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Bayesian Uncertainty Quantification for Anaerobic Digestion models

Abstract

Uncertainty quantification is critical for ensuring adequate predictive power of computational models used in biology. Focusing on two anaerobic digestion models, this article introduces a novel generalised Bayesian procedure, called VarBUQ, **ensuring a correct tradeoff between flexibility and computational cost**. A benchmark against three existing methods (Fisher's information, bootstrapping and Beale's criteria) was conducted using synthetic data. This Bayesian procedure offered a good compromise between fitting ability and confidence estimation, while the other methods proved to be repeatedly overconfident. The method's performances notably benefitted from inductive bias brought by the prior distribution, although it requires careful construction. **This article advocates for more systematic consideration of uncertainty for anaerobic digestion models and showcases a new, computationally efficient Bayesian method. To facilitate future implementations, a Python package called 'adug' is made available.**

Keywords: **Biochemical reaction networks**, Computational model, Predictive power, Confidence regions

1. Introduction

Computational modelling is now common practice in many areas of biology, including fields as diverse as environmental sciences, biotechnology and medical sciences (Sordo Vieira and Laubenbacher, 2022). These models are generally used to represent complex systems, such as gene regulation networks, ecological interactions, or biochemical reaction networks. In the field of environmental biotechnology, stan-

25 dard models based on ordinary differential equations have been adopted by the scien-
26 tific community for the most common bioprocesses such as anaerobic digestion (AD)
27 ([Bernard et al., 2001](#); [Batstone et al., 2002](#)). Historically, modelers interested in AD
28 have dedicated much effort over optimisation techniques, in order to efficiently cali-
29 brate these models, notably gradient-based and derivative-free methods ([see Donoso-](#)
30 [Bravo et al. \(2011\) for a survey](#)).

31 From a statistical viewpoint, the calibration of a number of parameters comparable
32 to the number of observations is a high dimensional estimation problem, where spe-
33 cial attention must be paid to the risk of overfitting. [Rieger et al. \(2012\)](#) indicates
34 good practices for conducting validation, notably using different datasets, working
35 under different conditions and operational parameters. In practice, observations can
36 be scarce, preventing experimenters to fully validate their model ([see Dochain and](#)
37 [Vanrolleghem, 2001](#)). This is notably the case when operating conditions are differ-
38 ent for training and testing datasets. This assumption is called dataset or distribu-
39 tion shift in learning theory ([Quinonero-Candela et al., 2008](#)). In this setting, how
40 much the predictions will diverge from the truth as time goes by can not be inferred
41 through validation, since validation data is assumed to be missing.

42 Uncertainty quantification (UQ) methods are essential tools to assess the quality of
43 the calibration. UQ is the quantitative analysis of the impact that sources of ran-
44 domness have on the calibration process. This randomness originates from the mea-
45 surements' noise as well as the stochastic nature of the future influent. UQ methods
46 estimate how far the calibrated set of parameter values as well as the predictions of
47 the calibrated model diverge from the truth, using statistical theory. Ideally, UQ on
48 the predictions should be robust to distribution shift, warning the user whenever the
49 calibration is no longer valid through an increase in predictions uncertainty.

50 Unfortunately, careful assessment of uncertainty is far from systematic in AD mod-

51 elling. Still, techniques have been used to quantify uncertainty for AD model calibra-
52 tion. The three prevalent methods in the field are based on Fischer’s information ma-
53 trix (FIM) (aka Cramér-Rao’s lower bound or information inequality, see Chapter 2
54 in Lehmann and Casella, 1998), a statistical criteria introduced in Beale (1960) (from
55 now on called Beale’s method), and bootstrapping. These methods infer uncertainty
56 on the parameters from residuals of the calibrated model. They are generally used to
57 provide UQ only for parameters which are fitted, *e.g.* those selected by a sensitivity
58 analysis (SA) routine. The remaining parameters are fixed at some default value, as
59 they are not deemed to have sufficient influence on predictions. But those parameters
60 actually have large uncertainty, since the data is not able to discriminate between
61 two widely different values. As the sensitivity of the model’s response to each param-
62 eter depends on operating conditions, the quality of extrapolations of the model on
63 new conditions can only be known if uncertainty is quantified on all parameters, or if
64 these operating conditions have been previously validated (Rieger et al., 2012).
65 Bayesian methods are designed to tackle the uncertainty on all parameters through-
66 out the training process, as they perform calibration and UQ jointly. The uncer-
67 tainty on parameters with little sensitivity impact on the model is controlled through
68 expert’s knowledge, encoded in a probability distribution called prior. The prior is
69 twisted into the posterior distribution through confrontation with the observations,
70 concentrating on sets of parameters likely to have generated them. The calibrated
71 model is no longer deterministic, but stochastic.
72 While uncommon, Bayesian flavoured techniques have already been used in the con-
73 text of AD modelling (Martin and Ayesa, 2010; Martin et al., 2011; Couto et al.,
74 2019; Pastor-Poquet et al., 2019). All these Bayesian inspired algorithms output the
75 uncertainty in the form of a sample. Statistical theory shows that satisfactory de-
76 scription of a generic distribution require a number of samples increasing at a more

