

# Invariant Image Reparameterisation: A Unified Approach to Structural and Practical Identifiability and Model Reduction

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**Abstract.** Both structural and practical parameter non-identifiability present fundamental challenges when using mathematical models to interpret data. This issue is particularly acute in complex, applied areas such as the life sciences or engineering, where determining appropriate model complexity is challenging. While several approaches exist for diagnosing and resolving parameter non-identifiability, including symbolic methods, profile likelihood analysis, and sloppiness analysis, these approaches have distinct limitations and are rarely combined. We present an integrated approach called Invariant Image Reparameterisation (IIR) that incorporates key elements of these methods in a new way. Our approach replaces symbolic computations with numerical calculations at a single reference estimate and an invariance condition that determines when this local calculation holds globally. Parameter combinations determined by this method are naturally ordered by degree of identifiability, and this supports model reduction by replacing a practically non-identified model with a structurally non-identified approximate model. This approximate model can be further parameterised in terms of identified parameters only. By treating parameter combinations determined by our approach as interest parameters within our established likelihood-based Profile-Wise Analysis (PWA) framework, we incorporate uncertainty quantification in terms of likelihood profiles and confidence sets. We provide a Julia library on [GitHub](#) demonstrating our methodology across a range of mathematical models.

**Key words.** Identifiability, Parameter estimation, Model reduction, Uncertainty quantification, Prediction

**1. Introduction.** Mechanistic mathematical models are widely used for interpreting experimental and observational data and learning about underlying causes of the observed phenomena. Such models are routinely used to provide insight into a broad range of applications including engineering (e.g. material science [36], fluid dynamics and transport phenomena [4, 28, 62, 6, 39]), ecology and population biology [38], disease transmission dynamics [56] as well as chemical reactions [35] and econometrics [32]. A fundamental challenge is determining whether available data contain enough information to yield unique or sufficiently precise parameter estimates, which are crucial both for understanding mechanisms and making predictions [64, 65].

Establishing whether model parameters are uniquely determined is often referred to as *structural identifiability analysis* in the modelling literature [5, 16, 45, 50, 51, 25], and is also simply referred to as identifiability analysis in the statistical literature [46]. In contrast, learning whether sufficiently precise parameter estimates are possible when working with finite noisy observations corresponds to the notion of *practical identifiability* (or estimability) analysis [33, 46, 70, 41].

Parameter non-identifiability occurs when different combinations of parameters produce

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identical, or sufficiently close, model outputs. making it impossible to uniquely determine the underlying mechanisms from observations [46, 65].

When model parameters are not identifiable, key questions arise: Can we identify certain parameter combinations even when individual parameters are non-identifiable [46, 17]? Can we perform model reduction to obtain simpler, identifiable models [13, 14, 27, 50, 51, 17]? Can we use practical non-identifiability to guide experimental design [63] or motivate approximate model reduction [49]?

Existing approaches include symbolic methods [13, 14, 18, 15], profile likelihood analysis [40, 60, 49, 64, 68], and sloppiness analysis [8, 31, 53]. Related work includes active subspaces [19] and likelihood-informed dimension reduction [23, 24] for large-scale inverse problems. While each approach has strengths, they also have limitations: symbolic methods typically apply only to idealised data/structural identifiability scenarios, profile likelihood methods usually require manual choice of target parameter to analyse, and sloppiness analysis may use non-parameterisation-invariant approximations for uncertainty quantification. Furthermore, the relationship between sloppiness and identifiability is not always clear, as sloppiness is a relative notion quantified in terms of ratios of eigenvalues (or singular values) models can be sloppy yet identifiable [16]. In applications of sloppiness and profile likelihood analysis to model reduction, users often simply set poorly-identified parameters to zero or some arbitrary value [42, 26, 69]. However, this can lead to setting individually poorly-identified parameters to values that jointly violate the requirements on possible values for the well-identified parameter combinations. Model reduction methods for inverse problems [19, 23], while powerful for computation, particularly Bayesian inverse problems, do not typically directly address identifiability questions and do not usually aim to provide interpretable parameter combinations for mechanistic models.

We present a novel approach that: (i) automatically identifies well-identified parameter combinations without symbolic computation; (ii) enables model reduction without requiring an explicit reduced form model; and (iii) provides statistically sound interval estimates for both parameters and predictions. Our method combines ideas from symbolic analysis and sloppiness literature to convert the general symbolic problem to a numerical one solvable at a single reference point. These parameter combinations then serve as interest parameters in our Profile-Wise Analysis (PWA) framework [65, 64]. For certain parameter combination classes, we recover structural identifiability analysis results to arbitrary accuracy, while still discovering useful approximate combinations in other cases.

**2. Methods.** Here, we outline the technical foundations of our ‘Invariant Image Reparameterisation’ approach, which builds on and extends the frameworks reviewed in [18], [17], [64], and, indirectly, [46, 47]. Our approach consists of four key components: (1) an auxiliary mapping connecting model parameters to observable quantities, (2) a general reparameterisation framework, (3) an initial parameter transformation to enable numerical computation, and (4) a singular value decomposition for implementing the reparameterisation in transformed parameter space. The identified parameter combinations can then serve as interest parameters in our Profile-Wise Analysis (PWA) workflow [64] or alternative approaches like Bayesian inference, which can also benefit from reparameterisation methods [29].

**2.1. Terminology.** We work relatively informally with (assumed-to-be) smooth mappings between finite-dimensional spaces [44], using standard terminology for submersions – mappings with full rank derivative – and immersions – mappings with injective derivative. The observed Fisher information measures parameter information content via the negative Hessian of the log-likelihood [58, 20, 59]. Informally, parameters or parameter combinations are identifiable if they can be uniquely determined from ‘perfect data’. In the context of a model mapping parameters to data distributions,  $\theta \mapsto p(y; \theta)$ , this is equivalent to the mapping, or more generally an induced relation in terms of parameter combinations, being injective [46].

**2.2. Model representation.** The auxiliary mapping  $\phi$  connects model parameters to data distribution parameters [64]:

$$(2.1) \quad \theta \mapsto \phi(\theta),$$

with density function

$$(2.2) \quad p(y; \phi),$$

inducing the probability model

$$(2.3) \quad p(y; \theta) = p(y; \phi(\theta)).$$

For spatial/temporal models, we use numerical solutions on a fine grid as the ‘exhaustive’ summary, evaluating derivatives via automatic differentiation in Julia [61]. Thus, while our approach is essentially identical to the ‘exhaustive summary’ approach reviewed by [18, 17], we generally avoid the need for explicit exhaustive summary methods such as Taylor series or generating series (as reviewed in the cited articles), though these can be used if available. In this context, we emphasise that automatic differentiation at the source code level is distinct from symbolic differentiation and only evaluates the numerical value of the derivative at a fixed input value [30].

The observed Fisher information in  $\theta$  coordinates is:

$$(2.4) \quad \mathcal{J}(\theta) = -H_l(\theta; y) = -\nabla_\theta(D_\theta l(\theta; y))^T = -\frac{\partial^2 l(\theta; y)}{\partial \theta \partial \theta^T}$$

where  $l(\theta; y)$  is the log-likelihood,  $D_\theta f$  is the Jacobian,  $\nabla_\theta f$  is the gradient, and  $H_f$  is the Hessian [48].

**2.3. Decomposition of the auxiliary mapping.** The auxiliary mapping can be decomposed as:

$$(2.5) \quad \phi(\theta) = \tilde{\phi}(\psi(\theta)),$$

where  $\psi(\theta)$  represents identifiable parameter combinations and  $\tilde{\phi}$  provides a one-to-one mapping to data distribution parameters. This decomposition is guaranteed by the epi-mono factorisation property of the general category of sets and mappings [43], where any mapping  $f : A \rightarrow B$  between sets  $A$  and  $B$  factorises as the composition:

$$(2.6) \quad f = m \circ e,$$

where  $e : A \rightarrow C$  is onto (epimorphic),  $m : C \rightarrow B$  is one-to-one (monomorphic), and  $C$  is some intermediate space, called the *image*,  $\text{im}(f)$ , in the context of category theory. Conceptually, this represents the possibility of a reduced model taking just the identified parameter combinations. Here we aim to determine this intermediate image by a local calculation that is ‘invariant’ to the choice of calculation point.

