Fast and Efficient Bayesian Analysis of Structural Vector Autoregressions Using the R Package bsvars (Version 3.2)

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Abstract

The R package **bsvars** provides a wide range of tools for empirical macroeconomic and financial analyses using Bayesian Structural Vector Autoregressions. It uses frontier econometric techniques and C++ code to ensure fast and efficient estimation of these multivariate dynamic structural models, possibly with many variables, complex identification strategies, and non-linear characteristics. The models can be identified using adjustable exclusion restrictions and heteroskedastic or non-normal shocks. They feature a flexible three-level equation-specific local-global hierarchical prior distribution for the estimated level of shrinkage for autoregressive and structural parameters. Additionally, the package facilitates predictive and structural analyses such as impulse responses, forecast error variance and historical decompositions, forecasting, statistical verification of identification and hypotheses on autoregressive parameters, and analyses of structural shocks, volatilities, and fitted values. These features differentiate **bsvars** from existing R packages that either focus on a specific structural model, do not consider heteroskedastic shocks, or lack the implementation using compiled code.

Keywords: Bayesian inference, Structural VARs, Gibbs sampler, exclusion restrictions, heteroskedasticity, non-normal shocks, forecasting, structural analysis, R.

1. Introduction

Since the publication of the seminal paper by Sims (1980) Structural Vector Autoregressions (SVARs) have become benchmark models for empirical macroeconomic analyses. Subsequently, they have found numerous applications in other fields and are now indispensable in everyday work at central banks, treasury departments and other economic governance institutions, as well as in finance, insurance, banking, and economic consulting.

The great popularity of these multivariate dynamic structural models was gained because they incorporate the reduced and structural forms into a unified framework. On the one hand, they capture the essential properties of macroeconomic and financial time series such as persistence, dynamic effects, system modelling, and potentially time-varying conditional variances. On the other hand, they control for the structure of an economy, system, or market through the contemporaneous effects and, thus, they identify contemporaneously and temporarily uncorrelated shocks that can be interpreted structurally. All these features make it possible to estimate the dynamic causal effects of the shocks on the measurements of

interest reliably. These effects are interpreted as the propagation of the well-isolated and unanticipated cause – a structural shock – in the considered system of variables throughout the predictable future.

This flexibility comes at a cost of dealing with local identification of the model, sharply growing dimension of the parameter space with the increasing number of variables, and the estimation of latent variables. Bayesian inference provides original solutions to each of these challenges often deciding on the feasibility of the analyses with a demanded model including many variables, conditional heteroskedasticity, and sophisticated identification of the structural shocks. In this context, Markov Chain Monte Carlo methods grant certainty of reliable estimation thanks to simple convergence diagnostics but they might incur substantial computational cost.

The paper at hand and the corresponding package **bsvars** by Woźniak (2024) for R (R Core Team 2021) provide tools for empirical macroeconomic and financial analyses using Bayesian SVARs. It addresses the considered challenges by choosing a convenient model formulation, applying frontier econometric and numerical techniques, and relying on compiled code written using C++ to ensure fast and efficient estimation. Additionally, it offers a great flexibility in choosing the model specification and identification pattern, modifying the prior assumptions, and accessing interpretable tabulated or plotted outputs. Therefore, the package makes it possible to benefit from the best of the two facilities: the convenience of data analysis using R and the computational speed using pre-compiled code written in C++.

More specifically, the package uses the SVAR models featuring a standard reduced form VAR equation following Bańbura, Giannone, and Reichlin (2010) (see also Woźniak 2016) and a structural equation linking the reduced form error term to the structural shocks via the structural matrix as in Lütkepohl, Shang, Uzeda, and Woźniak (2024) and Chan, Koop, and Yu (2024). The normal prior distribution for the autoregressive parameters implements the interpretability of the Minnesota prior by Doan, Litterman, and Sims (1984) by centring it around the mean that reflects unit-root nonstationarity or stationarity of the variables with an adjustable level of shrinkage depending on the equation and exhibiting exponential decay with the increasing autoregressive lag order. The prior distribution for the structural matrix is generalised-normal by Waggoner and Zha (2003a) which preserves the shape of the likelihood function (see Woźniak and Droumaguet 2015). Both of these priors are combined with the flexible three-level equation-specific local-global hierarchical prior distribution for the estimated level of shrinkage as in Lütkepohl *et al.* (2024) improving the model fit. The estimation of the level of shrinkage was shown to substantially improve forecasting performance of VAR models by Giannone, Lenza, and Primiceri (2015). Additionally, these specification choices lead to an efficient equation-by-equation Gibbs sampler for the posterior distribution of the autoregressive and structural parameters proposed by Chan *et al.* (2024) and Waggoner and Zha (2003a) respectively.

All the structural models in the **bsvars** package can be identified using highly adaptable exclusion restrictions proposed by Waggoner and Zha (2003a) and use the structural matrix sign normalisation by Waggoner and Zha (2003b). However, one might also choose to include additional sources of identification through heteroskedasticity following the ideas by Rigobon (2003) or by non-normal shocks as proposed by Lanne and Lütkepohl (2010). Therefore, the package offers a range of models for structural shocks conditional variance including a homoskedastic model with time-invariant variances. The list of heteroskedastic specifications is opened by Stochastic Volatility (SV) model in two versions: non-centred as in Lütkepohl

Figure 1: The hexagonal package logo features an impulse response that can be fully reproduced using the **bsvars** package following a script available at: github.com/bsvars/hex/blob/main/bsvars/bsvars.R

et al. (2024) and centred used by Chan *et al.* (2024), and is followed by the Markov-switching heteroskedasticity (MSH) model proposed by Brunnermeier, Palia, Sastry, and Sims (2021). The implementations of the MSH models follows that by Woźniak and Droumaguet (2015) in two versions: with stationary Markov process and its sparse version that facilitates the estimation of the number of states and non-parametric interpretations. Similarly, models with non-normal shocks are implemented in three versions including Student-t distributed shocks proposed by Lanne, Meitz, and Saikkonen (2017), and those following the normal mixture (MIX) model: with a finite number of components as in Frühwirth-Schnatter (2006) and in its sparse representation serving as an approximation of a non-parametric infinite mixture inspired by Malsiner-Walli, Frühwirth-Schnatter, and Grün (2016).

The R package **bsvars** implements a wide range of tools for structural and predictive analyses. The former encompasses the methods comprehensively revised by (Kilian and Lütkepohl 2017, Chapter 4: SVAR Tools) and include the impulse response functions, forecast error variance decompositions, historical decompositions, as well as the basic analysis of fitted values, structural shocks, conditional standard deviations and regime probabilities for MSH and MIX models. The predictive analysis includes Bayesian forecasting implemented through an algorithm sampling from the predictive density of the unknown future values of the dependent variables, and conditional forecasting of a number of variables given other variables' projections. Methods `summary()` and `plot()` support the user in the interpretations and visualisation of such analyses.