77 than exponential rate with the number of parameters fitted (see [appendix D](#)). This
78 heavily restricts the applicability of such algorithms for highly parameterized models.
79 [Variational Bayesian methods \(Hinton and Van Camp, 1993; Beal, 2003\)](#) learn the
80 [best approximation of the posterior amongst a class of distributions \(e.g., Gaussians,](#)
81 [Gaussians mixture\)](#). These structured posterior can be fully assessed using fewer
82 [model evaluations](#). The flexibility of the posterior (covariance structure, multimodal-
83 ity) is governed by the distribution class considered. For AD modelling, Gaussian
84 posteriors with block diagonal covariance present an interesting tradeoff, exploring
85 non trivial correlation structure while limiting the number of hyperparameters.
86 [A novel methodology for the joint calibration and UQ of AD models based on vari-](#)
87 [ational Bayes and learning theory, called Variational Bayesian Uncertainty Quan-](#)
88 [tification \(VarBUQ\), is introduced](#). The methodology is available as an open source
89 Python package and can be readily applied to any AD or biochemical reaction net-
90 work model. Its performance is compared to the prevailing *ad hoc* UQ [routines](#) (FIM,
91 Beale and Bootstrap), considering two AD models of varying complexity - Anaero-
92 bic Model 2 (AM2, [Bernard et al. \(2001\)](#)) and Anaerobic Digestion Model 1 (ADM1,
93 [Batstone et al. \(2002\)](#))-, using six synthetic datasets describing three different oper-
94 ating conditions and two sets of parameters monitoring the prior distribution's in-
95 ductive bias. Such synthetic data allows to assess the ability of the UQ methods to
96 recover the true parameter values, as well as their performance on test datasets. Spe-
97 cial attention is paid to the robustness of each UQ methods to distribution shift.

98 **2. Materials and Methods**

99 *2.1. Anaerobic Digestion models and data generation*

100 Observations used for calibration are generated using the AD model considered in
101 each benchmark (ADM1, AM2). The description of the intrans is likewise synthetic.

102 ADM1’s implementation is adapted from the PyADM1 package (<https://github.com/CaptainFerMag/PyADM1>). AM2’s implementation was written from scratch, using the formulation given in Bernard et al. (2001), with slight modifications to benefit from pH measurements and include microbial mortality (see appendix A). Both models are implemented in Python and are accessible on the following github repository: <https://github.com/BayesianUncertaintyQuantifAnaeroDig/AnaeroDigUQ>.

108 For each AD model, the modelled digester consists in a single stage digestion system with a liquid phase measuring 3400 cubic meter and a gas phase measuring 300 cubic meter. The temperature inside the digester is kept constant at 308.15 K. The frequency of the data was set to represent realistic monitoring data - respectively 24 hour and 6 hours between each data point for observations (e.g. biogas quality) and influent data (e.g. mass flow). 280 days are simulated, the first 70% (196 days) of which are used for calibration. The remaining part is used to assess the validity of the UQ methods on the predictions.

116 Each AD model is used to generate four datasets, describing two levels of intrans dynamics and two different sets of parameters. The datasets are denoted LN, HN, LF, HF, with L and H standing respectively for low and high dynamics of intrans, while N and F stands respectively for a set with parameter values near or far their default values. The same intrans was used for L datasets (respectively H datasets), while the same set of parameters is used to construct N datasets (resp. F datasets).

122 The N and F parameters are constructed using the prior distribution (see Section 2.2.1). The N (respectively F) parameter is drawn from the prior, and then renormalised in such a way that the χ^2 -test rejects the hypothesis that it is drawn from the prior with a p-value of 0.95 (resp 0.05).

126 The intrans datasets are constructed using sums of random sinusoids. The L and H datasets differ in terms of minimum HRT (30 days for L, 10 days for H). The intrans

128 is assumed to contain only carbohydrates, proteins and lipids, the remaining concen-
129 trations being set to 0. A detailed description is given in [appendix A](#).

130 To assess the robustness of the calibration and UQ methods under change of operat-
131 ing conditions, two additional datasets for each AD model are constructed by mod-
132 ifying the HRT of the L datasets during the test period. The HRT was lowered to
133 10 days gradually over two weeks. These datasets with varying levels of intransit dy-
134 namism are denoted LVN and LVF.

135 A specific initial state is constructed for each dataset by considering the steady state
136 result of the AD model, using the first characterisation of the intransit. After data has
137 been generated, a noisy copy of inputs, observations and initial states are used for the
138 calibration and UQ routines. The signals are noised in log-space using uniform noise:

$$\log(\text{Obs}_{i,t}) = \log(\text{AD}_{i,t}^*) + \mathcal{U}(-\sigma, \sigma). \quad (1)$$

139 For both AD models, the influent's noise level is 0.08, while the observations noise
140 level is 0.15. The noise levels and the distribution (log-uniform) are not assumed to
141 be known during the optimisation and UQ stages. Yet, the algorithms do rely on
142 the assumption that the observations are noised in log-space. As such, the statistical
143 model considered when performing FIM and Beale's UQ is

$$\log(\text{Obs}) = \log(\text{AD}(\theta^*, \text{Influent}, \text{Obs}_0)) + \sigma\varepsilon. \quad (2)$$

144 **Considering the influent description, none of the UQ method assumes any noise. Yet,**
145 **noise was still added to the influent data. Such noise is transformed in a non linear**
146 **way by the AD model into noise on the predictions. This makes the overall noise**
147 **structure more complex and closer to real world scenario - while the statistical model**
148 **considers a simplified, more tractable noise structure.**

149 Consistently with this model, the objective function or score function considered is
150 essentially a root mean square error in the log space, with slight adjustment to im-
151 prove stability (see [appendix B](#) for details). **The score can be roughly interpreted as**
152 **the mean relative error amongst all the predictions for small score values, *i.e.* a score**
153 **of $S \ll 1$ can be thought of as relative mean error of $100 \times S\%$.**

154 Predictions considered to compute the score for AM2 are the concentrations of solu-
155 ble compounds (S_1, S_2 in the original paper) and the gas flows (q_M and q_C) (784 ob-
156 servations), while the predictions used for ADM1 were VFA concentrations ($S_{va}, S_{bu},$
157 S_{pro}, S_{ac}), concentration of inorganic nitrogen (S_{IN}), gas flows (q_{gas}, q_{CH_4}) and partial
158 pressures ($p_{gas,CH_4}, p_{gas,CO_2}$) (1764 observations).