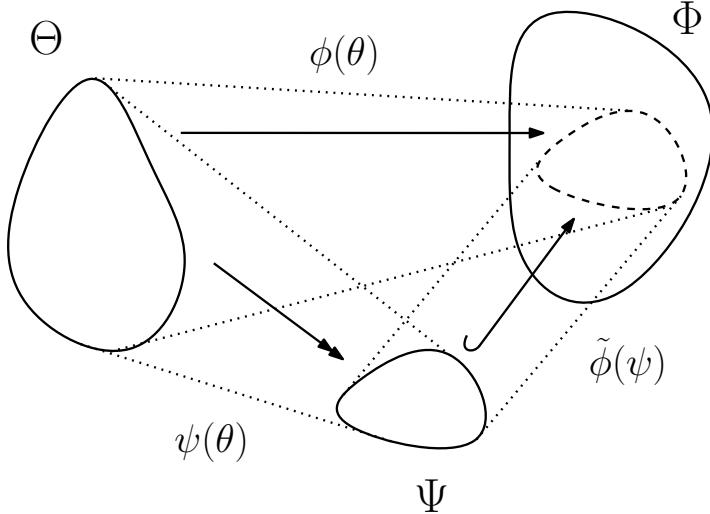


Figure 1: The basic decomposition of the auxiliary mapping into an identifiable reparameterisation followed by a reduced model mapping. Here  $\theta$  represent the original model parameters,  $\psi(\theta)$  represents identifiable parameter combinations, and  $\tilde{\phi}$  provides a one-to-one mapping from identifiable parameter combinations to data distribution parameters.

**2.4. Symbolic reparameterisation condition.** For smooth mappings with constant rank, we can strengthen the epi-mono factorisation by requiring  $\psi(\theta)$  to be a smooth submersion and  $\tilde{\phi}(\psi)$  to be a smooth immersion [44]. The chain rule then gives:

$$(2.7) \quad D_\theta \phi(\theta) = D_\psi \tilde{\phi}(\psi(\theta)) D_\theta \psi(\theta).$$

Since  $D_\psi \tilde{\phi}(\psi(\theta))$  is one-to-one, the rank of  $D_\psi \tilde{\phi}(\psi(\theta))$  and  $D_\theta \phi(\theta)$  are the same; furthermore, these derivatives share the same null space/kernel (see supplementary material):

$$(2.8) \quad \ker D_\theta \psi(\theta) = \ker D_\theta \phi(\theta).$$

Given null space vectors  $\alpha(\theta)$  obtained from  $D_\theta \phi(\theta)$ , we can then solve:

$$(2.9) \quad D_\theta \psi(\theta) \alpha(\theta) = 0,$$

for  $\psi(\theta)$ . This is equivalent to the conditions given by e.g. [12, 13], summarised by [18, 17]. It’s also equivalent to equating the rows of  $D_\theta \psi(\theta)$  to the vectors spanning the row space of  $D_\theta \phi(\theta)$ . The image of these vectors under  $\psi$  gives the intermediate ‘image’ component

$C$  of the epi-mono factorisation. As shown in detail in the supplementary material, we can also work directly with the observed Fisher information by solving a null space constraint in terms of the Fisher information rather than the Jacobian derivative of the auxiliary mapping. When we use the limiting Fisher information (i.e., as evaluated at the discretisation level of the solution grid), the approaches are equivalent; if not, the Fisher information formulation also includes additional finite data effects (see below).

**2.5. Parameter space linearisation.** Our goal is to determine identifiable parameter combinations without symbolic computation. While numerical methods typically provide only local reparameterisation information, we show that an initial coordinate transformation enables global results. Here we focus on the componentwise log transformation  $\log \theta = [\log \theta_1, \log \theta_2, \dots, \log \theta_p]^T$ , which linearises monomial parameter combinations in parameter space, though the overall function will still typically be a nonlinear function of the resulting linear combinations of log parameters. Reduced sets of monomial parameter combinations commonly arise in mechanistic models, e.g. via the Buckingham Pi theorem of dimensional analysis [10], and related asymptotic approximations and model reduction [3]. Such a log parameter transformation is commonly used in the sloppiness literature [7, 54, 69] and this also inspired our present approach. However, our basic approach can be applied if, e.g., only some components are logged or even if both logged and unlogged parameters are considered simultaneously.

Working in log coordinates, defining  $\theta^* = \log(\theta)$  to be the component-wise log of the parameter vector, models that can be written in terms of monomial parameter combinations take the form:

$$(2.10) \quad \phi(\theta) = \tilde{\phi}(\exp(A\theta^*)),$$

where  $A$  is a matrix of real coefficients. The chain rule gives:

$$(2.11) \quad D_{\theta^*}\phi_*(\theta^*) = D_{\psi_*}\tilde{\phi}(\psi_*(\theta^*))\text{diag}(\exp(A\theta^*))A,$$

leading to our key condition:

$$(2.12) \quad \ker A = \ker D_{\theta^*}\phi_*(\theta^*).$$

This follows since the first term on the right-hand side of the chain rule equation (2.11) is injective by assumption, and the second term is a diagonal matrix of (non-zero) exponentials and hence also injective. As before (see also supplementary material), these leave the null space of  $A$  unchanged. As the left-hand side of (2.12) is parameter-independent, the right-hand side must be too. We can hence evaluate the right-hand side derivative at any convenient point to determine the global, invariant null space, complementary row space and hence intermediate image, reducing what would be a PDE to an algebraic computation. If the model is assumed non-identifiable, the point used will generally be, e.g., any (non-unique) maximum likelihood estimate, and the Jacobian will be singular. This is expected and causes no issues in general.

While this condition does not uniquely determine  $A$ , as any basis for the null space (and complementary row space) can be used, it establishes the existence of a matrix capturing

non-identifiable and identifiable parameter combinations. While the coefficients in  $A$  are traditionally restricted to integers in dimensional analysis, here we allow them to be arbitrary real numbers and do not require the combinations to be dimensionless *a priori*. This relaxation facilitates numerical computation and provides more flexibility in discovering practically useful parameter combinations. However, we also consider *a posteriori* scaling and rounding operations to convert these real-valued coefficients to integers to aid interpretability while preserving key properties of the approximation.

The corresponding alternative route to the decomposition of the auxiliary mapping is illustrated in Figure 2.

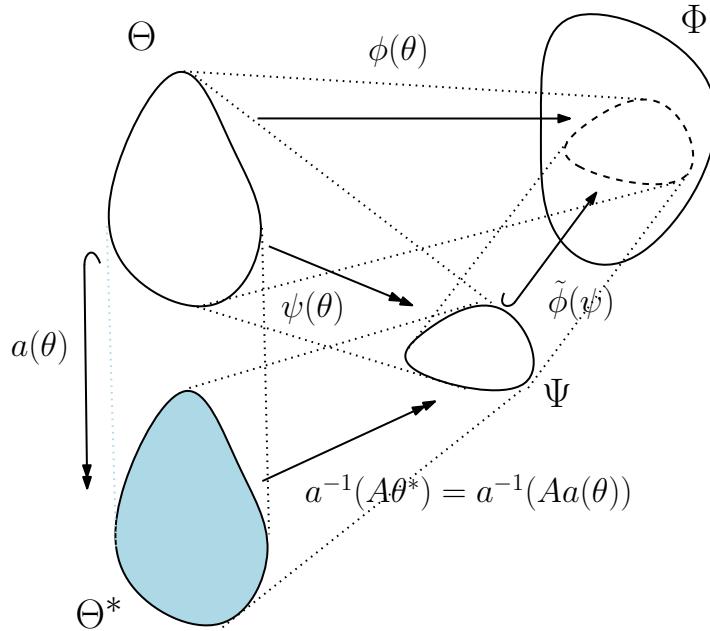


Figure 2: Implementation of parameter space linearisation using an initial componentwise transformation  $a(\theta)$ , typically log, followed by a linear transformation and componentwise inverse. The chain rule applied on the path from  $\Theta^*$  to  $\Phi$  allows us to equate the overall null space to that of the constant linear transformation  $A$ .