A distinguishing feature of the package are the Bayesian model diagnostic tools for the verification of identification and hypotheses on autoregressive parameters using posterior odds ratios. The posterior odds for hypotheses expressed as sharp restrictions on parameters are computed using Savage-Dickey Density Ratios (SDDRs) by Verdinelli and Wasserman (1995). The SDDRs representing Bayes factors are reliable, precisely estimated, and straightforward to compute once the posterior sample is available. As shown by Lütkepohl and Woźniak (2020) and Lütkepohl *et al.* (2024), SDDRs are a pragmatic tool for the Bayesian assessment of a null hypothesis of homoskedasticity in heteroskedastic models

allowing to verify partial or global identification through heteroskedasticity. A similar argument applies for the verification of identification in non-normal models. Additionally, the package's general implementation of SDDRs for the autoregressive parameters facilitates verification of restrictions on any conditional mean parameters of the model, such as e.g., hypotheses of exogeneity or Granger non-causality.

Finally, the package **bsvars** is highly integrated in terms of workflows, objects, and code compatibility with an R package **bsvarSIGNs** by Wang and Woźniak (2025b,a) focusing on SVAR models identified using sign (Rubio-Ramirez, Waggoner, and Zha 2010), sign and zero (Arias, Rubio-Ramírez, and Waggoner 2018), and narrative restrictions (Antolín-Díaz and Rubio-Ramírez 2018). The **bsvarSIGNs** package usage compatibility and its complementarity in terms of the implemented SVAR identification methods constitutes an additional appeal of the **bsvars** package.

Multivariate dynamic modelling, both Bayesian and frequentist, has found some traction in R in the recent years, which resulted in many new packages available on the CRAN repository. Two packages, **MTS** by Tsay, Wood, and Lachmann (2022) and **vars** by Pfaff (2008), cover a wide range of benchmark models for multivariate time series analysis in economics in finance. Other packages provide functionality for reduced-form models estimation and forecasting implementing regularisation, such as the **BigVAR** package by Nicholson, Matteson, Bien, and Wilms (2023), **bigtime** by Wilms, Matteson, Bien, Basu, Nicholson, and Wegner (2023), and **VARshrink** by Lee and Kim (2019), or Bayesian shrinkage, such as the **bvartools** package by Mohr (2022), **bayesianVARs** by Gruber (2024), or **BGVAR** by Boeck, Feldkircher, and Huber (2020). All of these specification are proven to be highly beneficial for forecasting in particular contexts.

Notable implementations of structural models include packages focusing on specific models important from the point of view of historical developments in the field, namely, the package **BVAR** by Kuschnig and Vashold (2021) providing tools for the estimation and analysis proposed by Giannone *et al.* (2015), package **bvarsv** by Krueger (2015) focusing on the heteroskedastic VAR proposed by Primiceri (2005), and package **FAVAR** by Chen and Chen (2022) implementing the factor-augmented model by Bernanke, Boivin, and Eliasz (2005). Other two packages that have been archived and are no longer available on CRAN are the package **MSBVAR** by Brandt (2006) focusing on the Markov switching model by Sims and Zha (2006) and package **VARsignR** by Danne (2015) provided a treatment of Bayesian SVARs identified via sign restrictions by Uhlig (2005), Rubio-Ramirez *et al.* (2010), and Fry and Pagan (2011). Some other packages focus on the implementation of research code for families of models focused around a theme, such as the aforementioned package **bsvarSIGNs** for sign-restricted SVARs, package **gmvarkit** by Virolainen (2024a) implementing frequentist SVARs with non-Gaussian identification by Kalliovirta, Meitz, and Saikkonen (2016) and Virolainen (2024d), or package **sstvars** by Virolainen (2024c) focusing on smooth-transition non-linearity in the structural models by Virolainen (2024b), Anderson and Vahid (1998), and Lütkepohl and Netšunajev (2017). Importantly, there exists a whole universe of MATLAB libraries for structural macroeconomics analyses. However, the code is available mostly from authors' websites and without structured documentation. This family of libraries is not surveyed here but we single out the **BEAR** toolkit by Dieppe and van Roye (2024) and **Dynare** by Dynare Team (2024) providing comprehensive set of methods and extensive documentation.

However, the most relevant package to compare **bsvars** to is the **svars** package by Lange,

Dalheimer, Herwartz, and Maxand (2021) focusing on frequentist inference for SVAR models identified via exclusion restrictions, heteroskedasticity, and non-normal shocks and implementing a range of models that are feasible to estimate using the maximum likelihood method. The similarity to the functionality of package **bsvars** include the selection of models, such as the MSH and with non-normal residuals, as well as the selection of tools for structural analyses including impulse responses, historical and forecast error variance decompositions. However, the package **svars** implements maximum likelihood and bootstrap procedures for the analysis of the model parameters and offers some specification testing procedures.

In this context, the **bsvars** package implements a range of novel solutions and models for Bayesian analysis. One differentiating example is the implementation of the SVAR models with SV that is not covered by the package **svars**. This model is particularly important in the context of recent developments clearly indicating that SV is the single extension of VARs leading to marginally largest improvements in the model fit and forecasting performance as shown e.g. by Clark and Ravazzolo (2015), Chan and Eisenstat (2018), Carriero, Clark, and Marcellino (2019), Chan (2020), and Bertsche and Braun (2022). Another such example are sparse MSH and MIX models based on hierarchical prior structures deciding on their frequentist implementation infeasibility. Additionally, the package **bsvars** provides unique Bayesian statistical procedures for the verification of partial identification through heteroskedasticity and non-normality using method `verify_identification()`. The verification of identification for such flexible models as those considered in the package is not feasible in the frequentist framework. Finally, the package benefits from the advantage of Bayesian approach that facilitates the estimation for models with potentially many variables, autoregressive lags inflating the dimension of parameters space, Markov-switching regimes or normal mixture components, all of which are the factors constraining the feasibility of maximum likelihood approaches.

2. Bayesian Analysis of Structural VARs

This section scrutinises the modelling framework used in the package focusing on the specification of the models, prior distributions, hypotheses verification tools, and estimation. The reader is referred to (Kilian and Lütkepohl 2017, Chapter 4: SVAR Tools) for the exposition of the standard tools for the analysis of SVAR models, such as the impulse responses, forecast error variance and historical decompositions, as their implementation in the package closely follows this resource.

2.1. Structural VARs

All of the models in the package **bsvars** share the reduced and structural form equations, as well as the hierarchical prior distributions for these parameters following Lütkepohl *et al.* (2024). The reduced form equation is the VAR equation with p lags specified for an N-vector $\mathbf{y}_t$ collecting observations on N variables at time t:

$$\mathbf{y}_t = \mathbf{A}_1\mathbf{y}_{t-1} + \cdots + \mathbf{A}_p\mathbf{y}_{t-p} + \mathbf{A}_d\mathbf{d}_t + \boldsymbol{\varepsilon}_t, \tag{1}$$

where $\mathbf{A}_i$ are $N \times N$ matrices of autoregressive slope parameters, $\mathbf{d}_t$ is a D-vector of deterministic terms, always including a constant term, and possibly dummy and exogenous

variables, $\mathbf{A}_d$ is an $N \times D$ matrix of the corresponding parameters, and $\boldsymbol{\varepsilon}_t$ collects the N reduced form error terms. Collect all the autoregressive matrices and the slope terms in an $N \times (Np + D)$ matrix $\mathbf{A} = \begin{bmatrix}\mathbf{A}_1 & \dots & \mathbf{A}_p & \mathbf{A}_d\end{bmatrix}$ and the explanatory variables in a $(Np + D)$-vector $\mathbf{x}_t = \begin{bmatrix}\mathbf{y}_{t-1}' & \dots & \mathbf{y}_{t-p}' & \mathbf{d}_t'\end{bmatrix}'$. Then equation (1) can be written in the matrix form as