159 *2.2. VarBUQ algorithm*

160 *2.2.1. Construction of the prior*

161 **Being a generalized Bayesian algorithm, VarBUQ requires a description of the a pri-**
162 **ori belief on the values of parameters in the form of a probability distribution, known**
163 **as the prior distribution.** For both AD models, the prior distribution consists in mul-
164 tivariate Gaussian distributions with a diagonal covariance structure on the log pa-
165 rameters. As such, the global prior draws each parameter independently from one
166 another. This follows the recommendations of [Tsigkinopoulou et al. \(2017\)](#). The indi-
167 vidual priors are constructed using previous description of default values and uncer-
168 tainty ([Rosén and Jeppsson \(2006\)](#); [Batstone et al. \(2002\)](#) for ADM1, [Bernard et al.](#)
169 [\(2001\)](#) for AM2). **Complete methodological details are given in [appendix A](#).**

170 *2.2.2. Variational formulation of generalized Bayes*

171 From a prior distribution, the Bayesian framework constructs a posterior distribution
172 by taking into account the observed data. Formally, it requires a statistical model,
173 in the form of a likelihood function $\ell(\theta, \text{Obs})$, which measures the affinity between
174 the set of parameters and observations. The posterior is then defined using Bayes'

175 formula, as

$$\hat{\pi} = \pi(\theta \mid \text{Obs}) \propto \ell(\theta, \text{Obs})\pi_0(\theta). \quad (3)$$

176 A celebrated result of the Bayesian framework is that, when the number of param-
177 eters is finite, the posterior distribution’s credible regions asymptotically behave like
178 true confidence regions, under mild assumptions on the model and the prior (Bernstein-
179 von Mises’s theorem, see chapter 12 of [Le Cam, 2012](#)). This implies that the poste-
180 rior concentrates around the true set of parameters, and that high probability regions
181 for the posterior can be used to adequately quantify the uncertainty on the parame-
182 ters, with asymptotical guarantees that these regions will have the required coverage.
183 Unfortunately, the Bayesian framework is not robust to improper statistical mod-
184 elling, as is the case in the context of AD. To address this shortcoming, different vari-
185 ants, such as tempered posteriors and Probably Approximately Correct (PAC)-Bayes,
186 were introduced (see [Guedj, 2019](#), for a survey). **A generic methodology popular in**
187 **environmental modelling, the Generalized Likelihood Uncertainty Estimation (GLUE)**
188 **framework, advocates replacing the modelling-based likelihood function by some user**
189 **chosen proxy ([Beven, 2018](#)). This core idea is also shared by the more theory oriented**
190 **PAC-Bayesian paradigm, where the likelihood is replaced by the empirical prediction**
191 **error, which acts as the standard measurement of affinity between data and set of pa-**
192 **rameters in learning theory.** A thoroughly studied case is the Gibbs posterior, defined
193 through

$$\hat{\pi}_\lambda(\theta) \propto \exp\left(-\frac{S(\theta)}{\lambda}\right)\pi_0(\theta).$$

194 By analogy with thermodynamics, λ is called the PAC-Bayesian temperature. **It**
195 **should not be confused with the temperature in the AD process, to which it is not**

196 **related**. It controls the amount of trust given to the observations: for large PAC-
197 Bayesian temperatures, the posterior is close to the prior, while for low PAC-Bayesian
198 temperatures it is similar to a Dirac distribution putting all its probability mass on
199 the minimizer of the score – the celebrated empirical risk minimizer.

200 While Bernstein-Von Mises’s theorem is no longer valid, some guarantees do exist for
201 PAC-Bayesian posteriors. These comes in the form of probably approximately correct
202 (PAC) generalisation bounds, controlling the mean error for the posterior on unseen
203 data. A variety of such bounds were constructed, first for independent, identically
204 distributed observations with bounded errors (McAllester, 1999; Seeger, 2002; Catoni,
205 2007), then under less stringent assumptions (Alquier and Wintenberger, 2012; Seldin
206 et al., 2012; Alquier and Guedj, 2018; Haddouche and Guedj, 2022). However, the
207 lack of an accepted model for intractable distributions makes it difficult to assess the va-
208 lidity of the assumptions even of the most general PAC-Bayes bounds. As such, the
209 PAC-Bayesian technique used does not come with any theoretical guarantee.

210 **Rather than relying on Markov chain Monte Carlo techniques which would construct**
211 **samples from the posterior, VarBUQ is inspired by the variational inference frame-**
212 **work, computing hyperparameters which define a distribution. The algorithm is based**
213 **on Catoni’s PAC-Bayes bound (Catoni, 2007), which interprets Gibbs posteriors as**
214 **result of penalized optimisation:**

$$\hat{\pi} = \arg \inf_{\nu \ll \pi} \nu[S] + \lambda \text{KL}(\nu, \pi_0)$$

215 where KL denotes the Kullback–Leibler divergence. **This penalization results in the**
216 **output (the posterior distribution) diverging from the input (the prior distribution)**
217 **only if the data shows that this is necessary. In other words, there is a tradeoff be-**
218 **tween ”fitting to the observations” and ”remaining close to the prior.” As such, the**
219 **prior gives inductive bias: it tells the algorithm where it should look for solutions,**

220 and how likely one deems each potential solution. This is different to the standard
221 empirical risk minimization algorithm, which does not come with inductive bias: the
222 algorithm will pick up any set of parameters, regardless of whether it would be deemed
223 plausible or not by an expert.

224 To obtain a result that is interpretable, computable and that can be easily saved and
225 reused, the minimisation problem is reduced to a parametric family of distributions.
226 Gaussian distributions with a covariance matrix satisfying some assumptions are con-
227 sidered. These distributions are defined on the unconstrained parametrisation - as the
228 transform between this representation and the standard parametrisation is bijective,
229 there is no difficulty in interpreting these distributions as distributions on the stan-
230 dard set of parameters.