**2.6. Singular value decomposition for nonlinear parameter combinations.** Given the Jacobian in log-parameters at reference point  $\hat{\theta}^*$ , we compute:

$$(2.13) \quad D_{\theta^*}\phi_*(\hat{\theta}^*) = U\Sigma V^T = U_r\Sigma_r V_r^T$$

Taking  $A = V_r^T$ , or any row-scaled version of this, ensures the same kernel as  $D_{\theta^*}\phi_*(\hat{\theta}^*)$ . The singular values provide a natural ranking of parameter combinations by identifiability, with zero or near-zero values indicating structural or practical non-identifiability respectively.

We can also partition parameters into identifiable and non-identifiable combinations using

the full rather than reduced SVD:

$$(2.14) \quad \theta \mapsto \begin{bmatrix} \psi(\theta) \\ \lambda(\theta) \end{bmatrix} = \exp(V^T \log(\theta))$$

where  $\psi(\theta)$  corresponds to non-zero singular values and associated singular vectors, and  $\lambda(\theta)$  to (near) zero values and associated singular vectors. This maintains compatibility with existing model codes while capturing the identifiability structure.

In the case of practical non-identifiability, or near non-identifiability, there will be singular values close to zero, and the corresponding singular vectors will be elements of the row space rather than the null space of the Jacobian. As the SVD leads to an orthogonal basis these singular vectors can still be considered to span a self-contained ‘practically non-identifiable’ parameter space (see e.g. [66]), and the remaining singular vectors will still span the well-identified parameter space.

As mentioned above, the null space and row space of the limiting observed Fisher information are the same as that of the auxiliary mapping, we can also extend this approach to work directly with the observed Fisher information (supplementary information). This may be more natural for many models.

**2.7. Practical vs structural identifiability and observation operators.** An important aspect of the relationship between practical and structural identifiability is represented by the need for observation operators such as:

$$(2.15) \quad \phi_{\text{obs}} = B_{\text{obs}} \phi_{\text{fine}}$$

where  $B_{\text{obs}}$  maps the fine-scale (numerical) solution to (experimental) observation points. The additional loss of information due to coarser observation scale can introduce additional null space components or poorly-identified parameters depending on the degree of additional discretisation. When we discuss the limiting observed Fisher information, we mean the observed Fisher information at the solution grid level; this is required for the Fisher information analysis to match the structural identifiability analysis, otherwise additional null space/poorly-identified components may be introduced.

When analysing at the solution grid level, our results should, to numerical approximation, recover those from an idealised structural identifiability analysis. However, for ill-posed problems or models with parameter-dependent limiting behavior, the distinction between practical and structural non-identifiability can blur [46]. The auxiliary mapping may have arbitrarily small singular values in certain parameter regions, making the distinction between practical and structural non-identifiability less clear. Furthermore, it is unclear if ideal structural identifiability results are useful in the absence of practical identifiability [46]. Our approach here is to use the auxiliary mapping (or limiting Fisher information) to determine the reparameterisation, but carry out the likelihood-based uncertainty analysis at the observation grid level. This provides a practical identifiability analysis that is consistent with the structural identifiability analysis

**2.8. Scaling and rounding.** For numerical implementation, we apply scaling and rounding to singular vectors to obtain interpretable parameter combinations, defaulting to the nearest

0.5 when scaling relative to the smallest non-zero singular value. The continuity of singular subspaces [66] ensures stable separation of parameter combinations in cases of near non-identifiability, with practically (non-)identifiable subspaces corresponding to structurally (non-)identifiable subspaces of the limit model.

**2.9. Profile-wise analysis.** We quantify uncertainty using our PWA framework [64], which connects identifiability, parameter estimation, and predictive uncertainty through likelihood-based confidence sets. This approach uses both the joint likelihood for all parameters and profiles of the likelihood – the likelihood as a function of a target parameter with the other ‘nuisance’ parameters maximised out [40, 60, 20, 59]. As the likelihood function is invariant to reparameterisation [58, 59, 20], reparameterisation of the full likelihood preserves all information in the original likelihood, unlike quadratic approximations based on the Fisher information. Rather, reparameterisation presents the information in the likelihood in a clearer form, while profile likelihoods reveal identifiability of individual parameters, or parameter combinations, separately from nuisance parameters [2].

**3. Example models.** Here, we describe three examples of varying areas of application and complexity, covering statistics and data science (parameterised normal distributions based on approximations to the binomial and Poisson models) [57, 2, 1], biochemistry and bioengineering (Michaelis-Menten kinetics) [52, 37], and physics and engineering (groundwater flow, heat conduction, diffusive and other transport modelling) [4, 28, 62, 11, 22, 6].

**3.1. Parameterised normal approximations.** Our first example considers estimating the number of trials  $n$  and success probability  $p$  in a continuous approximation to a binomial model. Near the Poisson limit (large  $n$ , small  $p$ ), maximum likelihood estimates become unstable [57], providing a case study in practical non-identifiability.

The model for a single (‘ $n$ -trial’) experiment is:

$$(3.1) \quad Y \sim \mathcal{N}(np, np(1 - np)),$$

with Poisson limit case:

$$(3.2) \quad Y \sim \mathcal{N}(np, np).$$

The auxiliary mapping connects the underlying  $(n, p)$  ‘mechanistic’ parameters to normal distribution parameters:

$$(3.3) \quad \phi : \begin{bmatrix} n \\ p \end{bmatrix} \mapsto \begin{bmatrix} np \\ np(1 - p) \end{bmatrix} = \begin{bmatrix} \mu \\ \sigma^2 \end{bmatrix}.$$

Although this is not really a ‘mechanistic’ model in the usual sense, one could consider an underlying binomial model is a lower-level mechanism that ‘generates’ the higher-level (approximately) normally distributed observations. The problem is to determine both  $n$  and  $p$  given  $k$  observations from the single experiment model given by (3.1) or (3.2).

**3.2. Michaelis-Menten kinetics.** Our second example is the Michaelis-Menten model [37, 52]. This equation describes substrate depletion:

$$(3.4) \quad \frac{dS}{dt} = -\frac{\nu S}{K + S},$$

where  $S$  is substrate concentration,  $\nu$  is maximum growth rate, and  $K$  is the half-saturation constant. For low substrate concentrations relative to  $K$ , this model has practical identifiability issues (see [34] in the context of microbial growth models), and the model approximately reduces to:

$$(3.5) \quad \frac{dS}{dt} = -\frac{\nu}{K}S.$$

The auxiliary mapping takes parameter vector  $\theta = [\nu, K]^T$  to a vector of solution values  $s(\theta)$  defined on a fine time grid. For simplicity, we assume a normal distribution error model with constant standard deviation  $\sigma = 0.05$ , though, e.g., log-normal errors or other error models can also be considered easily within our framework [55] (see also the next example). Observations then follow:

$$(3.6) \quad s_{\text{obs}} \sim \mathcal{N}(B_{\text{obs}}s(\theta), \sigma^2 I),$$

where  $B_{\text{obs}}$  maps to observation points and  $\sigma = 0.05$ .

In our present work we use the (structural) auxiliary mapping to determine the reparameterisation, but the point estimate is determined by using the likelihood based on the observed data distribution above.

**3.3. Flow in heterogeneous media.** Our final example models groundwater flow in a heterogeneous aquifer [4, 28, 62], governed by:

$$(3.7) \quad T_i \frac{d^2 h}{dx^2} + R = 0,$$

for regions  $i = 1, 2$ , with transmissivity  $T_i$  and recharge rate  $R$ . Boundary conditions enforce zero head at endpoints and continuity at the interface:

$$(3.8) \quad \begin{aligned} h_1(0) &= 0 \\ h_2(L) &= 0 \\ h_1(L/2) &= h_2(L/2) \\ -T_1 \frac{dh_1}{dx}(L/2) &= -T_2 \frac{dh_2}{dx}(L/2). \end{aligned}$$

Analogous models appear in heat conduction, diffusive transport, and other transport phenomena [11, 22, 6].

The solution (supplementary information) depends only on ratios  $R/T_1$  and  $R/T_2$ , indicating structural non-identifiability. Here we use a log-normal error model for the hydraulic head values with constant standard deviation  $\sigma$ . Observations then follow:

$$(3.9) \quad \log h_{\text{obs}} \sim \mathcal{N}(\log B_{\text{obs}}h(\theta), \sigma^2 I),$$

where  $\theta = [T_1, T_2, R]^T$ , and  $h(\theta)$  is the fine-scale solution.