$$\mathbf{y}_t = \mathbf{A}\mathbf{x}_t + \boldsymbol{\varepsilon}_t. \tag{2}$$

Each of the rows of the matrix $\mathbf{A}$, denoted by $[\mathbf{A}]_{n\cdot}$ follows a multivariate conditional normal prior distribution, given the equation-specific shrinkage hyper-parameter $\gamma_{A.n}$, with the mean vector $\underline{\mathbf{m}}_{n.A}$ and the covariance $\gamma_{A.n}\underline{\Omega}_A$, denoted by:

$$[\mathbf{A}]_{n\cdot}' \mid \gamma_{A.n} \sim \mathcal{N}_{Np+D}\left(\underline{\mathbf{m}}_{n.A}, \gamma_{A.n}\underline{\boldsymbol{\Omega}}_A\right), \tag{3}$$

where $\underline{\mathbf{m}}_{n.A}$ is specified in-line with the Minnesota prior by Doan *et al.* (1984) as a vector of zeros if all of the variables are stationary, or containing value 1 in its n^{th} element if the n^{th} variable is unit-root nonstationary. By default, $\underline{\boldsymbol{\Omega}}_A$ is a diagonal matrix with vector $\begin{bmatrix}\mathbf{p}^{-2\prime} \otimes \boldsymbol{\imath}_N' & 100\boldsymbol{\imath}_D'\end{bmatrix}'$ on the main diagonal, where $\mathbf{p}$ is a vector containing a sequence of integers from 1 to p and $\boldsymbol{\imath}_N$ is an N-vector of ones. Both, $\underline{\mathbf{m}}_{n.A}$ and $\underline{\boldsymbol{\Omega}}_A$ can be modified by the user. This specification includes the shrinkage level exponentially decaying with the increasing lag order, relatively large prior variances for the deterministic term parameters, and the flexibility of the hierarchical prior that leads to the estimation of the level of shrinkage as proposed by Giannone *et al.* (2015). The latter feature is facilitated by assuming a 3-level local-global hierarchical prior on the equation-specific reduced form parameters shrinkage given by

$$\gamma_{A.n} | s_{A.n} \sim \mathcal{IG}2\left(s_{A.n}, \underline{\nu}_A\right), \tag{4}$$

$$s_{A.n} | s_A \sim \mathcal{G}\left(s_A, \underline{a}_A\right), \tag{5}$$

$$s_A \sim \mathcal{IG}2\left(\underline{s}_{s_A}, \underline{\nu}_{s_A}\right), \tag{6}$$

where $\mathcal{G}$ and $\mathcal{IG}2$ are gamma and inverted gamma 2 distributions (see Bauwens, Richard, and Lubrano 1999, Appendix A), hyper-parameters $\gamma_{A.n}$, $s_{A.n}$, and s_A are estimated, and $\underline{\nu}_A$, $\underline{a}_A$, $\underline{s}_{s_A}$, and $\underline{\nu}_{s_A}$ are all set by default to value 10 to assure appropriate level of shrinkage towards the prior mean. The values of the hyper-parameters that are underlined in our notation can be modified by the user.

The structural form equation determines the linear relationship between the reduced-form innovations $\boldsymbol{\varepsilon}_t$ and the structural shocks $\mathbf{u}_t$ using the $N \times N$ structural matrix $\mathbf{B}_0$:

$$\mathbf{B}_0\boldsymbol{\varepsilon}_t = \mathbf{u}_t. \tag{7}$$

The structural matrix specifies the contemporaneous relationship between the variables in the system and determines the identification of the structural shocks from vector $\mathbf{u}_t$. Its appropriate construction may grant specific interpretation to one or many of the shocks. The package **bsvars** facilitates the identification of the structural matrix and the shocks via exclusion restrictions (see Kilian and Lütkepohl 2017, Chapter 8) and/or through heteroskedasticity or non-normal shocks (Kilian and Lütkepohl 2017, Chapter 14). The zero restrictions are imposed on the structural matrix row-by-row following the framework

proposed by Waggoner and Zha (2003a) via the following decomposition of the n^{th} row of the structural matrix, denoted by $[\mathbf{B}_0]_{n\cdot}$:

$$[\mathbf{B}_0]_{n\cdot} = \mathbf{b}_n \mathbf{V}_n, \tag{8}$$

where $\mathbf{b}_n$ is a $1 \times r_n$ vector collecting the elements to be estimated and the $r_n \times N$ matrix $\mathbf{V}_n$ including zeros and ones placing the estimated elements in the demanded elements of $[\mathbf{B}_0]_{n\cdot}$.

The structural matrix $\mathbf{B}_0$ follows a conditional generalised-normal prior distribution by Waggoner and Zha (2003a) recently revised by Arias *et al.* (2018) that is proportional to:

$$\mathbf{B}_0 \mid \gamma_{B.1}, \dots, \gamma_{B.N} \sim |\det(\mathbf{B}_0)|^{\underline{\nu}_B - N} \exp\left\{ -\frac{1}{2} \sum_{n=1}^{N} \gamma_{B.n}^{-1} \mathbf{b}_n \underline{\mathbf{\Omega}}_{B.n}^{-1} \mathbf{b}_n' \right\}, \tag{9}$$

where $\underline{\mathbf{\Omega}}_{B.n}$ is an $r_n \times r_n$ scale matrix set to the identity matrix by default, $\underline{\nu}_B \geq N$ is a shape parameter, and $\gamma_{B.n}$ is an equation-specific structural parameter shrinkage. The shape parameter $\underline{\nu}_B$ set to N by default makes this prior a conditional, zero-mean r_n-variate normal prior distribution for $\mathbf{b}_n$ with the diagonal covariance and the diagonal element $\gamma_{B.n}$. The shape parameter can be modified by the user though.

This prior specification is complemented by a 3-level local-global hierarchical prior on the equation-specific structural parameters shrinkage given by

$$\gamma_{B.n} | s_{B.n} \sim \mathcal{IG}2\left(s_{B.n}, \underline{\nu}_b\right), \tag{10}$$
$$s_{B.n} | s_B \sim \mathcal{G}\left(s_B, \underline{a}_B\right), \tag{11}$$
$$s_B \sim \mathcal{IG}2\left(\underline{s}_{s_B}, \underline{\nu}_{s_B}\right), \tag{12}$$

where hyper-parameters $\gamma_{B.n}$, $s_{B.n}$, and s_B are estimated and $\underline{\nu}_b$, $\underline{a}_B$, $\underline{s}_{s_B}$, and $\underline{\nu}_{s_B}$ are fixed to values 10, 10, 1, and 100 respectively to assure a flexible dispersed distribution *a priori* but they can be modified by the user.

Finally, all of the models share the zero-mean conditional normality of the structural shocks given the past observations with the diagonal covariance matrix containing the N-vector of structural shock variances, $\boldsymbol{\sigma}_t^2$, on the main diagonal:

$$\mathbf{u}_t \mid \mathbf{x}_t, \boldsymbol{\sigma}_t^2 \sim \mathcal{N}_N\left(\mathbf{0}_N, \operatorname{diag}\left(\boldsymbol{\sigma}_t^2\right)\right). \tag{13}$$

The diagonal covariance matrix, together with the joint normality, implies contemporaneous independence of the structural shocks which is the essential feature allowing for the estimation of dynamic effects to a well-isolated cause that is not influenced by other factors in the SVAR models.