231 In order to keep the dimension of the parametric family of Gaussian reasonable, the
232 covariance matrices were constrained to be block diagonal. The blocks are constructed
233 by clustering parameters having direct impact on the same reactions (see [appendix](#)
234 [B](#)). Parameters belonging to different blocks are drawn independently from one an-
235 other. The Bayesian calibration problem is therefore simplified to

$$\hat{\pi}_\lambda = \arg \min_{\gamma} \pi(\gamma)[S] + \lambda \text{KL}(\pi(\gamma), \pi_0), \quad (4)$$

236 where γ is the hyperparameter describing the distribution. This is solved using ac-
237 celerated gradient descent. Indeed, since the prior is also Gaussian, the KL admits
238 a closed form expression, whose gradient with respect to the distribution's parame-
239 ters can be computed explicitly. The derivative of the integral with respect to $\pi(\gamma)$
240 can be estimated using an independent sample of sets of parameters θ drawn from
241 $\pi(\gamma)$. This estimate is unbiased, and its variance scales in the inverse of the number
242 of samples points. The number of calls to the AD model, which is usually the com-
243 putational bottleneck ([Rosén and Jeppsson, 2006](#)), equals at each step the number of

244 sample points generated. These evaluations can be fully parallelized. To be able to
 245 keep this number of model evaluation reasonable, mechanisms are used to recycle the
 246 evaluations (see [appendix B](#)).

247 For each dataset, the gradient descent procedure runs for 250 steps. For AM2 (resp.
 248 ADM1), 256 (resp. 160) samples are generated at each step, amounting to 64000
 249 (resp. 40000) calls to the AD model. A full description of the hyperparameters is
 250 given in [appendix B](#).

251 The choice of the PAC-Bayesian temperature is done a priori. The criteria used to
 252 define this PAC-Bayesian temperature is based on Catoni’s PAC-Bayes generalisation
 253 bound ([Catoni, 2007](#)). This bound, valid for scores defined as a mean of N indepen-
 254 dent, identically distributed losses bounded by C , states that

$$\mathbb{E}_S[\nu[S]] \leq \nu[S] + \lambda \text{KL}(\nu, \pi_0) + \frac{C}{\lambda 8N} + \lambda \log(\delta^{-1}) \quad (5)$$

255 is valid simultaneously for any distribution ν with probability at least $1 - \delta$. The
 256 generalisation guarantee involves the term $\frac{C}{\lambda 8N}$. This implies vacuous generalisation
 257 guarantees if the PAC-Bayesian temperature chosen is too low. The PAC-Bayesian
 258 temperature is chosen in such a way that $\frac{1}{\lambda 8N} < 0.1$, which implies for ADM1 that
 259 $\lambda \geq 0.0007$ and for AM2 that $\lambda \geq 0.0016$. A safety margin was added, and PAC-
 260 Bayesian temperatures of $\lambda_{\text{ADM1}} = 0.001$ and $\lambda_{\text{AM2}} = 0.002$ were used. For ADM1,
 261 PAC-Bayesian temperatures two and eight times larger were also investigated. It
 262 should be stressed that this a priori choice of PAC-Bayesian temperature is debat-
 263 able, since Catoni’s bound assumptions are not met: data is not independent, not
 264 identically distributed, and the score was not a sum of contributions, but the square-
 265 root of a sum.

266 For ADM1, the initial distribution’s parameters were obtained through a specific al-
 267 gorithm, which was able to efficiently reduce the mean score. This was based on the

268 approach described in [Leurent and Moscoviz \(2022\)](#), which uses large samples of sets
269 of parameters to completely redefine Gaussian distributions. The procedure stops
270 when the objective in Equation (4) starts increasing. Such an approach proved nec-
271 essary since the gradient descent procedure struggled for ADM1 to quickly concen-
272 trate the distribution around a satisfactory set of parameters when initiating from the
273 prior.

274 *2.3. Other UQ routines included in the benchmark*

275 Three UQ routines are considered to benchmark VarBUQ: FIM, Beale and Bootstrap.
276 The detailed description of these methods is provided in [appendix C](#). Bootstrap was
277 not evaluated for ADM1, due to excessive computation time.

278 *Contrary to Bayesian joint UQ and calibration, these UQ routines are carried out*
279 *after model calibration. This non-Bayesian calibration was performed by minimizing*
280 *the score function (see [appendix B](#)). As these methods do not follow the Bayesian*
281 *paradigm, they do not require constructing a prior distribution and therefore can be*
282 *easier to implement.*

283 *Selecting parameters to calibrate through sensitivity analysis can mitigate the risk*
284 *of overfitting. The more parameters are selected, the smaller the empirical score of*
285 *the calibrated model will be.* For ADM1, a global sensitivity analysis based on Morris
286 method ([Morris, 1991](#)) is performed to select the parameters to calibrate (with 96
287 repetitions). The minimum and maximum values considered for each parameter are
288 coherent with the prior used by VarBUQ, being two standard deviations below and
289 above the reference value. *Details on the implementation can be found in [appendix](#)*
290 *[B](#).*

291 *2.4. Assessment of parameters uncertainty*

292 *AD model parameters describe quantities which have a physical or biological interpre-*
293 *tation, and inform on properties of the AD process. As such, the uncertainty on the*

294 calibrated parameter values is an important consideration.

295 Each UQ method is assessed through computation of p-values for tests of the hypoth-
296 esis that the true set of parameter is θ^* . If the UQ method performs as it should,
297 these p-values should be uniformly distributed between 0 and 1. Small p-values in-
298 dicate that the UQ is overconfident, as the true set of parameters would be rejected,
299 while large p-values indicate that the UQ is underconfident.