**4. Results and Discussion.** Here we present the results of our analysis of the three example models described in Section 3. The first example is simple but illustrates many of the key conceptual components of our approach, including both structural and practical non-identifiability; the second involves a differential equation in time that is solved numerically and utilises automatic differentiation to compute the Jacobian of the auxiliary mapping; and the third involves a differential equation in space that can be solved analytically but involves three parameters and structural non-identifiability. For this last example, we show how parameter non-identifiability and predictive uncertainty are related using the PWA approach.

**4.1. Parameterised Normal Models.** These examples are sufficiently simple that we can illustrate the core ideas analytically, and so we first outline some analytical results. We then present numerical results, produced without assuming these analytical results were available, using generic model-agnostic code.

We focus our analytical illustration on the Poisson limit model for simplicity, defined by (3.2). In this model, we expect only  $np$  to be identifiable, as the variance is equal to the mean. We will show that both symbolic (original parameters) and numerical (log-transformed parameters) approaches obtain this result.

We also present the results of numerical, likelihood-based analysis of both parameterised normal models. We consider the likelihood functions in both original parameterisation and our reparameterisations. Although the likelihood is invariant to reparameterisation, we see how the reparameterisation ‘brings out’ the separation of information concerning the identifiable and non-identifiable parameters.

**4.1.1. Analytical results: Poisson limit model, original parameterisation.** To first obtain the symbolic result we note, as above, that the auxiliary mapping in terms of untransformed parameters is given by

$$\phi(n, p) = \phi\left(\begin{bmatrix} n \\ p \end{bmatrix}\right) = \begin{bmatrix} np \\ np \end{bmatrix}.$$

The Jacobian of this mapping is given by

$$(4.1) \quad D\phi(n, p) = \begin{bmatrix} p & n \\ p & n \end{bmatrix}.$$

This is a function of  $n$  and  $p$  and clearly has a non-trivial null space for all  $n$  and  $p$ . As the Jacobian and the associated null space depend on (are given as a function of)  $n$  and  $p$  we refer to this as the ‘symbolic’ null space of the model. We can determine this by inspection, noting that vectors of the form

$$(4.2) \quad \alpha(n, p) = \begin{bmatrix} n \\ -p \end{bmatrix}$$

satisfy  $D\phi(n, p)\alpha(n, p) = 0$  for all  $n$  and  $p$ . Thus the symbolic null space has dimension one and is spanned by the vector  $\alpha(n, p)$ ; furthermore, the row space of  $D\phi(n, p)$  hence has dimension one and is spanned by a symbolic vector orthogonal to  $\alpha(n, p)$ . This implies that  $\psi(n, p)$  is scalar-valued and can be determined by equating the (unknown) single row of  $D\psi(n, p)$  to

the (transpose of the) vector spanning the (known) row space of  $D\phi(n, p)$ . By inspection, we see that the row space of  $D\phi(n, p)$  is spanned by the vector  $[p, n]^T$ , which is orthogonal to  $\alpha(n, p) = [n, -p]^T$ .

Thus we can determine  $\psi(n, p)$  equating the rows of  $D\psi(n, p)$  to the vectors spanning the row space of  $D\phi(n, p)$ , or by solving the partial differential equation

$$(4.3) \quad \frac{\partial \psi}{\partial n} n + \frac{\partial \psi}{\partial p} (-p) = 0,$$

based on the orthogonality of the rows of  $D\psi(n, p)$  and the vectors spanning the null space of  $D\phi(n, p)$ . By inspection, we see that  $\psi(n, p) = np$  is a solution to these equations, and hence the identifiable parameterisation is given by  $\psi(n, p) = np$ , as expected. This approach is equivalent to that of [13, 27, 18, 17] but, as with their approach, requires symbolic determination of the Jacobian and the solution of partial differential equations. We now show how our numerical approach can determine the same result without symbolic manipulation.

**4.1.2. Analytical results: Poisson limit model, log-transformed parameterisation.** We now consider the Poisson limit model in log-transformed parameters. By definition (specifically, from parameterisation invariance) the auxiliary mapping in terms of log-transformed parameters satisfies

$$(4.4) \quad \phi_*(n^*, p^*) = \phi_* \left( \begin{bmatrix} n^* \\ p^* \end{bmatrix} \right) = \phi \left( \begin{bmatrix} n \\ p \end{bmatrix} \right) = \phi \left( \exp \left( \begin{bmatrix} n^* \\ p^* \end{bmatrix} \right) \right),$$

where  $n^* = \log n$  and  $p^* = \log p$  and where  $\exp$  is the componentwise exponential function.

The right-hand side of the above equation is obtained from the definition of the auxiliary mapping in terms of untransformed parameters:

$$(4.5) \quad \phi \left( \begin{bmatrix} n \\ p \end{bmatrix} \right) = \begin{bmatrix} np \\ np \end{bmatrix} = \begin{bmatrix} \exp(n^*) \exp(p^*) \\ \exp(n^*) \exp(p^*) \end{bmatrix} = \begin{bmatrix} \exp(n^* + p^*) \\ \exp(n^* + p^*) \end{bmatrix}.$$

Thus the Jacobian of the auxiliary mapping in terms of log-transformed parameters is given by

$$(4.6) \quad D\phi_*(n^*, p^*) = \begin{bmatrix} \exp(n^* + p^*) & \exp(n^* + p^*) \\ \exp(n^* + p^*) & \exp(n^* + p^*) \end{bmatrix} = \exp(n^* + p^*) \begin{bmatrix} 1 & 1 \\ 1 & 1 \end{bmatrix}.$$

As expected, this takes the SVD form (up to normalisation of the singular vectors):

$$(4.7) \quad D\phi_*(n^*, p^*) = \underbrace{\begin{bmatrix} 1 \\ 1 \end{bmatrix}}_{D_{\psi_*} \tilde{\phi}(\psi_*(\theta^*))} \underbrace{\exp(n^* + p^*)}_{\text{diag}(\exp(A\theta^*))} \underbrace{\begin{bmatrix} 1 & 1 \end{bmatrix}}_A,$$

where  $\theta^* = [n^*, p^*]^T$ ,  $A$  is the matrix of the constant linear transformation component of the reparameterisation and  $D_{\psi_*} \tilde{\phi}(\psi_*(\theta^*))$  is the Jacobian of the auxiliary mapping in terms of the transformed, identifiable parameters. The diagonal ‘matrix’ is a scalar in this case as the

intermediate image is represented by a single parameter. Since  $\psi_*(n^*, p^*) = \exp(n^* + p^*)$ , and the output of the auxiliary mapping is

$$(4.8) \quad \phi_*(n^*, p^*) = \begin{bmatrix} \exp(n^* + p^*) \\ \exp(n^* + p^*) \end{bmatrix} = \begin{bmatrix} \psi_*(n^*, p^*) \\ \psi_*(n^*, p^*) \end{bmatrix},$$

we have that  $D_{\psi_*}\tilde{\phi}(\psi_*(\theta^*))$  is also constant in this case. In more general classes of models, the  $A$  matrix will remain constant, but the Jacobian of the auxiliary mapping in terms of the identifiable parameters will depend on the parameters.

Thus we conclude that the identifiable parameterisation is given by

$$(4.9) \quad \psi_*(n^*, p^*) = \exp(A\theta^*) = \exp\left(\begin{bmatrix} 1 & 1 \end{bmatrix} \begin{bmatrix} n^* \\ p^* \end{bmatrix}\right) = \exp(n^* + p^*) = \exp(\log n + \log p) = np.$$

This is the same result as obtained in the symbolic analysis above. However, as the  $A$  matrix here is constant, and corresponds (up to normalisation) to the singular vector of the Jacobian of the auxiliary mapping in log-transformed parameters, we can determine it with a single numerical evaluation of the Jacobian. This is the key advantage of our numerical approach.

