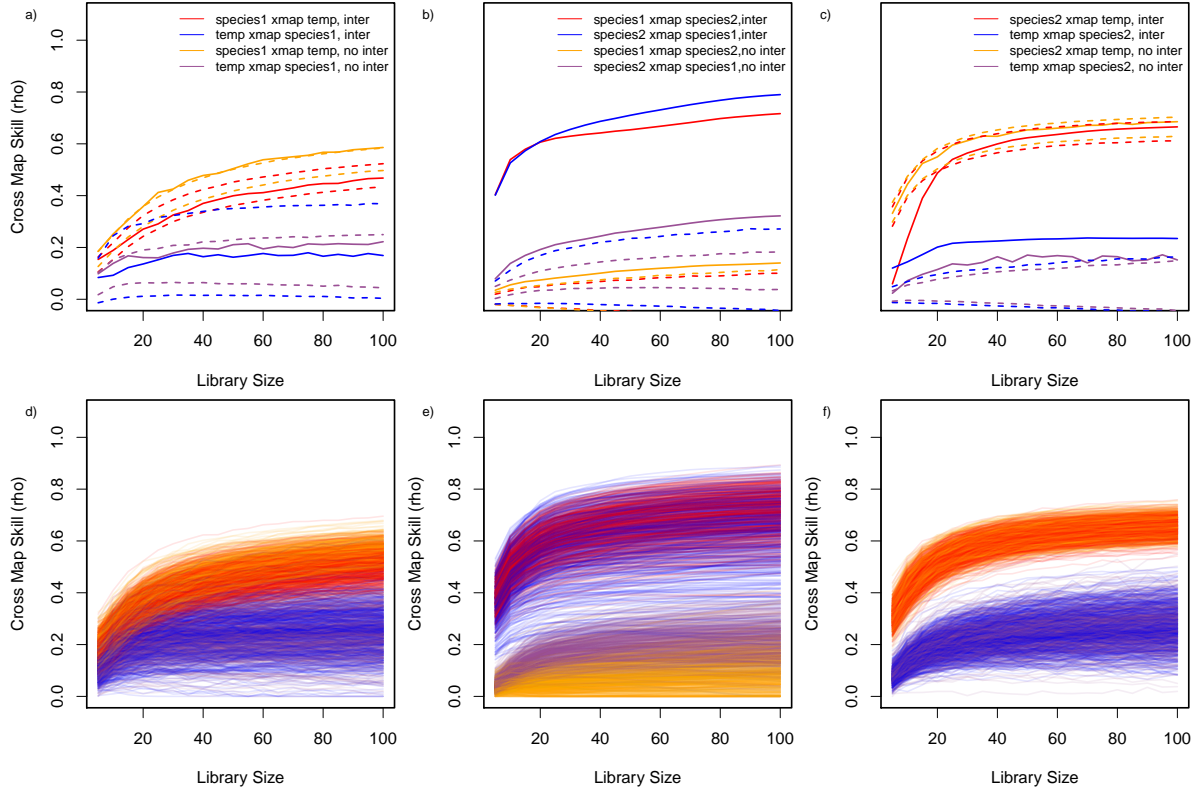


Figure 7: Convergent cross-mapping for the two species forced by an environmental driver (denoted as temp), when interactions are present (blue, red) and when interactions are absent (purple, orange), for 500 simulations. Dashed lines indicate the 10% interval for rho-values obtained from surrogate values.