The model parts described in the current section are common to all the models considered in the package **bsvars**. Note that identification of the structural matrix here must be assured by the exclusion restrictions only in the homoskedastic model. Heteroskedastic and non-normal specifications might not require the exclusion restrictions to identify the structural matrix. Still, such restrictions might occur beneficial from the point of view of the model fit sharpening shock identification. Such alternative model specifications are distinguished by the characterisation of the conditional variances collected in vector $\boldsymbol{\sigma}_t^2$.

2.2. Models for Conditional Variances

The **bsvars** package offers a selection of alternative specifications for structural shocks conditional variance process.

Homoskedastic model

The first such specification is a homoskedastic model for which the conditional variance of every shock is equal to

$$\sigma^2_{n.t} = 1 \tag{14}$$

for all t. This setup results in a simple SVAR model that is quick to estimate. Note that in this model, the conditional covariance of the data vector, $\mathbf{y}_t$ is equal to $(\mathbf{B}_0'\mathbf{B}_0)^{-1}$. The point at which this model is standardized as in equation (14) is the benchmark value for the all other heteroskedastic models whose conditional variances hover around value 1.

Stochastic Volatility

The heteroskedastic model with Stochastic Volatility is implemented in two versions: non-centred by Lütkepohl *et al.* (2024) and centred Chan *et al.* (2024). In these models, the conditional variances for each of the shocks are given by

$$\text{non-centred:} \qquad \sigma^2_{n.t} = \exp\left\{\omega_n h_{n.t}\right\} \tag{15}$$

$$\text{centred:} \qquad \sigma^2_{n.t} = \exp\left\{\tilde{h}_{n.t}\right\}, \tag{16}$$

where the parameter ω_n denotes the plus-minus square root of the conditional variance for the log-conditional variance process and will be referred to as the *volatility of the log-volatility*, whereas $h_{n.t}$ and $\tilde{h}_{n.t}$ are the log-volatility processes following autoregressive equations

$$\text{non-centred:} \qquad h_{n.t} = \rho_n h_{n.t-1} + v_{n.t}, \qquad v_{n.t} \sim \mathcal{N}\left(0, 1\right) \tag{17}$$

$$\text{centred:} \qquad \tilde{h}_{n.t} = \rho_n \tilde{h}_{n.t-1} + \tilde{v}_{n.t}, \qquad \tilde{v}_{n.t} \sim \mathcal{N}\left(0, \sigma^2_v\right) \tag{18}$$

with the initial values $h_{n.0} = \tilde{h}_{n.0} = 0$, where ρ_n is the autoregressive parameter, $v_{n.t}$ and $\tilde{v}_{n.t}$ are the SV normal innovations, and σ^2_v is the conditional variance of $\tilde{h}_{n.t}$ in the centred parameterisation.

The priors for these models include a uniform distribution for the autoregressive parameter

$$\rho_n \sim \mathcal{U}(-1, 1), \tag{19}$$

which assures the stationarity of the log-volatility process and sets its unconditional expected value to $E[h_{n.t}] = E[\tilde{h}_{n.t}] = 0$. The prior distribution for the volatility of the log-volatility parameter in the non-centred and the conditional variance of the log-volatility in the centred parameterisation follow a multi-level hierarchical structures given by:

$$\text{non-centred:} \quad \omega_n \mid \sigma^2_{\omega.n} \sim \mathcal{N}\left(0, \sigma^2_{\omega.n}\right), \qquad \sigma^2_{\omega.n} \mid s_\sigma \sim \mathcal{G}(s_\sigma, \underline{a}_\sigma), \qquad s_\sigma \sim \mathcal{IG}2(\underline{s}, \underline{\nu}) \tag{20}$$

$$\text{centred:} \quad \sigma^2_v \mid s_v \sim \mathcal{IG}2(s_v, \underline{a}_v), \qquad s_v \mid s_\sigma \sim \mathcal{G}(s_\sigma, \underline{a}_\sigma), \qquad s_\sigma \sim \mathcal{IG}2(\underline{s}, \underline{\nu}) \tag{21}$$

where parameters $\sigma^2_{\omega.n}$ and s_v follow gamma distribution with expected value equal to $s_\sigma \underline{a}_\sigma$. In this hierarchical structure the hyper-parameters ω_n, $\sigma^2_{\omega.n}$, σ^2_v, s_v, and s_σ are estimated,

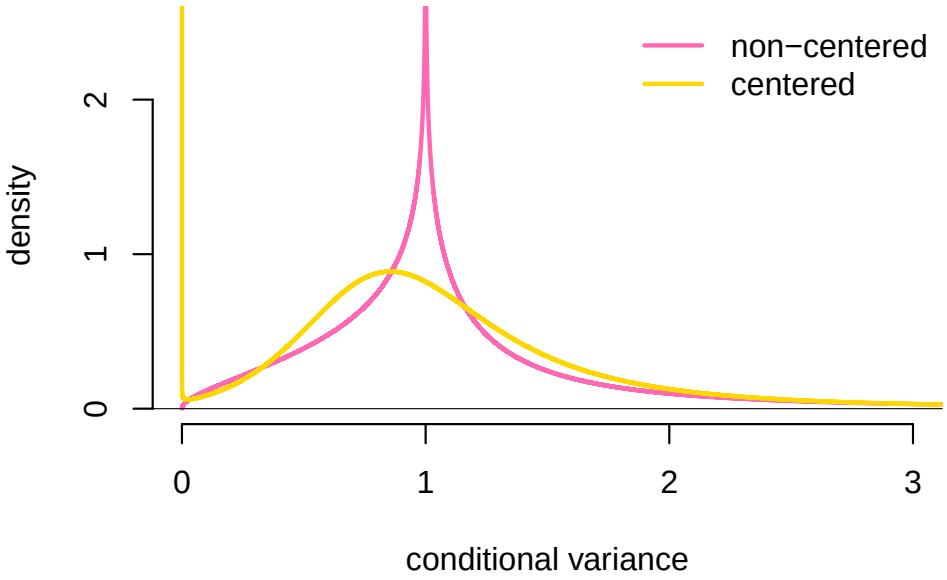

Figure 2: Marginal prior density of a structural shock conditional variance in the two SV models. Source: Lütkepohl et al. (2024).

while $\underline{a}_v$, $\underline{a}_\sigma$, $\underline{\nu}$, and $\underline{s}$ are set to values 1, 1, 1, and 0.1, respectively, by default and can be modified by the user.