We can also determine the non-identifiable parameters by considering the full SVD of the Jacobian (or by finding orthogonal vectors to the identifiable parameter combination). As before, this implies that the non-identifiable parameter combination is given by

$$(4.10) \quad \lambda_*(n^*, p^*) = \exp\left(\begin{bmatrix} 1 & -1 \end{bmatrix} \begin{bmatrix} n^* \\ p^* \end{bmatrix}\right) = \exp(n^* - p^*) = \frac{n}{p}.$$

**4.1.3. Numerical results: Poisson limit model.** Below we present the results of our numerical analysis of the Poisson limit model. We show the likelihood functions in both the original parameterisation and the ‘invariant image’ reparameterisation in Figure 3. We used true parameter values of  $n = 100$  and  $p = 0.2$ , and a sample size of 10. We also imposed bounds of  $[0, 500]$  and  $[0, 1]$  for  $n$  and  $p$ , respectively. For reproducibility, the data realisation used was  $[21.9, 22.3, 12.8, 16.4, 16.4, 20.3, 16.2, 20.0, 19.7, 24.4]$ . This was generated from the *non-limit* model, i.e. treating the limit model as an approximation at the analysis rather than data generation stage. The analysis can be found in the [repository](#) at `examples/stat_model.jl`.

The top row of Figure 3 shows the likelihood in the original parameterisation,. We see a long ‘banana’ shaped likelihood contour in the  $(n, p)$  plane, illustrating the existence of (approximately) equivalent parameter combinations lying along a curved relationship. The profile likelihoods for each parameter illustrate the individual non-identifiability of the parameters. The likelihood is completely flat for both parameters, other than where the bounds of the parameter space are reached. Together these results imply that the two parameters are not individually identifiable in this model, though there may be some combination of parameters that is identifiable (i.e.  $np$ , as we have shown analytically).

The bottom row of Figure 3 shows the likelihood in reparameterised space. We see the likelihood is constant in the vertical,  $\frac{n}{p}$ , direction and varies only in the horizontal,  $np$ , direction. This reflects the identifiability of the parameter combination  $np$ , and the non-identifiability of the parameter combination  $n/p$ . Furthermore, this structure means the information concerning the identifiable and non-identifiable parameters is completely separated, as the likelihood

factors into a product of a function of  $np$  and a (constant) function of  $n/p$  (see e.g. the discussion in [2, 21]). Thus we can, in principle, construct an autonomous reduced model based on the identifiable parameter combination  $np$  (as can be seen analytically).

The profile likelihoods for the new parameters, shown in the bottom row of Figure 3 further illustrate the distinct identifiability properties of these parameter combinations. The profile likelihood for  $np$  is a simple Gaussian-like function, showing good estimability, while the profile likelihood for  $n/p$  is completely flat, demonstrating non-identifiability.

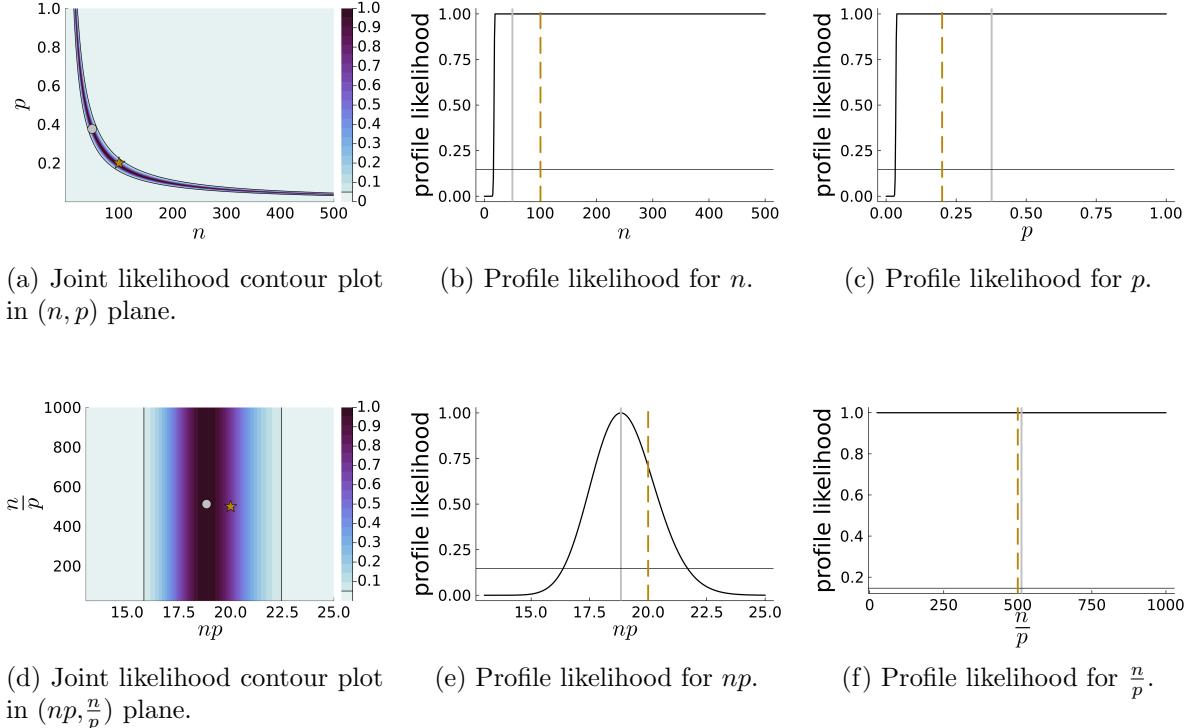


Figure 3: Poisson-limit example analysis in original (top row) and reparameterised (bottom row) parameter spaces. For the contour plots (left column), gold stars show the true parameter value, silver circles show the maximum likelihood estimate, and the colour bar represents the relative likelihood. For all plots, black contour/horizontal lines indicate the 95% confidence interval threshold. For profile likelihood plots (centre, right columns), the solid silver vertical line indicates the maximum likelihood estimate, and the dashed gold vertical line indicates the true parameter value.

**4.1.4. Numerical results: non-limit model.** We now consider the non-limit model, defined by (3.1). This model is now technically identifiable – for example, the mean and variance are now distinct as  $np \neq np(1 - p)$  for  $p \neq 0$ , and we can solve for  $n$  and  $p$  separately from these two quantities. However, near the Poisson limit, we also expect the parameters to be practically non-identifiable, i.e. poorly-identified. In this setting, the well-identified parame-

ter determined from the SVD will be close but not exactly equal to  $np$ , while there will be a poorly identified parameter close to but not exactly equal to  $n/p$ . We can either work with the exact SVD singular vectors obtained, e.g., for our point estimate, or use the heuristic rounding approach to obtain the approximate reparameterisation. Here we find that our rounding heuristic (dividing by smallest non-zero entry and rounding to nearest 0.5) indeed recovers the previous identifiable and non-identifiable parameter combinations, but these now correspond to ‘well-identified’ and ‘poorly but structurally identified’ parameters, respectively.

For these results, again, we used true parameter values of  $n = 100$  and  $p = 0.2$ , a sample size of 10, and the same parameter bounds. For reproducibility, the data realisation used was (again) [21.9, 22.3, 12.8, 16.4, 16.4, 20.3, 16.2, 20.0, 19.7, 24.4]. The analysis can again be found in the [repository](#) at `examples/stat_model.jl`.

These results can be seen in Figure 4, and largely mirror those of the Poisson limit model. The well-identified parameter  $np$  and the poorly identified parameter  $n/p$  are again clearly separated in the reparameterised space. However, in this case, the separation is not exact, and the poorly identified parameter is not completely flat in the profile likelihood. We also see *one-sided identifiability* in both the original parameterisation and in the poorly identified parameter in the reparameterised model – the likelihood is much flatter on one side of the maximum likelihood estimate than the other. We can attribute this to the model becoming poorly identified in the Poisson limit, which occurs asymmetrically in parameter space.