Larger interaction webs

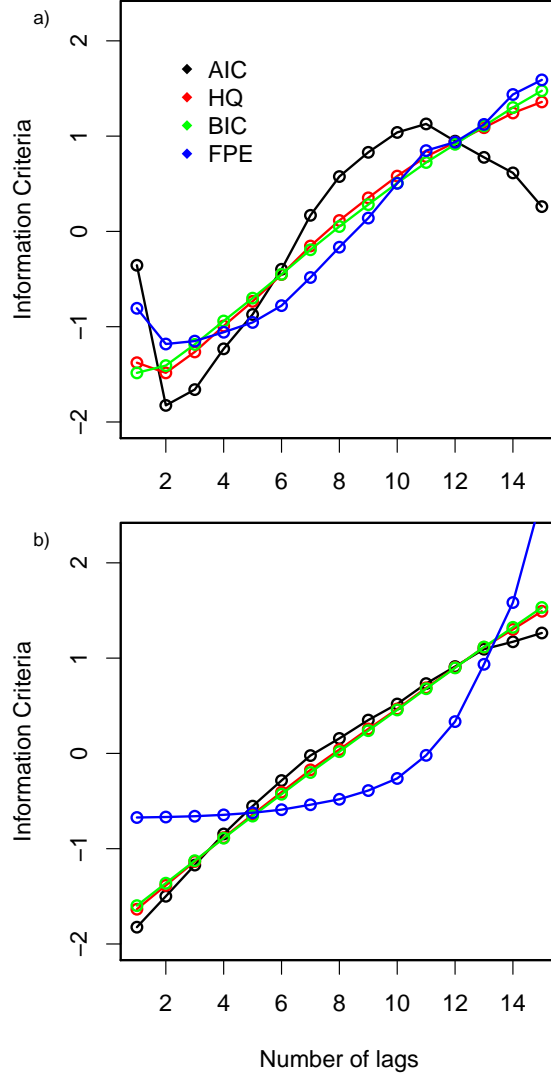
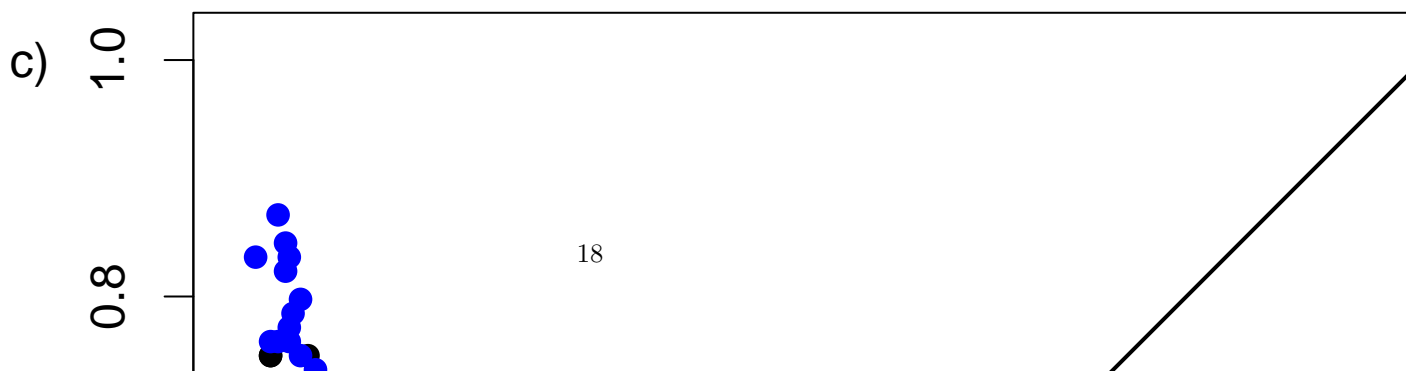
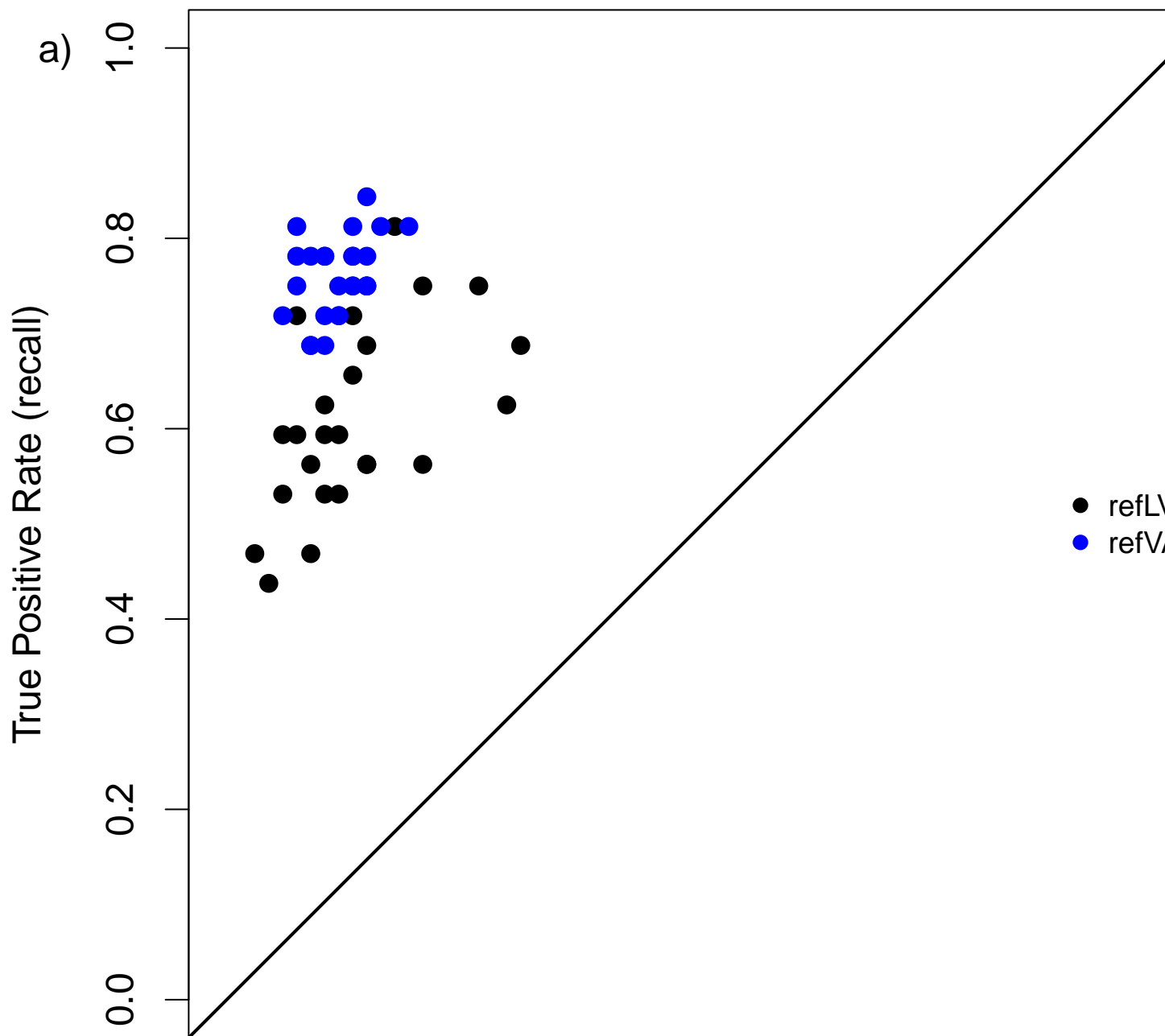


