Analysing Conceptual Climate Models with Monte Carlo Basin Bifurcation Analysis (MCBB)

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Based on M. Gelbrecht, J. Kurths, F. Hellmann: “Monte Carlo Basin Bifurcation Analysis”
Monte Carlo basin bifurcation analysis

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Abstract

Many high-dimensional complex systems exhibit an enormously complex landscape of possible asymptotic states. Here, we present a numerical approach geared towards analyzing such systems. It is situated between the classical analysis with macroscopic order parameters and a more thorough, challenging for high-dimensional systems. Further, for high-dimensional systems, often one is also more interested in classes of asymptotic states such as synchronized versus unsynchronized states of oscillator networks or states that share a common symmetry. Here, we explain in section 2.4 a number of paradigmatic examples that showcase the wide variety of possible realizations. A generalized Stuart–Landau oscillator network, each exhibiting a complex behavior, is used. For such systems, the classical analysis with macroscopic order parameters is not sufficient and the study of the basin stability is often challenging for high-dimensional systems. Thus, we can regard MCBB as a way to interpolate between detailed studies of asymptotic states and only tracking changes in a single order parameter or the climate system. Our machine learning approach, Monte Carlo Basin Bifurcation Analysis (MCBB), allows for tracking changes in asymptotic structure on the one hand, and statistical physics using specialized order parameters to study the macroscopic behavior at the other end. The method is available to use as a package for the Julia programming language.

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Motivation

- **Multistability** is a universal phenomenon of complex systems.
- Magnetism, human brain, gene expression networks, human perception, power grids, climate systems and many more exhibit multistable regimes.

- Volume of the basin of attraction often interesting as well.
Motivation

- For high-dimensional systems a traditional bifurcation analysis is often challenging.
- Often one is also interested in classes of asymptotic states instead of every single possible asymptotic state.

**Aim:**

- Fill gap between thorough bifurcation analysis and macroscopic order parameters.
- Learn classes of similar attractors that collectively have the largest basin of attraction.
- Understand how their *basin volumes change as a function of the parameters*.
- Get insights into the dynamics of these classes of asymptotic states.
- Apply it to climate dynamics.
Method

• **Idea:**
  • Combine a sampling based approach with a clustering analysis
  • Don’t compare the high-dimensional trajectory tails with each other directly but with per-dimension measures
Algorithm

Given:

- system $\dot{x} = F(x, t; p)$
  or $x_{n+1} = F(x_n, x_{n-1}, \ldots; p)$
- with system dimension $N_d$
- A set of $N_m$ statistics $\{S_i\}$ on the components $\mathbb{R}^{N_t} \to \mathbb{R}$ (e.g. mean and variance)
- Distribution $U_{IC}$ of the initial conditions and parameters $U_p$

sample $N$ initial conditions and $N$ parameters from $U_{IC}$ and $U_p$

for every sample $i \in [1, N]$

- solve system for a long trajectory, only save the tail $x(t; p)$

for every system dimension $i_d \in [1, N_d]$ and for every statistic $i_m \in [1, N_m]$

- compute matrix of statistics $S_{i, i_d, i_m} = S_i(x_{i_d})$

Obtained: $N \times (N_d \times N_s)$ - matrices $S_i$

compute $N \times N$ distance matrix $D$ of all $S_i$ to each other

Density-based clustering of $D$ (e.g. DBSCAN)

analyse cluster memberships and measures for each cluster dependent on $p$
## Algorithm

**Given:**

- System \( \dot{x} = F(x, t; p) \)
  - or \( x_{n+1} = F(x_n, x_{n-1}, \ldots; p) \)
  - with system dimension \( N_d \)
- A set of \( N_m \) statistics \( \{S_i\} \)
  - on the components \( \mathbb{R}^{N_d} \rightarrow \mathbb{R} \)
  - (e.g. mean and variance)
- Distribution \( U_{IC} \)
  - of the initial conditions and parameters \( U_p \)

**Sample** \( N \) initial conditions and \( N \) parameters from \( U_{IC} \) and \( U_p \)

**For every sample** \( i \in [1, N] \)

- Solve system for a long trajectory, only save terminal position \( x_N \)
  - for every system dimension \( i_d \in [1, N_d] \)
  - compute matrix of statistics \( S_{i_d, i_m} \)

**Obtained:** \( N \times (N_d \times N_s) \) - matrices \( S_i \)

**Compute** \( N \times N \) distance matrix \( D \) of all \( S_i \) to each other

**Density-based clustering of** \( D \) (e.g. DBSCAN)

**Analyse** cluster memberships and measures for each cluster dependent on \( p \)

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**Note:** More detailed information in the paper [https://doi.org/10.1088/1367-2630/ab7a05](https://doi.org/10.1088/1367-2630/ab7a05)
Software Implementation: MCBB.jl

- Open Source software package MCBB.jl available
- Julia lang, easy to read and write, fast programming language
- Excellent state-of-the-art differential equations solvers (thanks to DifferentialEquations.jl)

GitHub repository

https://github.com/maximilian-gelbrecht/MCBB.jl

Documentation

https://maximilian-gelbrecht.github.io/MCBB.jl/dev/
Applications

- MCBB is a modular, flexible method suitable for many different kinds of mid- to high-dimensional complex systems
- Maps, ODEs, ...

**Examples**
- Dodds-Watts model of social and biological contagion
- Kuramoto network
- Stuart-Landau oscillator network
- conceptual climate models (work in progress)
- modified Lorenz 96 model (here)

\[ \text{paper} \]
Application: Dodds Watts model

- Dodds-Watts model of social and biological contagion
- Generalisation of SI(RS) models from epidemiology
- Population with N Individuals that can be either Susceptible, Infected or Recovered
- Dodds-Watts model introduces a dosage memory into these models (all details see Dodds, Watts [arXiv:1705.10783](https://arxiv.org/abs/1705.10783))
Application: Dodds Watts model - MCBB results

- Area in the plot corresponds to the basin volume

- Additional tools to identify the dynamics of the individual classes of the asymptotic states in the paper / library

- Here, coexistence of states where the population is fully healthy (green), only some individuals are infected (red) and fully infected (blue)
Application: Lorenz 96

- 1-Layer Lorenz 96 model coupled to a simple EBM
- add an additional “wiggle” to the EBM to invoke more stable states than the regular cold / warm state
- add noise -> SDE

\[ dX_k = \left( -X_{k-2}X_{k-1} + X_{k+1}X_{k+1} - X_k + F \right)dt + \sigma_X dW \]

- Lorenz 96
- Noise

\[ dF = \left( EBM(X, F) + A \cdot \sin(\omega(F - F_0)) \right)dt + \sigma_{EBM} dW \]

- Additional Wiggle
- Noise
Application: Lorenz 96

\[ \sigma_{EBM} = 0 \]

\[ \sigma_{EBM} \text{ large} \]

- Sinus wiggle introduces many additional stable states
- For large noise amplitudes only the “deepest” states in the EBM are relevant and the sinus-wiggle is not important anymore
- Further analysis with MCBB possible (and also experiments with two parameters)