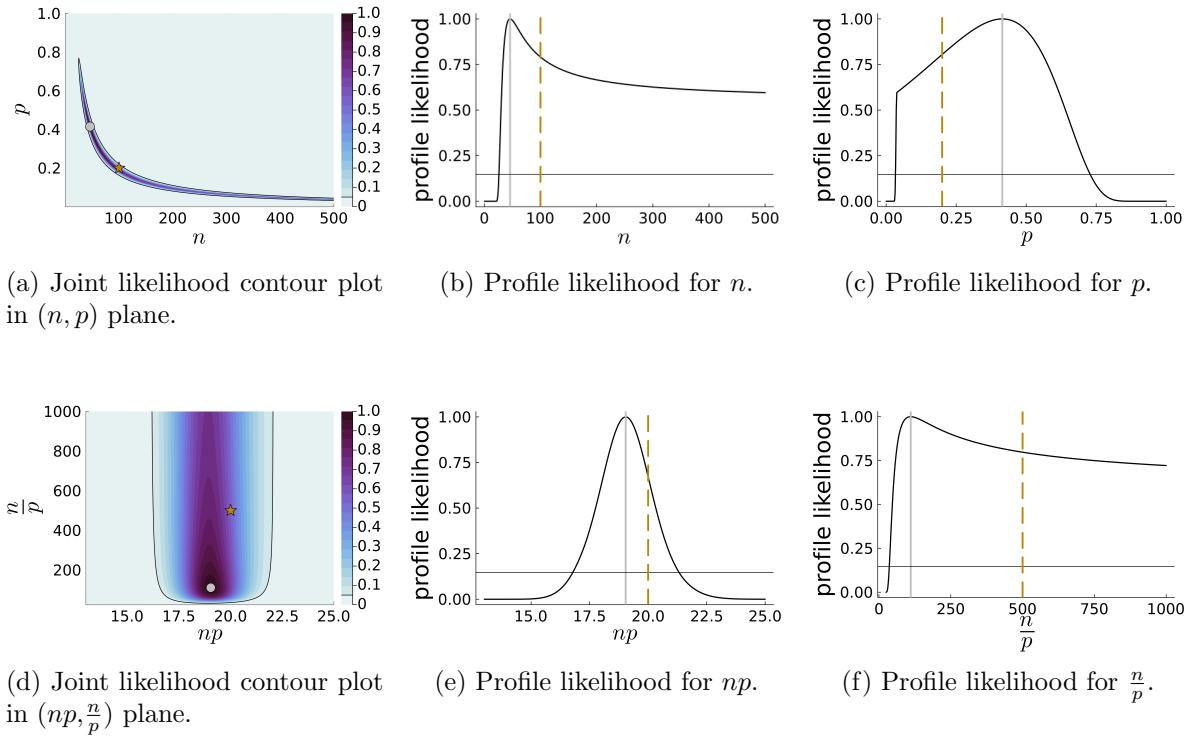


Figure 4: Non-limit (approximate Binomial) example analysis in original (top row) and reparameterised (bottom row) parameter spaces. For the contour plots (left column), gold stars show the true parameter value, silver circles show the maximum likelihood estimate, and the colour bar represents the relative likelihood. For all plots, black contour/horizontal lines indicate the 95% confidence interval threshold. For profile likelihood plots (centre, right columns), the solid silver vertical line indicates the maximum likelihood estimate, and the dashed gold vertical line indicates the true parameter value.

**4.2. Michaelis-Menten kinetics.** We now consider the Michaelis-Menten kinetics model, defined by (3.4). This model is structurally identifiable but practically non-identifiable in the limit regime where the initial substrate concentration,  $S(0)$ , is low relative to the half-saturation constant,  $K$ . For this example, we first focus on results from the non-reduced model before considering the reduced model. This reflects the more natural process of analysis, where identifiability analysis suggests the possibility of a reduced, structurally non-identified model, which could be investigated subsequently.

For these results, we used an initial concentration of  $S(0) = 1$ , a true half-saturation constant of  $K = 5.0$ , and a maximum growth rate of  $\nu = 1.0$ . We used a normal observation model with standard deviation  $\sigma = 0.05$ , and observed the concentrations at 11 equally spaced time points between 0 and 20. We used a fine time grid of 201 points between 0 and 20 for the model solution in the auxiliary mapping computations. This regime is relatively close to the limit regime, but not so close that the effects are negligible. We expect the parameters

to be potentially practically non-identifiable in this regime, but structurally identifiable. Our analysis can be found in the [repository](#) at `examples/mm_model.jl`.

The top row of Figure 5 shows the results of the non-reduced model analysis in the original parameterisation. We see that the joint likelihood contours in the  $(\nu, K)$  plane consist of ‘fanning’ lines, indicating the existence of parameter combinations having similar likelihood values. The profile likelihoods for each parameter show that the maximum likelihood estimate is close to the true parameter value in this particular case but that the likelihood is very flat to one side (excluding the effects of parameter bounds) and shows characteristic ‘one-sided identifiability’, i.e. limiting non-identifiability.

The bottom row of Figure 5 shows the results of the non-reduced model analysis in reparameterised space. Here the parameter combinations identified are  $\frac{K}{\nu}$  (well-identified) and  $\nu K$  (poorly identified). The first parameter represents the time scale associated with the limit model. We see a similar likelihood contour shape to the previous model analysis, with an apparent limiting regime where the parameters are decoupled and one parameter is well-identified while the other is poorly identified. Outside of the limit regime, the relationship between the parameters is more complex, and the parameters are not as clearly separated. Since the likelihood is invariant to reparameterisation, analysis of the non-reduced model in any coordinate system is equally valid. The role of reparameterisation is to bring out the separation of information concerning the potentially identifiable and non-identifiable parameters.

Although only approximate, these results do suggest a structurally non-identified reduced model may be useful, in the limit as  $K\nu$  becomes large while  $\frac{K}{\nu}$  stays constant. This corresponds to the limit model mentioned in the model description section above.

Figure 6 shows the results of the limit (reduced) model analysis in the reparameterised space. We see the likelihood contours agree well in the limit regime, while keeping the separation of parameters in the non-limit regime where the approximation technically breaks down. The profile likelihoods show full non-identifiability of the poorly identified parameter, and good identifiability of the well-identified parameter. This is consistent with the expected behaviour of the reduced, structurally non-identifiable model.

For this model, we provide prediction results using PWA in the supplementary material and provide more detailed prediction results for the transport model next.

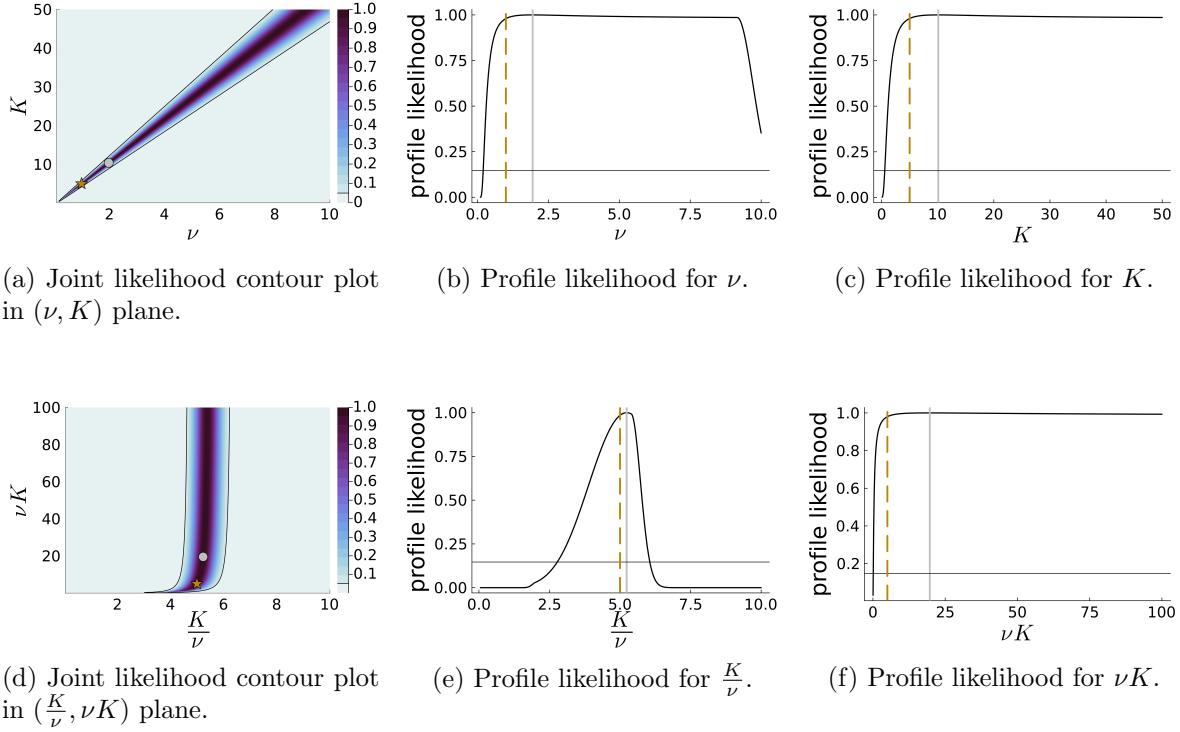


Figure 5: Michaelis-Menten example analysis in original (top row) and reparameterised (bottom row) parameter spaces. For the contour plots (left column), gold stars show the true parameter value, silver circles show the maximum likelihood estimate, and the colour bar represents the relative likelihood. For all plots, black contour/horizontal lines indicate the 95% confidence interval threshold. For profile likelihood plots (centre, right columns), the solid silver vertical line indicates the maximum likelihood estimate, and the dashed gold vertical line indicates the true parameter value.