300 2.5. Assessment of uncertainty on predictions

301 The performance of each UQ method is also assessed on predictions using the test set
302 (84 days). The uncertainty on the prediction is obtained by transferring the uncer-
303 tainty on the parameter, through linear uncertainty transport for FIM, and through
304 the evaluation of multiple sets of parameters for all remaining methods. Pseudo 95%
305 confidence intervals (CIs) were then constructed for each prediction by considering
306 quantiles, and their ability to cover the unnoised signal is assessed.

307 Predictions are regrouped as gas flows (q_M , q_C for AM2, q_{gas} , q_{CH_4} for ADM1) and
308 soluble compounds (S_1 , S_2 for AM2, the four main VFAs, S_{bu} , S_{va} , S_{ac} , S_{pro} for ADM1)
309 to assess quality.

310 For each group of predictions, four indicators are computed:

- 311 • The coverage of the CIs, *i.e.* the fraction of predictions inside the CIs,
- 312 • The width of the CIs,
- 313 • The prediction error of the calibrated model,
- 314 • The residual error of the CIs.

315 The residual error of the CI is computed by replacing the standard residuals by the
316 distance between the ground truth and the CI. Notably, if the confidence interval
317 completely covered the truth, the residual error of the CI would be 0.

318 **3. Results and discussion**

319 *3.1. Calibration results on training set*

320 For ADM1, the global sensitivity analysis selected from 9 to 14 parameters depending
321 on the datasets. Only 14 parameters were at least selected once (K_{S_c4+} , k_{m_c4+} , K_{S_ac} ,
322 k_{m_ac} , K_{S_pro} , k_{m_pro} , k_{m_su} , k_{m_aa} , k_{dec} , $K_{I,NH3}$, $pH_{UL:LL\ aa}$, $pH_{LL\ aa}$, $pH_{UL:LL\ ac}$, $pH_{LL\ ac}$
323 in the original paper). Details on parameters selected for calibration for each datasets
324 can be found in [appendix B](#).

325 Once calibrated, the models obtained scores of about 0.09 for AM2 and 0.095 for
326 ADM1. This is slightly above the contribution of the noise on the observations (~~the-~~
327 ~~oretically, 0.087 based on the selected noise level on observations alone~~). This implies
328 ~~that the noise on the influent did increase the overall noise on observations~~. As ex-
329 pected, the optimisation based calibration routine succeeded in finding sets of param-
330 eters achieving a lower score than the one obtained using the true set of parameters.
331 The mean score for VarBUQ is slightly above the score of the true set of parameters
332 for all datasets at the reference PAC-Bayesian temperature (about 0.005 higher for
333 both AM2 and ADM1, implying an absolute increase of 0.5% to the relative error).
334 Doubling the PAC-Bayesian temperature had moderate effect on the train perfor-
335 mance of the posterior, with an increase in the score of about 0.005. Increasing the
336 PAC-Bayesian temperature to eight time its reference value had a more noticeable
337 effect, with a mean score up to 0.024 higher.

338 *3.2. Uncertainty on parameters values*

339 The capacity of the UQ methods to capture the true set of parameters was assessed
340 by computing p-values for tests indicating whether the true set of parameters be-
341 longed to the confidence regions. These p-values are tabulated in Section 4.
342 Ad-hoc confidence regions constructed after standard calibration could generally not
343 account for the large deviations between the true set of parameters and optimised set

344 of parameters for ADM1. This results in FIM’s confidence regions systematically fail-
345 ing to cover the true set of parameters for ADM1, where deviations are particularly
346 noticeable for k_m , K_S couples. This finding remains mostly valid in the case of AM2,
347 since the confidence level must be chosen above the standard 95% criteria in order to
348 cover the true set of parameters with FIM and Bootstrap confidence regions.

349 The results of Beale’s method are of particular interest. As the p-values were con-
350 structed using the theoretical criteria rather than any approximation, its failure to
351 englobe the true set of parameters directly implies that the non linearity in the AD
352 models offers opportunities to reduce the noise significantly more than a linear model.
353 Half of the p-values obtained were orders of magnitude lower than the 0.05 threshold
354 considered, being on two occasions equal to the machine precision ($2.2e - 16$). On the
355 remaining datasets, only one p-value was above the threshold (0.3), while the three
356 others were of order $1e - 3$.

357 Confidence regions constructed with Bootstrap failed to cover the true parameter for
358 any confidence level in three of four cases. Correcting for the number of bootstrap
359 samples generated, the 95% confidence upper bound on the p-values was above the
360 standard 0.05 threshold for only one dataset out of four. This could be related to spe-
361 cific implementation choices designed to mitigate the computation time (see [appendix](#)
362 [C](#)). Bootstrap method are by construction computationally intensive, requiring multi-
363 ple model calibrations, which in the context of AD might prove prohibitive. The com-
364 putational cost of the bootstrap routine could be improved by considering different
365 calibration techniques or laxer termination criteria. However, no satisfactory tradeoff
366 between performance and computational cost was found during the present study.

367 Of all UQ methods, VarBUQ gave the best results for parameter recovery. For ADM1,
368 the results remained unsatisfactory. Using the reference PAC-Bayesian temperature,
369 only one p-value was above the threshold (compared to none for all remaining meth-

370 ods), while two of them were equal to the machine epsilon, and the last one of order
 371 1e-6. This was improved by doubling the PAC-Bayesian temperature, which brought
 372 little train performance loss, though there was still only a single p-value above the
 373 threshold. p-values were further increased by raising the PAC-Bayesian temperature
 374 to eight times the reference, at the cost of noticeable decrease on train performances.
 375 In that last setting, two p-values were above the threshold, while the two remaining
 376 ones are of order 4e-3. For AM2, VarBUQ with reference PAC-Bayesian temperature
 377 obtained satisfactory performance, with p-values all of order 0.9, both for L and F
 378 datasets. For the latter ones, the prior would obtain p-value of 0.05, implying that
 379 the posterior did more than inherit the induction bias.