Both of the SV models share a number of features, such as the flexibility of hierarchical priors with estimated hyper-parameters granting better fit to data and improved forecasting performance, and they facilitate the identification of the structural matrix $\mathbf{B}_0$ and shocks through heteroskedasticity following the original ideas by Bertsche and Braun (2022) and Lewis (2021). However, they differ with respect to the features analysed by Lütkepohl *et al.* (2024) that are presented in Figure 2 plotting the marginal prior distribution of the conditional variances, $\sigma^2_{n.t}$, in the two SV models. These densities are implied by the SV model specifications presented in this section. The centred parameterisation concentrate the prior probability mass around point 1 only mildly and goes to infinity when the conditional variance goes to zero. The non-centred parameterisation, on the other hand, concentrates the prior probability mass around point 1 more strongly, goes to zero when the conditional variance goes to zero, and features fat right tail. Finally, in the non-centred parameterisation homoskedasticity can be verified by checking the restriction $\omega_n = 0$ (see Lütkepohl *et al.* 2024).

Markov-switching heteroskdasticity

In another heteroskedastic model, the MSH one, the time-variation of the conditional variances is determined by a discrete-valued Markov process s_t with M regimes:

$$\sigma^2_{n.t} = \sigma^2_{n.s_t}. \tag{22}$$

All of the variances switch their values at once according to the latent Markov process takes the values $s_t = m \in \{1, \dots, M\}$. The properties of the Markov process itself are determined by the transition matrix $\mathbf{P}$ whose $[\mathbf{P}]_{i.j}$ element denotes the transition probability from regime i to regime j over the next period. The process' initial probabilities are estimated and denoted

by the M-vector $\boldsymbol{\pi}_0$. In this model used by Brunnermeier *et al.* (2021), the variances in the n^{th} equation sum to M, each of them has the prior expected value equal to 1, and their regimes are given equal prior probabilities of occurrence equal to M^{-1}. Therefore, the prior for the conditional variances is the M-variate Dirichlet distribution:

$$M^{-1}\left(\sigma_{n.1}^2,\dots,\sigma_{n.M}^2\right) \sim \mathcal{D}irichlet_M(\underline{e}_\sigma,\dots,\underline{e}_\sigma), \tag{23}$$

where the hyper-parameter $\underline{e}_\sigma = 1$ is fixed. Each of the rows of the transition matrix as well as the initial state probabilities follow the Dirichlet distribution as well:

$$[\mathbf{P}]_{m\cdot} \sim \mathcal{D}irichlet_M(\underline{e},\dots,\underline{e}) \tag{24}$$

$$\boldsymbol{\pi}_0 \sim \mathcal{D}irichlet_M(\underline{e}_0,\dots,\underline{e}_0). \tag{25}$$

The package **bsvars** offers two alternative models based on MSH. The first is characterised by a stationary Markov process with no absorbing state, and with a positive minimum number of regime occurrences following Droumaguet, Warne, and Woźniak (2017). In this model, the hyper-parameter $\underline{e} = \underline{e}_0$ is fixed to 1 by default and can be modified by the user. The other model represents a novel proposal of a sparse representation that fixes the number of regimes to an over-fitting value $M = 20$ (or specified by the user). In this model, many of the regimes will have zero occurrences throughout the sample, which allows the number of regimes with non-zero occurrences to be estimated following the ideas by Malsiner-Walli *et al.* (2016). Its prior specification is complemented by a hierarchical prior for the hyper-parameter $\underline{e}$:

$$\underline{e} \sim \mathcal{IG}2\left(\underline{s}_e, \underline{\nu}_e\right). \tag{26}$$

Due to its construction, the sparse MSH model excludes regime-specific interpretation of parameters. Instead, the estimated sequence of conditional variances, $\sigma_{n.t}^2$, enjoys standard interpretations. Furthermore, both MSH models provide identification through heteroskedasticity following the ideas by Lanne, Lütkepohl, and Maciejowska (2010) and Lütkepohl and Woźniak (2020). The latter paper provides framework for verifying the identification, which in the **bsvars** package is implemented by verifying the homoskedasticity hypothesis represented by a restriction setting the conditional variances to 1, $\sigma_{n.m}^2 = 1$ for all m.

2.3. Models with Non-Normal Shocks

Identification of the structural shocks through non-normality is implemented in the package using the mixture of normal component model (MIX) following the proposal by Lanne and Lütkepohl (2010) and the Student-t distributed shocks as suggested by Lanne *et al.* (2017).

Mixture of normal components

In this model, the structural shocks follow a conditional N-variate normal distribution given the state variable $s_t = m \in \{1,\dots,M\}$;

$$u_t \mid \mathbf{x}_t, s_t = m, \boldsymbol{\sigma}_m^2 \sim \mathcal{N}_N\left(\mathbf{0}_N, \text{diag}\left(\boldsymbol{\sigma}_m^2\right)\right), \tag{27}$$

and where the states are predicted to occur in the next period with probability $\boldsymbol{\pi}_0$. The prior specification for these models closely follows that for the MSH models, with the Dirichlet

prior for the regime probabilities, $\boldsymbol{\pi}_0$, as in (25), and that for the conditionals variances, $\boldsymbol{\sigma}_m^2$, as in (23).

As long as the predictive state probabilities are constant in these models the classification of the observations into the regimes is performed using filtered and smoothed probabilities, or the posterior realisations of the state allocations s_t (see Song and Woźniak 2021, for a recent review of the methods).

The MIX model comes in two versions as well. The first is the finite mixture model (see e.g. Frühwirth-Schnatter 2006) in which the number of states, M, is fixed and the unconditional state probabilities, $\boldsymbol{\pi}_0$, are strictly positive. The latter condition requires non-zero regime occurrences over the sample, a condition that is imposed in the package implementation. An alternative specification is referred to as the sparse mixture model and is based on the proposal by Malsiner-Walli *et al.* (2016). In this model, the number of the finite mixture components is set to be larger than the real number of the components. Consequently, the number of components with non-zero probability of occurrence is estimated, which is facilitated by allowing the remaining components to have zero occurrences. This sparse structure of normal components implemented thanks to the prior specified for the hyper-parameter $\underline{e}$ of Dirichlet distribution as in equation (26).

The MIX models facilitate the identification through non-normality as proposed by Lanne and Lütkepohl (2010). The hypothesis of normality for a shock, contradicting its identification, is verified by checking whether restriction $\sigma_{n.m}^2 = 1$ holds for all m.

Student-t shocks

The Bayesian implementation of the Student-t model follows closely that by Geweke (1993) and is implemented using an inverse gamma scale of normal distribution. Therefore, the conditional normality of the structural shocks from equation (13) is complemented by the marginal prior distributions for variances

$$\sigma_{n.t}^2 \mid \nu_n \sim \mathcal{IG}2(\nu_n - 2, \nu_n). \tag{28}$$

Such a construction of the structural shock density results in a marginal density for the nth shock being a zero-mean, unit-variance Student-t distribution with equation-specific degrees of freedom, $\nu_n > 2$, (see Bauwens *et al.* 1999)

$$u_{n.t} \mid \mathbf{x}_t, \nu_n \sim t\left(0, 1, \nu_n\right). \tag{29}$$

In this model, the only role of $\sigma_{n.t}^2$ is to be integrated out for the sake of specifying the demanded marginal density for the structural shocks.

The prior distribution for the degrees of freedom parameter is set to

$$p(\nu_n) = \frac{1}{(\nu_n - 1)^2}. \tag{30}$$

This prior density is proper and setting it implies the estimation of the degrees of freedom parameters. Its particular form is further motivated by the fact that it facilitates identification through non-normality verification for a shock by checking the restriction $\nu \to \infty$ (see also Jensen and Maheu 2013).