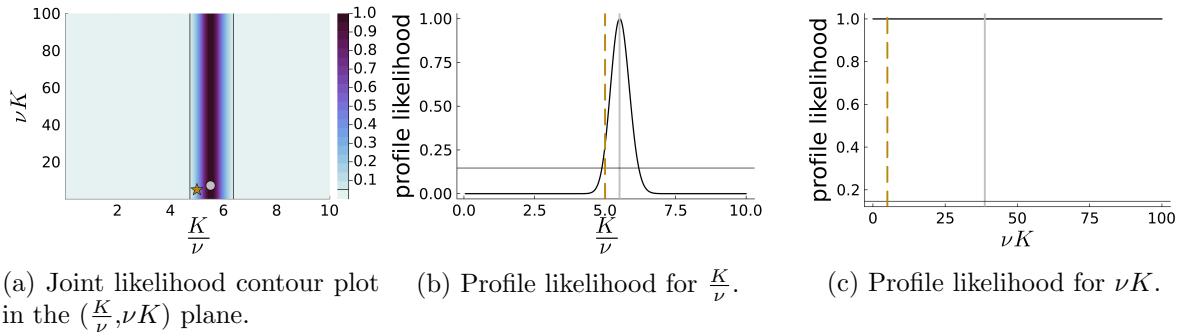


Figure 6: Reparameterised Michaelis-Menten limit example: (Left) joint contour in the  $(\frac{K}{\nu}, \nu K)$  plane. The gold star indicates the true parameter value, and the silver circle indicates the maximum likelihood estimate. The colour bar represents the relative likelihood. (Centre and right) profile likelihoods. The solid silver vertical line indicates the maximum likelihood estimate, and the dashed gold vertical line indicates the true parameter value. For all plots, black contour/horizontal lines indicate the 95% confidence interval threshold.

**4.3. Flow in heterogeneous media.** Here we consider the groundwater model, representing flow in heterogeneous media, defined by (3.7). As discussed in the model section, and shown in the supplementary material, this model is structurally non-identifiable, and can be written in terms of a reduced set of monomial functions of the parameters. Rather than consider further analytical results, we proceed directly to the numerical analysis of the model and verify that our numerical approach can uncover the non-identifiability of the model and suggest a reduced parameterisation.

For these results we used a true parameter value of  $T_1 = 3.0$ ,  $T_2 = 1.0$ , and  $R = 1.0$ , with parameter bounds of  $[0.1, 5]$  for all quantities. We considered a fine grid of 201 points between  $x = 0$  and  $x = L = 100$ , and an observation grid of 19 equally-spaced points, excluding the endpoints. We used a normal observation model with standard deviation  $\sigma = 0.2$  and a single, spatial sample (i.e. a single observation of the model solution at the observation points, giving a data vector of length 19). For reproducibility, the data realisation used was [186.4, 402.6, 505.2, 756.1, 1144.1, 790.9, 1283.5, 1647.6, 872.3, 1144.4, 1691.2, 1352.7, 1519.9, 1316.0, 1437.1, 726.7, 952.3, 759.4, 272.0]. [repository](#) at `examples/transport_model.jl`.

The first two rows of Figure 7 show the results of the analysis in the original parameterisation. For visualisation we consider each of the three joint two-dimensional likelihood profiles with the third parameter ‘profiled out’. We see that the joint profile likelihood contours in the  $(T_1, T_2)$  plane show a ‘fanning out’ of the likelihood contours, indicating the existence of parameter combinations having similar likelihood values. Similarly for  $(T_1, R)$ . For  $(T_2, R)$  we see more concentrated contours, indicating that some combination of these parameters may be better identified. We also show the one-dimensional profile likelihoods for each parameter. These all show largely flat likelihoods, other than decreases induced by bounding constraints, indicating that these parameters are not individually identifiable in this model.

The second two rows of Figure 7 show the analysis in the reparameterised space. The repa-

rameterisation suggested by the SVD is  $(\frac{T_2}{R}, \frac{T_1}{\sqrt{T_2 R}}, T_1 T_2 R)$ , with the first having a singular value two-three orders of magnitude larger than the second, and the third being numerically equivalent to zero (order  $10^{-14}$ ). This indicates that one parameter combination is very well identified, the second somewhat identified, and the third completely unidentifiable. The first two combinations from the SVD reparameterisation are different to the reduced parameter pair that appear in the analytical results, i.e. to  $(\frac{T_1}{R}, \frac{T_1}{R})$ , though these are in one-to-one correspondence. This reflects that the SVD aims to find an orthogonal (in log-parameter space in the present work) reparameterisation in which the information on each parameter combination is maximally separated. Both pairs of parameter combinations are orthogonal to the non-identified parameter combination  $T_1 T_2 R$  in log-space, and are linearly independent, and hence provide a valid basis for the identified subspace. Here the two parameterisations lead to visually indistinguishable results, and so we only show the results of the SVD reparameterisation.

Notably, the reparameterised results indicate possible one-sided identifiability of the less well (but still) identified parameter  $\frac{T_1}{\sqrt{T_2 R}}$ , in addition to the structural non-identifiability of  $T_1 T_2 R$ . This suggests a further reduced limiting model may exist. Here the true value of the first transmissivity parameter  $T_1$  is somewhat larger than the second (three vs one), and the limit suggested by the one-sided non-identifiability is to take  $T_1$  large relative to  $T_2$  and  $R$ . Thus the smaller transmissivity parameter  $T_2$  becomes the limiting factor in the model, and the model can be reduced to a simpler form. This reinforces that profile likelihood-based practical identifiability methods can help determine limiting models, as in [49] and as in the previous examples, though for this example we do not pursue this further.

Finally, we show the profile-wise prediction intervals for the full model in the reparameterised space in Figure 8. We provide the profile-wise prediction intervals for the original parameterisation in the supplementary material. We use a degree of freedom of two for all of the prediction intervals (i.e. number of non-zero singular values and hence intrinsic dimensionality; see also [67]). In the original space the prediction intervals are driven by all three parameters (supplementary material). In the reparameterised space, however, we see that the non-identified parameter  $T_1 T_2 R$  has no effect on the prediction intervals. This is true of both the individual profile-wise prediction interval based on  $T_1 T_2 R$  in the bottom row, and the joint prediction intervals involving  $T_1 T_2 R$  in the top row, which closely match the individual profile-wise prediction intervals for the other parameter in each case.