380 Plots of the confidence regions constructed through each UQ method for the AM2
 381 model (Figure 2) yield qualitative insight on their performances. VarBUQ benefits
 382 from inductive bias as exhibited in figs. 2a, 2b and 2e to 2h, where the confidence
 383 region constructed using the posterior remains almost entirely in the confidence re-
 384 gion constructed using the prior. Still, VarBUQ performed satisfactorily in settings
 385 where the true set of parameters is on the boundary of the prior’s confidence regions
 386 (figs. 2c and 2g). The remaining UQ methods are almost ordered, with FIM’s confi-
 387 dence region nearly englobing Beale’s, which in turn englobes those constructed by
 388 the Bootstrap method. While this seems incoherent with the p-values obtained in
 389 section 4, this could be explained by the additional approximation step required to
 390 construct Beale’s confidence regions. While all UQ method indicate strong correlation
 391 between maximum growth rate and Monod constant, the exact form of the confidence
 392 regions differs. By construction, FIM’s confidence regions are ellipsoidal, while Var-
 393 BUQ’s confidence regions are ellipsoidal in log-space. Interestingly enough, this sec-
 394 ond shape-constraint seems better suited to describe the relationship between the two
 395 parameters, since both Beale and Bootstrap, which outputs confidence regions with

396 no shape constraints, obtain a somewhat similar curvature (figs. 2b to 2f and 2h).
397 Since FIM’s confidence regions are constructed by extrapolating a local linear approx-
398 imation, they can include non physical parameter values (i.e. negative values), as is
399 the case in figs. 2e and 2f and, to a lesser degree, in fig. 2g.

400 Overall, Figure 2 highlights two factors which contribute to VarBUQ’s superior per-
401 formance in comparison to the ad-hoc UQ methods for the AM2 datasets. First, the
402 confidence region it constructed tend to be larger than those constructed using other
403 UQ methods. Second, VarBUQ’s confidence regions are also better centered around
404 the true parameter values, implying that the Bayesian procedure offered a better
405 calibration than the standard calibration procedure. This second feature can be at-
406 tributed to the inductive bias brought by the prior: out of two sets of parameters
407 yielding similar outputs, VarBUQ will favor the one deemed most likely by the ex-
408 perts, even if slightly less performant.

409 3.3. Uncertainty on prediction values

410 As complex AD models such as ADM1 are known to have identifiability issues, as-
411 sessing the performance of the UQ on the parameter is not sufficient. Indeed, since
412 different sets of parameters may still result in similar predictions, confidence regions
413 centered around an incorrect set of parameters could still encapsulate the uncertainty
414 on the predictions. Still, recovering the true set of parameters is the only way to pro-
415 vide full guarantees on the performance of the model on any future dataset.

416 Amongst all UQ methods tested, VarBUQ was best able to recapture the underlying
417 signal. The coverage of its 95% confidence intervals are significantly higher than the
418 other methods for both AD model (see Figure 3b), achieving an overall mean cov-
419 erage of 69%, compared to 38% for FIM, 35% for Beale and 30% for Bootstrap. For
420 each method, the CIs obtained higher coverage for soluble compounds than gas flows
421 - this can be explained by the smaller sensitivity of gas flows to parameter values, as

422 non-biological gas-related parameters such as K_p were assumed to be constant, and
423 higher sensitivity to the input noise.

424 The higher coverage obtained by VarBUQ is coherent with the larger width of its CIs
425 (see Figure 3d). While for the gas flows, these remain too small to fully capture the
426 signal at the target 95% level, VarBUQ's CIs can be large for soluble compounds
427 (up to $\pm 10\%$ for AM2 and $\pm 17.5\%$ for ADM1). Notably, for AM2, VarBUQ's CIs
428 systematically had 100% coverage, indicating underconfidence in the results. Other
429 UQ methods constructed CIs achieving above 95% coverage which were more than 3
430 times smaller for one dataset. Oracle symmetric confidence intervals achieving 100%
431 coverage could be up to 5.6 times smaller, implying that the methodology can still
432 be improved upon. Still, no other UQ method was able to obtain consistently high
433 coverage for soluble compounds. For ADM1, the large width of VarBUQ's CIs ap-
434 pear necessary to obtain the required coverage. In the single case where another UQ
435 method covered more than 90% of the data (Beale for acetate concentration, HN),
436 CIs' width was larger than the one obtained by VarBUQ (0.29 vs. 0.23), for lower
437 coverage (92% vs. 95%).

438 VarBUQ was able to maintain a high level of coverage when the operating condi-
439 tions change, for a reasonable increase in the width of the CIs. CIs constructed using
440 Fisher's information matrix reacted drastically to changes of operating conditions.
441 The width of the CIs reached very high levels for S2 in the AM2 model (resp. 2.2
442 and 3.0 for LVN and LVF, implying an average factor of 8 and 20 between the lower
443 and upper bound on the prediction). This phenomenon is also observed, though to a
444 lesser degree, for ADM1. This could be explained by FIM using linear extrapolation
445 of local changes in the predictions, which do not take into account saturation effects.
446 This interpretation is corroborated by the fact that Beale's CIs' width do not evolve
447 in such a way - resulting in a drop in coverage.