Figure 8: Lag order selection for the 10-species (a) and [one of the] 20-species stochastic community model (b).

Here we report the results of analyses for 10 and 20 species modular interaction webs (5 species as in Sugihara et al. done in Supplement SXX). Lag order selection revealed that low-order $MAR(p)$ models were selected (Fig. 8), hence we have focused on $MAR(1)$ models. The high-dimensional $S \times S$ $MAR(1)$ models include clustering (see Appendix SXX) because the basic LASSO-penalized $VAR(1)$ models poorly identify modular interactions webs (REFs).

ROC Simone



Discussion

We have shown above that MAR(p) modelling and Granger causality testing are fairly robust to nonlinearities in ecological dynamics, when applied on the appropriate logarithmic-abundance scale, and combined with model selection by information criteria. This is true for many nonlinear simulation models, including deterministic chaos. This confirms and extends findings from an investigation of the robustness to nonlinearities of log-linear MAR(1) models (with p restricted to 1 lag, Certain et al. 2017 MEE). Comparison to the CCM framework by Sugihara et al. further revealed that CCM and MAR(p)/Granger causal modelling can in fact - surprisingly - yield relatively similar results in nonlinear and stochastic dynamical systems of interacting species. Evidence for this comes from highly nonlinear systems for which CCM and GC both infer interactions, but also from cases where both seem to fail (two competing species forced by a very similar environmental driver). Therefore, both Granger causality and CCM might yield reasonable inferences on similar datasets.

Moreover, we use here false discovery rates and regularized models (i.e., LASSO-penalized MAR(1) models developed for modular interaction networks, Chiquet XXXX) to tackle relatively-high dimensional models (5, 10 and 20 species). This allows to better infer Granger causality in these contexts that, we surmise, will be most exciting to ecologists working on interacting species using community-level data. The results demonstrate that simple pairwise Granger causality (i.e., using 2×2 MAR(p) models) are almost as good as the penalized MAR(1) models in finding the interaction network.