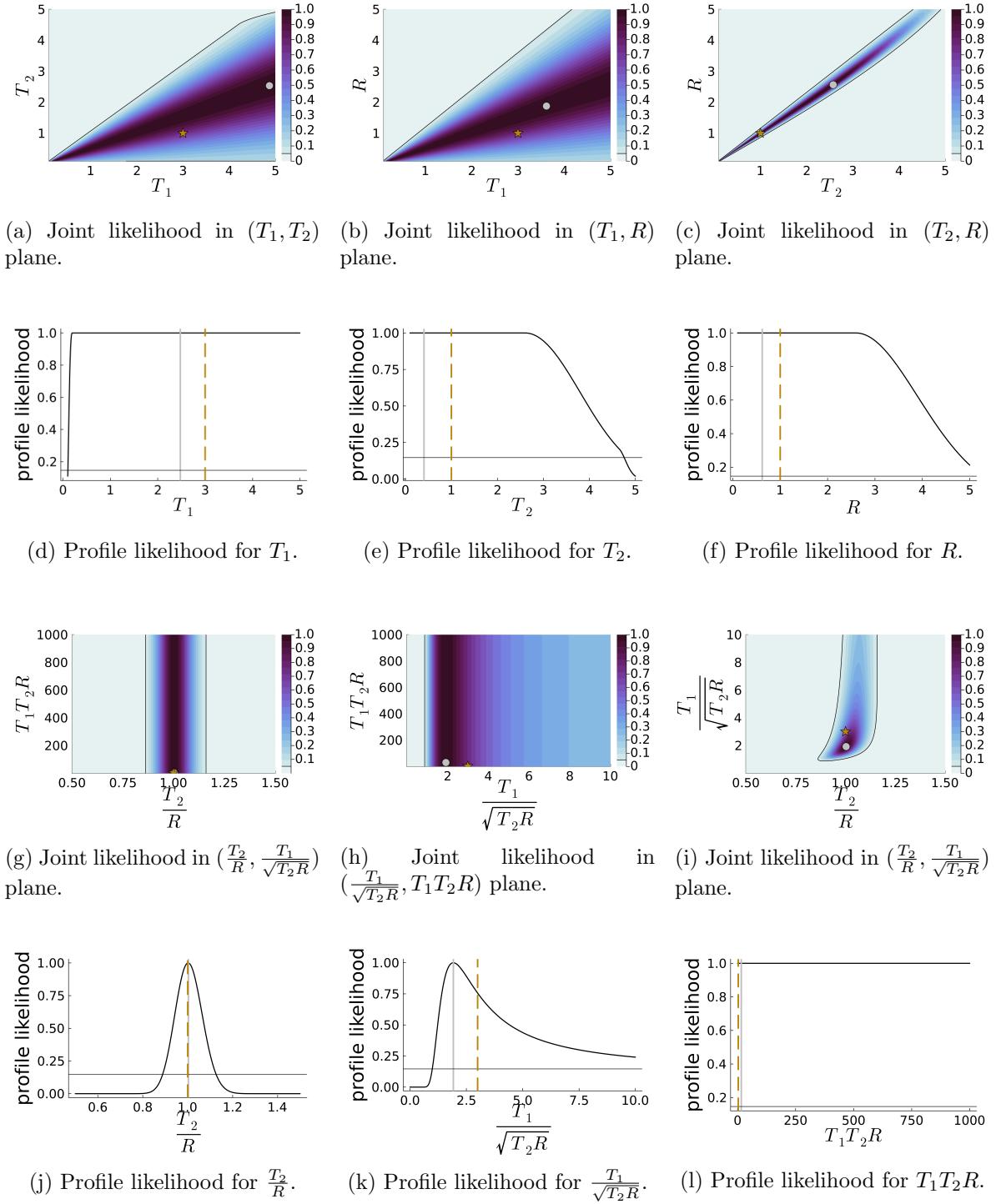


Figure 7: Flow in heterogeneous media example analysis in original (top two rows) and reparameterised (bottom two rows) parameter spaces. First and third rows show joint likelihood contours; second and fourth rows show profile likelihoods. For contour plots, gold stars show the true parameter value, silver circles show the maximum likelihood estimate, and colorbars represent relative likelihood. For all plots, black contour/horizontal lines indicate the 95% confidence interval threshold. For profile likelihood plots, solid silver vertical lines show maximum likelihood estimates and dashed gold vertical lines show true parameter values.

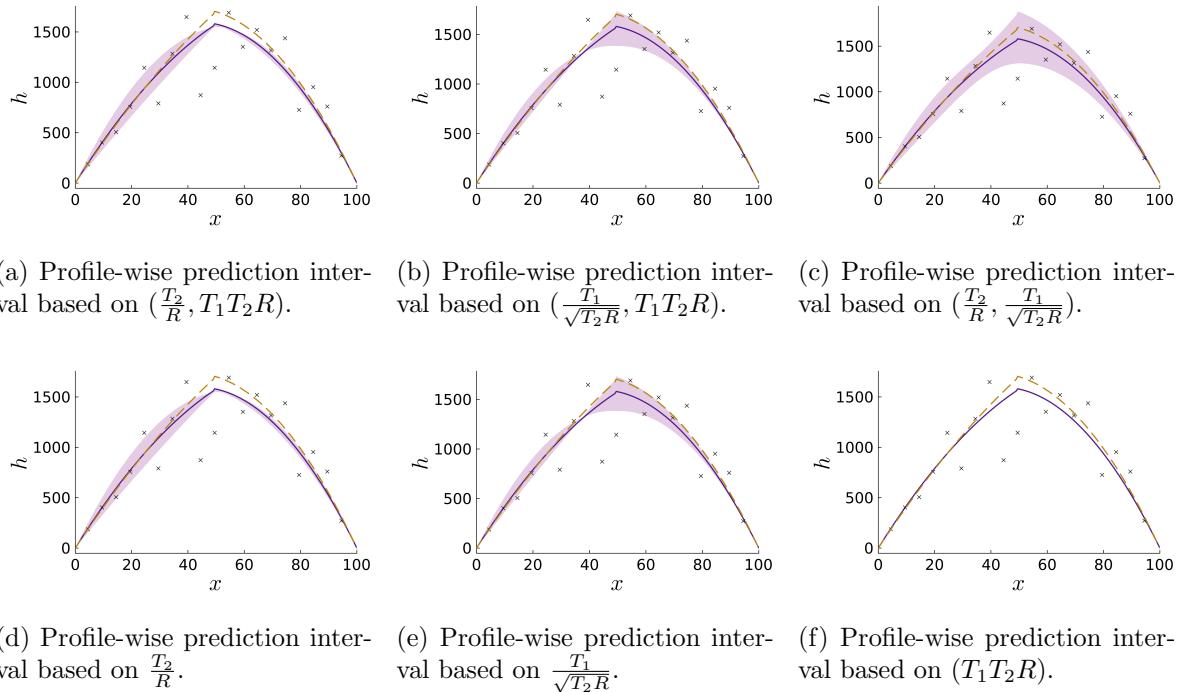


Figure 8: Profile-wise prediction intervals for the mean in the flow in heterogeneous media example in reparameterised space. Top row shows joint prediction intervals; bottom row shows individual parameter prediction intervals. In all plots, gold trajectories show the true mean function, dark purple trajectories show the maximum likelihood estimate, and purple shaded regions represent approximate 95% (predictive) confidence intervals for the mean.

**5. Conclusion and Future Work.** Here we have presented Invariant Image Reparameterisation (IIR), an approach to parameter identifiability analysis that bridges structural and practical identifiability analysis, and symbolic and numerical approaches to implementation. We show how an initial coordinate transformation converts the symbolic approach of discovering identifiable parameter combinations into numerical computation at a single reference point. This numerical approach recovers symbolic results for a common class of parameter combinations while providing a natural ranking of such parameter combinations by their degree of identifiability in general and in cases of practical non-identifiability.

We find that practical non-identifiability, particularly when one-sided or asymmetric, is closely related to the existence of potential model reductions, mirroring observations by [49] on using profile likelihood for model reduction. Our use of profile-likelihood-based Profile-Wise Analysis for uncertainty quantification, in addition to Fisher information-based reparameterisation, reveals such asymmetric limits in terms of likelihood contours and profiles, in contrast to approaches focusing solely on Fisher-information/Hessian analysis.

As in [64], our approach extends to more complex models such as stochastic differential equations or simulation-based models, given an appropriate auxiliary mapping. Here, we used

the full model solution as our ‘exhaustive summary’, while stochastic or simulation-based models generally need more carefully defined data distribution parameters such as moment dynamics equations [9]. Additionally, while our approach applies in principle to larger models, we deliberately considered examples with low parameter dimension, as even these give complex results. Further work could explore applications to larger models and spatially/temporally varying parameters, as well as improving scaling and rounding heuristics for interpretable parameter combinations.

The provided Julia implementation makes our methodology accessible for both analysis and further development. We believe IIR will prove valuable for model development and analysis across the quantitative sciences, particularly in complex applications where symbolic approaches may be impractical.

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**8. Competing interests.** The authors declare that they have no competing interests.

**9. Data and materials availability.** All data needed to evaluate the conclusions in the paper are present in the paper and/or the supplementary material. Julia code associated with this paper is available from GitHub at <https://github.com/omaclarens/reparam>.

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