448 Both the standard calibration and VarBUQ obtained low errors on test sets similar
449 to the train sets, with average prediction errors remaining lower than 0.021 for AM2,
450 0.04 for ADM1. While VarBUQ slightly underperformed when the test sets were sim-
451 ilar to the training sets (obtaining prediction scores on average 15% higher), it exhib-
452 ited stronger robustness to change of operating conditions. For those datasets, the
453 average prediction errors of the standard optimisation was 0.041 for AM2 and 0.097
454 for ADM1, respectively 53% and 84% higher than the prediction errors of VarBUQ.
455 The residual prediction error computed after projecting on the CIs is globally smaller
456 using VarBUQ (see Figure 3c). Notably, it was the only method able to obtain resid-
457 ual prediction errors to a low level (< 0.05) for all predictions. Since the predictions
458 are already small when the test influent is similar to the train influent, this indicator
459 is more relevant for the T datasets. For AM2, Bootstrap, Beale and FIM obtained
460 their worst performance on the same variable, S1 (for LVN dataset), of respectively
461 0.15, 0.10 and 0.087, indicating a sizeable gap between the signal and the CIs. For
462 ADM1, Beale and FIM obtained non negligible residual prediction error for the con-
463 centrations of acetate (0.22 and 0.18 respectively). Beale's UQ also failed to properly
464 account for the propionate (0.19).

465 Overall, VarBUQ's UQ was best able to capture the discrepancy between the predic-
466 tions and the true signal. Both FIM and Beale slightly outperformed the Bootstrap
467 method. While FIM and Beale obtained similar performances, FIM reacted better to
468 the change in intrans characteristic, obtaining higher level of coverage.

469 Figure 4 represents the CIs for the predictions of the three main VFAs (butyrate,
470 propionate and acetate) obtained by VarBUQ, FIM and Beale on ADM1, for LN
471 and LVN datasets. Without distribution shift (figs. 4a to 4c), the CIs constructed by
472 VarBUQ englobe those constructed through FIM, which were on average larger than
473 those constructed by Beale's method. All CIs exhibited high frequencies, due to the

474 noisy intrans description. While only VarBUQ’s CIs adequately covered the true sig-
475 nal, the remaining methods still obtained satisfactory performances as the calibrated
476 model’s predictions were suitable. Under distribution shift (figs. 4d to 4f), the cali-
477 brated model’s prediction diverged significantly from the truth. FIM’s CIs widened
478 sufficiently to take into account this discrepancy for butyrate and propionate concen-
479 trations, but not for acetate concentrations. The width of Beale’s CIs remained no-
480 ticeably too small. On the other hand, VarBUQ’s CIs were centered around the true
481 signal, and englobed it adequately.

482 *3.4. Computational cost*

483 Computations were carried out using Microsoft Azure, on virtual machines with 32
484 cores, 64 Gb ram and 256 Gb of memory. Routines fully benefit from parallelisation
485 and one can assume that the number of cores have an almost linear impact on their
486 durations. All durations are supplied in **supplementary materials**.

487 VarBUQ was more computationally intensive than the standard calibration, requir-
488 ing an average of 1 h 40 minutes for AM2 (resp. 30 minutes for standard calibration)
489 and 5 hours for ADM1 (resp. 2 h 30 minutes). This is mitigated once UQ is taken
490 into account. While FIM method’s duration is negligible, Beale’s method required 50
491 minutes for AM2 and more than an hour and a half for ADM1, bridging a large part
492 of the gap. The Bootstrap procedure required prohibitive computational power. As
493 such, this method was only assessed for AM2, with computations lasting about two
494 days. While this computation time could be diminished, by either by reducing the
495 number of Bootstrap procedure or relaxing convergence criteria, this would have seri-
496 ous consequences on the quality of the UQ.

497 *3.5. Potential bias related to calibration method*

498 The performance of the UQ methods benchmarked are impacted by the calibration
499 method. As such, the empirical risk minimisation approach used here should be deemed

500 in part responsible for the obtained results. This choice of calibration method was
501 driven by two considerations. First and foremost, it is a quite common approach
502 in the field, and therefore the results are hopefully representative of the difficulties
503 of obtaining proper UQ for AD models. A second point is that Beale’s UQ method
504 takes its origin in the behavior of the minimiser of mean squared errors objective. To
505 limit confounding factors when assessing the UQ methods, the calibration derived
506 from Beale’s method was therefore used also for FIM and Bootstrap, while VarBUQ
507 uses the same scoring function.

508 For FIM, such a calibration is actually ill suited to the method’s hypothesis, since
509 the requirement that the estimator be unbiased is not met. However, **it should be**
510 **stressed** that this hypothesis will rarely be realistic in the context of AD models,
511 most of all for highly parametrized models. Constructing an unbiased estimator might
512 not be feasible, even when considering a simple statistical model such as Equation (2)
513 - and since the statistical models used have only limited validity, there is little point
514 in trying. Moreover, from a statistical viewpoint, the well known bias–fluctuation
515 tradeoff indicates that biased estimator can give better performances.

516 One important difficulty with the optimisation based procedure used was that it
517 could result in unrealistically high parameter values for the k_m , K_S couples. This was
518 treated by imposing an upper bound on those values when optimising. This could ex-
519 plain why the optimisation procedure had poor robustness when testing on a different
520 intrans. This hints that the calibration could benefit from penalization, in order to
521 favour explanations remaining closer to the standard values.

522 *3.6. Limitations of synthetic datasets*

523 Knowledge of the true set of parameters being primordial when assessing UQ meth-
524 ods for parameter recovery, the benchmark was conducted using synthetic datasets.
525 This implies some debatable modelling decisions. A first decision concerned the mod-

526 elling of the noise. The signal was noised in log space. While not strictly accurate,
527 this implies that the measurement noise will typically be better represented consider-
528 ing relative error. A strong hypothesis was to use the same noise level for all types of
529 observations. This is actually a key requirement in order to use Beale's UQ technique
530 when using different types of predictions. Adapting Beale's method when the noise
531 levels vary is not straightforward, as a core aspect of the method consists in bypass-
532 ing the estimation of the noise levels. A uniform noise structure was preferred to the
533 standard Gaussian noise, so as to test whether this slight change would give an edge
534 to the Bootstrap procedure, specifically designed to deal with unknown noise struc-
535 ture.

