`pomp`: an R package for time series analysis using POMP (Partially Observed Markov Process) models

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- A platform supporting model development, statistical methodology development, and data analysis, for nonlinear non-Gaussian models.
- New methods have enabled previously infeasible analysis:
  - iterated filtering (`mif`)
  - particle Markov chain Monte Carlo (`pmcmc`)
  - approximate Bayesian computation (`abc`)
- A cost of generality: pomp has focused on flexible computational tools, such as sequential Monte Carlo (SMC), which are exponentially costly in the state dimension.

rprocess, dprocess, rmeasure, dmeasure

- A pomp model is defined by user-specified functions.
- **Plug-and-play** inference algorithms can be written in terms of the model functions
  - rprocess: simulates the latent Markov process.
  - rmeasure: simulates the measurement model.
  - dmeasure: evaluates the measurement model density.
- Some methods, such as expectation-maximization (EM) and standard MCMC algorithms, also require dprocess. This is problematic for models more easily characterized via simulation algorithms.

Categories of POMP methodologies

(a) Plug-and-play

	Frequentist	Bayesian
Full information	iterated filtering (`mif`)	PMCMC (`pmcmc`)
Feature-based	nonlinear forecasting (`nlf`) probe matching & synthetic likelihood (`probe.match`)	ABC (`abc`)

(b) Not plug-and-play

	Frequentist	Bayesian
Full information	EM and Monte Carlo EM Kalman filter	MCMC
Feature-based	Trajectory matching (`traj.match`) extended Kalman filter Yule-Walker equations	

Systems studied using pomp

- Disease ecology: cholera, dengue, influenza, malaria, measles, pneumonia, polio, rabies.
- Population ecology: Nicholson's blowflies.
- finance: stochastic volatility models.