2.4. Hypothesis Verification Using SDDRs

The **bsvars** package includes unique procedures for the verification of identification and hypotheses on autoregressive parameters. They are based on posterior odds ratio computed using the SDDR by Verdinelli and Wasserman (1995). Consider a general specification of a hypothesis represented by sharp restrictions on the parameters of the model, denoted by $\mathcal{H}_0$, and its complement denoted by $\mathcal{H}_1$. The SDDR is specified by

$$\frac{\Pr[\mathcal{H}_0 \mid data]}{\Pr[\mathcal{H}_1 \mid data]} = SDDR = \frac{p(\mathcal{H}_0 \mid data)}{p(\mathcal{H}_0)}, \tag{31}$$

where the LHS equality represents its interpretation as the posterior odds ratio, whereas the RHS equality provides the equivalent form that makes its computation straightforward. Consequently, SDDRs report the ratio of the posterior probability of the restriction to the posterior probability of the unrestricted model. Therefore, a value of the SDDR greater than one provides evidence in favour of the restriction $\mathcal{H}_0$, whereas its value less than one provides evidence against this hypothesis, or in favour of $\mathcal{H}_1$.

The SDDR computation requires the estimation of the unrestricted model under $\mathcal{H}_1$ and the computation of the ratio of the marginal posterior ordinate to the marginal prior ordinate both evaluated at the restriction $\mathcal{H}_0$. The specification of the models included in the **bsvars** package facilitate fast estimation of both ordinates using the estimator proposed by Gelfand and Smith (1990).

Identification verification

In order to verify the identification of structural shocks through time-varying volatility (or non-normality) one needs to verify the hypothesis of homoskedasticity (normality) of individual shocks, which allows them to make probabilistic statements regarding partial or global identification (see Lütkepohl and Woźniak 2020; Lütkepohl *et al.* 2024; Lanne *et al.* 2017). The model is globally identified iff no more than one structural shock is homoskedastic (normal). An individual shock is identified iff it is heteroskedastic (non-normal) or if it is the only homoskedastic (normal) shock in the system.

According to Lütkepohl *et al.* (2024) the hypothesis of homoskedasticity of the nth shock in the non-centred SV model is represented by the restriction

$$\mathcal{H}_0: \quad \omega_n = 0 \tag{32}$$

whereas in the MSH models it given by

$$\mathcal{H}_0: \quad \sigma^2_{n.1} = \ldots \sigma^2_{n.M} = 1. \tag{33}$$

The verification of normality of the nth shock in the MIX models is performed using the restriction in equation (33), whereas in the Student-t model it is given by

$$\mathcal{H}_0: \quad \nu_n \to \infty, \tag{34}$$

as in the limit, the Student-t distribution becomes normal. The model specification makes Bayesian verification of this uncommon restriction straightforward.

Verifying autoregressive specification

Finally, the package makes it possible to verify restrictions on the autoregressive parameters in the form of

$$\mathcal{H}_0: \quad \mathbf{S}\text{vec}(\mathbf{A}) = \mathbf{r}, \tag{35}$$

where $\text{vec}(\mathbf{A})$ is a vectorised matrix $\mathbf{A}$, $\mathbf{S}$ is an $r \times N(Np + D)$ selection matrix picking r elements of $\mathbf{A}$ to be restricted to the values in the r-vector $\mathbf{r}$. Note that the specification of the hierarchical prior leading to the estimated level of autoregressive shrinkage makes the verification of such restrictions less depending on arbitrary choices.

2.5. Posterior Samplers and Computational Details

In this section, we explain **bsvars** package's implementation of fast and efficient estimation algorithms obtained thanks to the application of appropriate model specification and frontier econometric techniques best described in Lütkepohl *et al.* (2024) and Woźniak and Droumaguet (2015).

The objective for choosing the model equations and the prior distributions was to make the estimation using Gibbs sampler technique (see e.g. Casella and George 1992) and well-specified easy-to-sample-from full conditional posterior distributions. Therefore, the package relies on the reduced form equation (2) for the VAR model. This choice is fairly uncommon in the SVAR literature but it simplifies the estimation of the autoregressive parameters $\mathbf{A}$ directly in the form as they are used for the computations of impulse responses or forecast error variance decomposition. This choice combined with the prior in (3) and specification of the structural form equation (7) facilitates the application of the row-by-row sampler by Chan *et al.* (2024). As shown by Carriero, Chan, Clark, and Marcellino (2022), relative to the joint estimation of the matrix $\mathbf{A}$ in one step, a usual practice in reduced form VARs, the row-by-row estimation in SVARs can reduce computational complexity of Bayesian estimation from $\mathcal{O}(N^6)$ to $\mathcal{O}(N^4)$.

The estimation of the structural form equation (7) is implemented following the quickly converging, efficient, and providing excellent mixing sampling algorithm by Waggoner and Zha (2003a). It offers a flexible framework for setting exclusion restrictions and was also adapted to the SVARs identified through heteroskedasticity and non-normality by Woźniak and Droumaguet (2015). The unique formulation of this equation is particularly convenient for complex heteroskedastic models facilitating the row-by-row estimation of matrix $\mathbf{A}$ and Gibbs sampler for the heteroskedastic process.

The estimation of the Stochastic Volatility models is particularly requiring due to the N independent T-valued latent volatility processes estimation that it involves. The implementation of crucial techniques is particularly important here. The sampling algorithms use the 10-component auxiliary mixture technique by Omori, Chib, Shephard, and Nakajima (2007) that facilitates the estimation of the log-volatility using the simulation smoother by McCausland, Miller, and Pelletier (2011) for conditionally Gaussian linear state-space models greatly speeding up the computations (see Woźniak 2021, for the computational times comparison for various estimation algorithms). Application of appropriate numerical techniques reduces the complexity from $\mathcal{O}(T^3)$ to $\mathcal{O}(T)$.

Additionally, our specification facilitates the algorithms to estimate heteroskedastic process if the signal from the data is strong, but it also allows them to heavily shrink the posterior

towards homoskedasticity, as in equation (14), otherwise. The package implements the adaptation of the ancillarity-sufficiency interweaving strategy that is shown by Kastner and Frühwirth-Schnatter (2014) to improve the efficiency of the sampler when heteroskedasticity is uncertain. Our implementation of the sampling algorithm closely follows the algorithms from package **stochvol** with adaptations necessary for the SVAR modelling.

The estimation of the Markov switching and mixture models benefits mainly from the implementation of the forward-filtering backward-sampling estimation algorithm for the Markov process s_t by Chib (1996) in C++. However, an additional step of choosing the parameterisation of the conditional variances as in equation (23), requiring sampling from a new distribution defined by Woźniak and Droumaguet (2015), assures excellent mixing and sampling efficiency improvements relative to alternative ways of standardising these parameters.