We elaborate on these results and possible explanations below. Sugihara *et al.* (2012) suggested that Granger causality would work well for simulated (log)-linear systems while CCM would work well for nonlinear dynamical systems. Reality, however, is less clear-cut. We reported above on results where even deterministic chaos can be identified by MAR(p) models / GC inference. But the converse is also true: some log-linear cases can also be well-identified by CCM, which relies upon the possibility to reconstruct an attractor in state space, which seems to work even in those noisy cases. Of course, as CCM has been developed specifically from nonlinear dynamical systems theory (and relies upon state-space reconstruction of chaotic models), it seems more appropriate for highly nonlinear and weakly stochastic cases, while MAR(p) models are best performers in weakly nonlinear and more stochastic situations. Nonetheless, it was surprising to see how well MAR(p) models can perform in deterministic chaos in a number of cases, unlike what could have been expected from the previous study of Sugihara *et al.* (2012). Though we clearly acknowledge that some chaotic scenarios may inevitably lead to a difficulty in GC inference.

Several recent attempts to perform nonlinear inference of interactions support our findings. Suzuki *et al.* (2017) use stochastic GLV models and a model selection algorithm derived from Fisher & Mehta (2014), and

even though they use the S-map, because their evaluation is based on prediction, they actually perform a nonlinear Granger inference. . The neuroscience, gene regulation networks and related dynamical systems literature is awash with nonlinear GC inferences, often confirmed by simulations of nonlinear stochastic systems (Marinazzo *et al.*, 2008; Yang *et al.*, 2017) [some more examples here]. Hence there is fairly good evidence that either log-linear (power-law) or nonlinear GC inference is possible for nonlinear stochastic systems of interacting species.

Here, we would like to go back to the heart of the issue that Sugihara *et al.* (2012) highlighted, causality reversion in nonlinear dynamical systems. The standard Granger causality holds that whenever a model $Y_{t+h}|(Y_t, X_{t \in A_t})$ better predicts the observed time series (y_t) than a model $Y_{t+h}|(Y_{t \in A_t})$, then x is causal for y . CCM instead holds that whenever $\rho(x, \hat{x}|M_Y)$ increases strongly with the library size L use to reconstruct x from the shadow manifold M_Y . It seems that in the latter method, x causes y whenever knowledge about y can be used to reconstruct x . However, verbal reasoning is treacherous there. To determine whether x causes y :

- GC compares knowledge about Y_t vs. knowledge about X_t, Y_t in prediction of Y_{t+h}
- CCM compares knowledge about Y_t vs. no knowledge about Y_t in prediction of X_t .

Using a standard autoregressive model, the equivalent of a CCM test $x \rightarrow y$ would be predicting X_t by a model $X_t|Y_t$ vs X_t . There is no conditionality upon past X_t values in the prediction step of the algorithm. Thus there is no causality reversion that is intrinsic to nonlinear dynamic testing: GC and CCM are simply two different types of causality testing that are based upon *different assumptions on the conditioning set and ways to select models*. We therefore conclude for these methods and concepts to work relatively similarly, they must share some underlying similarities that not yet evident to theoretical and statistical ecologists. More mathematical research on the possible connections and differences between these methods is obviously needed to better see in which scenarios each should be favored.

Based on our simulations, complemented with those of the neuroscience literature (Ding *et al.*, 2006; Chen *et al.*, 2006; Barnett & Seth, 2014; Marinazzo *et al.*, 2008), we suggest that Granger causality, in its log-linear (this paper) or nonlinear varieties (Marinazzo *et al.*, 2008; Suzuki *et al.*, 2017), is appropriate to infer ecological interactions. CCM is another interesting method to infer interactions. Although it has been shown that some scenarios like seasonal forcing might render interaction inference difficult (Cobey & Baskerville, 2016), we think that as always details of implementation are important, thus it is important not to disqualify a method in the early stages of its development.

From an almost sociological viewpoint, we conclude that recommending to abandon established statistical methods like GC, or linear modelling after transformation more generally, in favor of promising yet not fully

tested statistical methods may not always help ecological science. More fruitful methodological development might highlight the pros and cons of new developments in statistical inference under a broad range of simulated scenarios.