All of the estimation routines for the Markov chain Monte Carlo estimation of the models and those for low level processing of the rich estimation output are implemented based using compiled code in **C++**. This task is facilitated by the **Rcpp** package by Eddelbuettel, François, Allaire, Ushey, Kou, Russel, Chambers, and Bates (2011) and Eddelbuettel (2013). The **bsvars** package relies heavily on linear algebra and pseudo-random number generators. The former is implemented using the package **RcppArmadillo** by Eddelbuettel and Sanderson (2014) that is a collection of headers linking to the C++ library **armadillo** by Sanderson and Curtin (2016), as well as on several utility functions for operations on tri-diagonal matrices from package **stochvol** by Hosszejni and Kastner (2021). The latter refers to the algorithms from the standard normal distribution using package **RcppArmadillo**, truncated normal distribution **RcppTN** by Olmsted (2017) implementing the efficient sampler by Robert (1995), and generalised inverse Gaussian distribution using package **GIGrvg** by Leydold and Hörmann (2017) implementing the sampler by Hörmann and Leydold (2014). All of these developments make the algorithms computationally fast. Still, Bayesian estimation of multivariate dynamic structural models is a requiring task that might take a little while. To give users a better idea of the remaining time the package displays a progress bar implemented using the package **RcppProgress** by Forner (2020). Finally, the rich structure of the model specification including the prior distributions, identification pattern, and starting values, as well as the rich outputs from the estimation algorithms are organised using dedicated classes within the **R6** package by Chang (2021) functionality.

3. Workflows for SVAR analysis

The **bsvars** package allows the users to design their workflows in several ways. The three main stages include model specification, estimation, and post-estimation analysis.

3.1. The Basic Workflow (also with a Pipe)

The basics of the workflow are presented for the case of a simple homoskedastic SVAR model. Begin by uploading the package and a sample data matrix for the analysis of the US fiscal policy, and setting the seed for the sake of reproducibility:

```
R> library(bsvars)
```

```
R> data(us_fiscal_lsuw)
R> set.seed(1)
```

Specify the SVAR model with a lower triangular structural matrix and one autoregressive lag both being the default settings by executing:

```
R> spec = specify_bsvar$new(us_fiscal_lsuw)
```

```
The identification is set to the default option of lower-triangular structural matrix.
```

The object `spec` includes a number of objects that define the model, such as the data matrices, fixed hyper-parameters of the prior distribution, identification pattern, and starting values. The estimation of the model using the Monte Carlo Markov Chain (MCMC) methods is performed in two steps. First, the object `spec` with model specification is provided to the `estimate()` function to perform `1000` iterations of the Gibbs sampler. This burn-in stage is run for the algorithm to achieve convergence to the stationary posterior distribution. In the second step, the object `burn` is provided to the `estimate()` function to perform `10000` iterations of the Gibbs sampler and save them in the object `post`:

```
R> burn = estimate(spec, 1000)
R> post = estimate(burn, 10000)
```

In the latter case, the function `estimate()` extracts the last draw of the parameters from the previous run, uses it as starting values for the final run of the estimation algorithm, and continues the Markov chain providing sample from the target posterior distribution. This way of designing the `estimate()` function allows the user to run the estimation in several steps, which is particularly useful for the models requiring longer runs of the sampling algorithm to achieve convergence. The user can discard the draws from the previous step and continue the estimation in as many subsequent `estimate()` function runs as required.

The posterior output is normalised with respect to the signs of the structural matrix following the procedure by Waggoner and Zha (2003b) in an automated way by running function `normalise_posterior()` within the execution of the function `estimate()`.

Subsequently, use the estimation output to forecast, say, four periods ahead:

```
R> fore = forecast(post, 4); summary(fore)
```

compute and plot impulse responses:

```
R> irfs = compute_impulse_responses(post, 4); plot(irfs)
```

verify whether the third variable Granger causes the first:

```
R> H0   = matrix(NA, 3, 4); H0[1,3] = 0
R> sddr = verify_autoregression(post, H0)
R> summary(sddr)
```

or perform any other post-estimation analysis.

The same workflow can be coded using the `|>` pipe. We propose that the user binds the model specification with the estimation:

```
R> set.seed(1)
R> us_fiscal_lsuw |>
+   specify_bsvar$new() |>
+   estimate(S = 1000) |>
+   estimate(S = 10000) -> post
```

to obtain exactly the same draws from the posterior distribution as in the previous workflow collected in object `post`. The post-estimation analysis can then be executed by:

```
R> post |> forecast(horizon = 4) |> summary()
R> post |> compute_impulse_responses(horizon = 4) |> plot()
R> post |> verify_autoregression(hypothesis = H0) |> summary()
```

User preferences, convenience, and specific project requirements should decide on the implementation of the procedure in a script.

3.2. Customizing The Workflow

The package offers a range of models, post-estimation methods, and a set of functions for each of the stages of analysis. The full extent of workflow customization is presented in Figure 3.

The top of the Figure presents functions to specify the model. Here users can choose a homoskedastic model, one with normal mixture (MIX), Markov-switching heteroskedasticity (MSH), Stochastic Volatility (SV), or t-distributed errors. Then the model can be estimated using the `estimate()` function repeatedly as long as necessary to obtain S draws from the posterior distribution in the final run. It is recommended then that the user verifies the draws of the $N \times N$ structural matrix contained in an $N \times N \times S$ array `post$posterior$B` for unimodality. The lack of thereof may indicate that the automated manner of normalising the posterior draws using function `normalise_posterior()` was not successful and more work needs to be done here. The default calibration of this algorithm is found to be sufficient for models with exclusion restrictions though.

Given the posterior output, the user can proceed to forecasting, hypotheses verification, or analysis of interpretable quantities. No particular ordering of the operations is recommended and users should implement their competence in the subject matter and consider their project's requirements here. Forecasting is performed using the `forecast()` function and includes the possibility of generating conditional predictions given future projections of some of the variables provided in argument `conditional_forecast`. The user can verify hypotheses about the model parameters using the `verify_autoregression()` and `verify_identification()` functions implementing the computation of SDDRs. Finally, the user can compute interpretable quantities such as structural shocks' conditional standard deviations, fitted values, historical decompositions, impulse responses, MIX and MSH models' regime probabilities, structural shocks, and forecast error variance decompositions using an appropriate method listed in the last block in Figure 3. The