From a statistical perspective, looking at the various implementations of GC and CCM, it seems that the hardest methodological choice to make is almost invariably not the type of functional form or embedding (linear, nonlinear, etc.) but the conditioning set, i.e. the information that is considered to be known for the prediction (Eichler, 2013). Strategies to better understand how to choose the conditioning set when doing causal inference will be, we believe, a very important feature of ecological interaction inference for the years to come.

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Appendices, Supplements

Transfer entropy and nonlinear Granger causality

Transfer entropy can be defined as

$$\mathcal{T}_{x \rightarrow y|z} = H(\mathbf{y}^{t_m+1} | \mathbf{y}^{t_m}, \mathbf{z}^{t_m}) - H(\mathbf{y}^{t_m+1} | \mathbf{y}^{t_m}, \mathbf{x}^{t_m}, \mathbf{z}^{t_m})$$

where $\mathbf{y}^{t_m+1} = (y_2, \dots, y_{t_m+1})$ and $\mathbf{y}^{t_m} = (y_1, \dots, y_{t_m})$. The quantity $H(x|y) = H(x, y) - H(y)$ is a conditional entropy, defined with $H(x)$ the Shannon entropy. It has then been shown that the Granger causal measure $\mathcal{G}_{x \rightarrow y|z} = \ln(\frac{\sigma_y^2}{\sigma_\epsilon^2})$ where the residuals errors are take from eqs. 2 can be generalized to $\mathcal{T}_{x \rightarrow y|z}$. In the linear case, Barnett *et al.* (2009) proved that $\mathcal{G}_{x \rightarrow y|z} = 2\mathcal{T}_{x \rightarrow y|z}$, so that Granger causality through MAR(1) modelling is a special case of causality defined through transfer entropy.

In general, any method which evaluates whether adding a new time series \mathbf{x} to a dynamical system for variables y_1, \dots, y_n improves prediction of y_i can be defined as a generalised GC method $x \rightarrow y_i | (y_1, y_2, \dots, y_{i-1}, y_{i+1}, \dots, y_n)$. Quite a number of nonlinear Granger causality inference techniques then fall within this category (e.g., Marinazzo *et al.*, 2008; Paluš, 2008).

Example of 2-species stochastic model

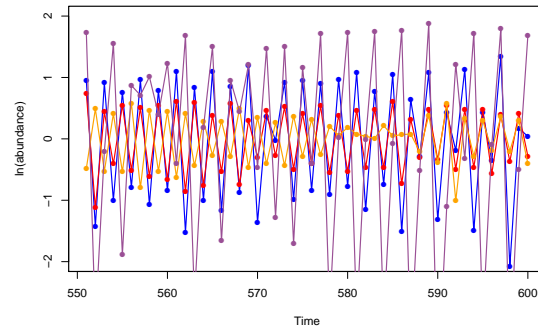


Figure 10: 2-species model with (blue, red) and without (purple, orange) competition

Effect of log-transformation on CCM

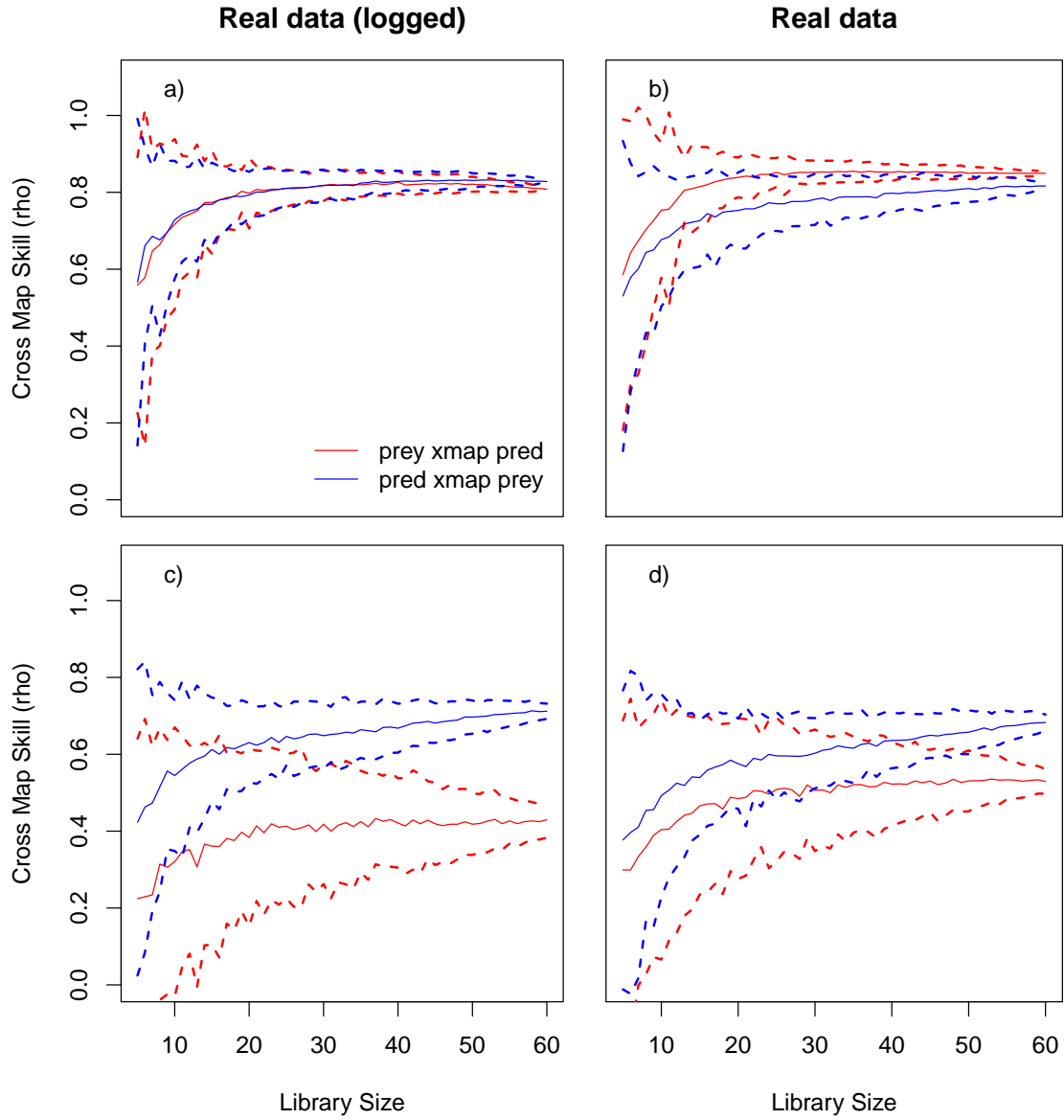


Figure 11: Convergent Cross-Mapping with (left) and without (right) \ln -transform of the data for the Veilleux dataset

Lag-choice for the deterministic model

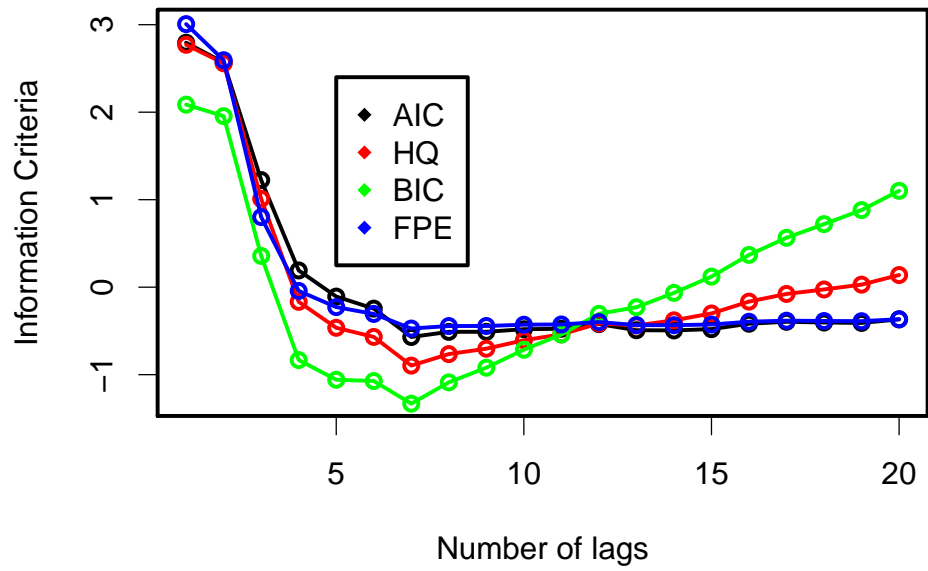


Figure 12: Results of model information criteria vs. lag order for the simulated deterministic competition data