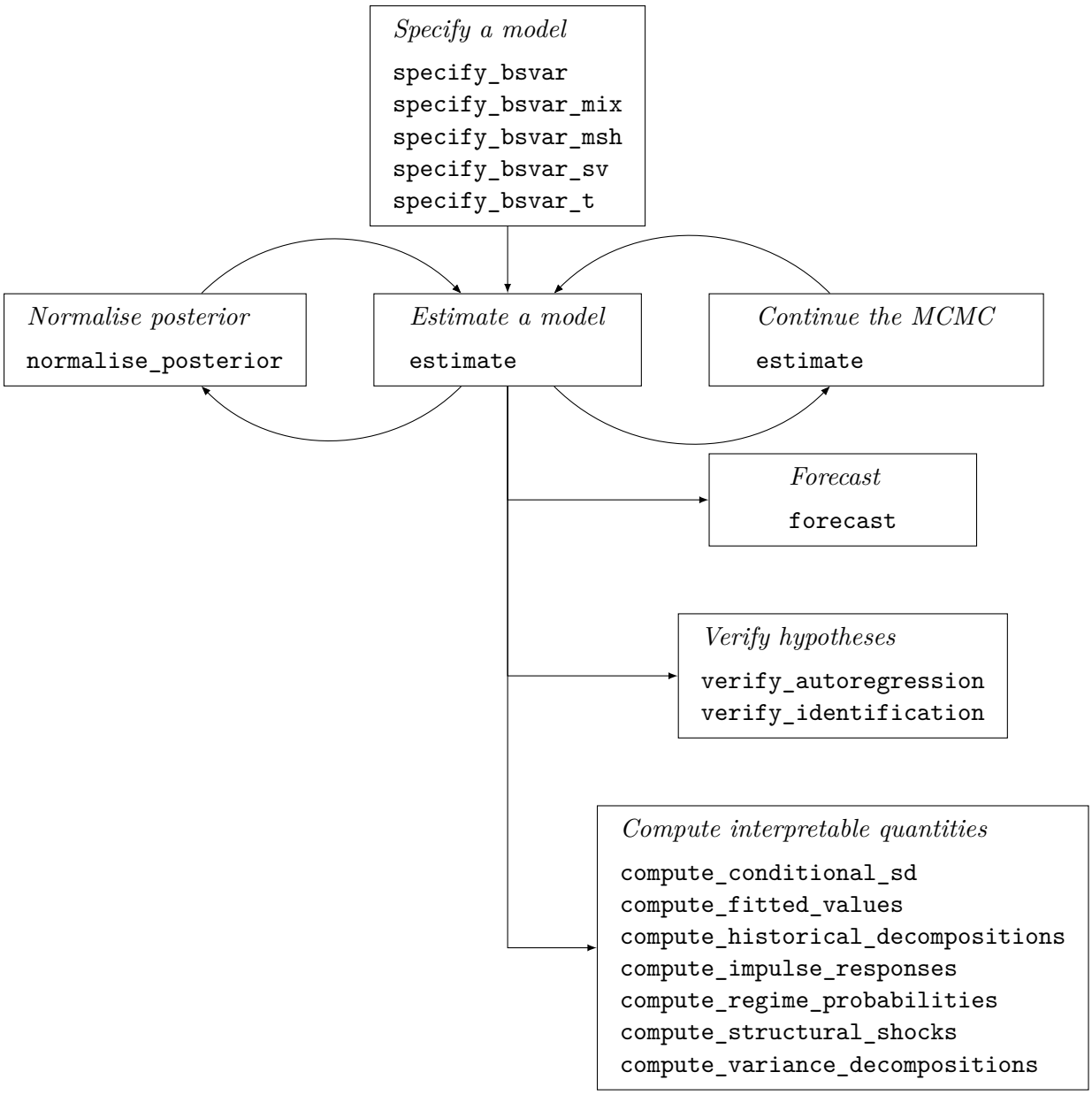

Figure 3: Workflow for SVAR analysis

package documentation provides all the necessary details on the arguments and outputs of the functions, which enables further customization of the workflow.

3.3. Generics, Methods, and Functions

The workflows described in this section are possible thanks to a deliberate design of the package's generics, methods, and functions listed in Table 1. The functions specifying the model are created using the **R6** classes to facilitate the management of this complicated object. All the specification details can be adjusted by the user by modifying the elements

Table 1: Summary of package's generics, methods, and functions

generic or function	first argument class	output class	plot	summary
	Specify a model			
`specify_bsvar`	`matrix`	`BSVAR`, `R6`		
`specify_bsvar_mix`	`matrix`	`BSVARMIX`, `R6`		
`specify_bsvar_msh`	`matrix`	`BSVARMSH`, `R6`		
`specify_bsvar_sv`	`matrix`	`BSVARSV`, `R6`		
`specify_bsvar_t`	`matrix`	`BSVART`, `R6`		
	Estimate a model			
`estimate`	(model classes)	(posterior classes)		✓
	(posterior classes)	(posterior classes)		✓
	Normalise posterior output (if necessary)			
`normalise_posterior`	(posterior classes)	(posterior classes)		
	Forecast			
`forecast`	(posterior classes)	`Forecasts`	✓	✓
	Compute interpretable quantities			
`compute_conditional_sd`	(posterior classes)	`PosteriorSigma`	✓	✓
`compute_fitted_values`	(posterior classes)	`PosteriorFitted`	✓	✓
`compute_historical_decompositions`	(posterior classes)	`PosteriorHD`	✓	✓
`compute_impulse_responses`	(posterior classes)	`PosteriorIR`	✓	✓
`compute_regime_probabilities`	(posterior classes)	`PosteriorRegimePr`	✓	✓
`compute_structural_shocks`	(posterior classes)	`PosteriorShocks`	✓	✓
`compute_variance_decompositions`	(posterior classes)	`PosteriorFEVD`	✓	✓
	Verify hypotheses			
`verify_autoregression`	(posterior classes)	`SDDRautoregression`		✓
`verify_identification`	(posterior classes)	(sddr classes)		✓
	Classes explanation			
(model classes) include `BSVAR`, `BSVARMIX`, `BSVARMSH`, `BSVARSV`, `BSVART`				
(posterior classes) include `PosteriorBSVAR`, `PosteriorBSVARMIX`, `PosteriorBSVARMSH`, `PosteriorBSVARSV`, `PosteriorBSVART`				
(sddr classes) include `SDDRidSV`, `SDDRidMIX`, `SDDRidMSH`, `SDDRidT`				

Note: The last two columns indicate availability a dedicated `plot` or `summary` method.

of the specification object, such as the `spec` object, that is of a class indicating the specified model, e.g. `BSVAR`, `BSVARSV`, ... These objects inherit properties of the `list` class as well.

All other functions listed in Table 1 define generics that find their particular methods depending on the class of their first argument. Such a construction assures that appropriate estimation algorithm is applied to the model specified by the user. This applies, to all the subsequent stages of the workflow, such as forecasting, hypotheses verification, and computation of interpretable quantities that are performed using the exact algorithms required by the particular specification.

This can be illustrated for the workflow described in the current section. Executing the specification function `specify_bsvar$new()` creates an object of class `BSVAR`. Therefore, in the second step the `estimate()` generic implements method for homoskedastic SVAR model coded in `estimate.BSVAR()` creating object of class `PosteriorBSVAR`, which is followed by execution of the method `estimate.PosteriorBSVAR()` that continues the model estimation using MCMC methods. Consequently, the forecasting is performed using method `forecast.PosteriorBSVAR()`, impulse responses are computed for this model using method `compute_impulse_responses.PosteriorBSVAR()`, and the SDDR is estimated using the algorithm dedicated to this particular model using method `verify_autoregression.PosteriorBSVAR()`. A dedicated set of `summary()` and `plot()` methods greatly simplifies the user experience and their workflows.

Finally, generics are designed to be used in other packages with the first implementation in the R package **bsvarSIGNs** by Wang and Woźniak (2025b,a) providing methods for SVAR models identified with sign, zero, and narrative restrictions.

4. Conclusion

The **bsvars** package offers fast and efficient algorithms for Bayesian estimation of Structural VARs with a range of specifications for the volatility or distributions of the structural shocks. Thanks to the application of the frontier econometric and numerical techniques the package makes the estimation of multivariate dynamic structural models feasible even for a larger number of variables, complex identification strategies, and non-linear specifications. Its strong reliance on algorithms written in C++ makes it possible to benefit from the best of the two worlds: the convenience of data analysis using R and the computational speed using pre-compiled code written in C++. Finally, the package provides essential generics for applied analyses that facilitate developing coherent workflows for the dependent packages, such as the **bsvarSIGNs**, package greatly extending the set of models available to the users.

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