536 Noise on the input data resulted in prediction CIs with little smoothness. While the
537 influent signals could have been smoothed, this could have added less detectable bi-
538 ases to the analysis of the results (e.g. choice of the smoothing bandwidth). In prac-
539 tice, observations on the influent might be scarce or exhibit high frequency noise, and
540 as such, the modelling did not seem too unrealistic.

541 Another consideration is that the performance of calibration and UQ using real world
542 data will depend on the mismatch between the computational model and the physical
543 model. Still, the experiments conducted inform on the quality of the UQ methods. A
544 method struggling with synthetic data is unlikely to fare better with real world data.

545 Finally, the methodology used to construct the true set of parameters might favor
546 the Bayesian framework, insofar as the prior is used. This was mitigated by assess-
547 ing the performance on a set of parameters which was deemed unlikely to have been
548 drawn from the prior (p-value of 0.05). Still, any Bayesian framework is expected to
549 work poorly if the prior is badly constructed and is either much too large (resulting
550 in underconfidence) or much too small (resulting in both poor calibration perfor-
551 mances and overconfidence). Constructing adequate priors is therefore a key chal-

552 lenge for the use of Bayesian methods with real data. Thorough bibliographical work
553 is needed to make use of numerous previous works and obtain a state of the art prior.
554 The benchmark's results show that such work could prove valuable; although the
555 other UQ methods can be implemented more easily as they do not require a prior,
556 the Bayesian procedure benefitted from the prior, obtaining confidence regions better
557 centered around the true sets of parameters and confidence intervals on predictions
558 more robust to distribution shift. Notably, it prevents including sets of parameters
559 which an expert would consider unrealistic.

560 3.7. VarBUQ compared to previous Bayesian routines for Anaerobic Digestion

561 Before the present work, Bayesian flavoured techniques had already been used in the
562 context of AD modelling. [Martin and Ayesa \(2010\)](#) developed a Matlab implemen-
563 tation of Monte Carlo methods which could calibrate a 2-parameters AD model accu-
564 rately while also assessing parameter uncertainty, adapt to non-identifiable situations,
565 as well as construct proper and tight confidence regions for predictions ([Martin et al.,](#)
566 [2011](#)). [Couto et al. \(2019\)](#) use a Bayesian framework to fit five parameters in ADM1.
567 [Pastor-Poquet et al. \(2019\)](#) implemented an *ad hoc* Approximate Bayesian Computa-
568 tion (ABC) algorithm to calibrate 14 parameters on a high-solids AD model. Due to
569 implementation choices, the actual algorithm's UQ presents characteristics between
570 Beale and Bayesian methods. The resulting mean parameter was found to offer good
571 predictive power for methane production, though the authors also noted discrepancies
572 in volatile fatty acids (VFA) simulations which could be due to modelling issues.
573 These Bayesian inspired algorithms output the uncertainty in the form of a sample.
574 Conversely, VarBUQ does not output a sample. The algorithm computes hyperpa-
575 rameters defining a probability distribution belonging to a user chosen parametric
576 class (e.g. multivariate gaussian). This offers a more interpretable description of the
577 uncertainty, able to effortlessly generate any number of samples from the posterior.

578 This description can be furthermore stored and used for further calibration, assuming
579 more data has been collected; as such, the algorithm can easily be used in an online
580 learning set-up. In addition, VarBUQ considers a simplified Bayesian framework lim-
581 iting the interactions between parameters to specific cases, chosen through expert
582 knowledge. For instance, in this study, only interactions between parameters acting
583 on the same biological reaction were allowed. This was implemented by considering
584 gaussian distributions with block diagonal covariance, which significantly reduce the
585 number of hyperparameters. This more rigid set-up limits the ability of the poste-
586 rior to fit the data, but reduces the number of model evaluations needed compared to
587 learning a full covariance matrix or general distribution.

588 *3.8. Improving VarBUQ*

589 The Bayesian paradigm showcased here can be improved both in terms of methodol-
590 ogy and implementation. A key aspect is the construction of the prior, which could
591 take into account observed correlations between parameters. This would help the pos-
592 terior further concentrate by removing unlikely combinations of parameters. Another
593 leverage for improvement is the procedure choosing the PAC-Bayesian temperature.
594 Informally, the choice of PAC-Bayesian temperature should be guided by how much
595 training data is used and how far the data ought to be trusted. Quantifying this con-
596 fidence one would be much harder in real world scenario. Using a validation set to
597 select the PAC-Bayesian temperature might be an option, though this would be com-
598 putationally costly.

599 The computational cost of the procedure could be reduced. A promising option con-
600 sists in building surrogate models able to approximate the error of the model for a
601 fraction of the computational cost. A simple method consists in increasing the max-
602 imal time step of the ordinary differential equation solvers at the core of both AD
603 models. This could help quickly building good approximations of the posterior.

604 The variational class plays an important role both in terms of computational com-
605 plexity and performance. The choice investigated here, Gaussian distributions with
606 block diagonal covariance matrix, appeared a good compromise. The block covari-
607 ance structure prevented the posterior from learning spurious correlations between
608 variables, while it was still able to investigate non identifiable cases. Gaussian dis-
609 tributions are also easier to manipulate compared to the prevalent choice in the AD
610 literature, where a combination of uniform and log-uniform distributions are used to
611 construct the prior (Martin et al., 2011; Pastor-Poquet et al., 2019; Tolessa et al.,
612 2023). This choice is usually motivated by the lack of prior knowledge on the parame-
613 ter values beyond their plausible range, hence the use of a so called uninformed prior.
614 On the other hand, covariance plays a crucial role in bypassing AD models' identi-
615 fiability issues. Gaussian distributions offer a simple way to model covariance while
616 uniform distributions do not. To conciliate flat priors with covariance, new parametri-
617 sations of AD models could be considered. For instance, parametrisations considering
618 the ratio of the maximum growth rate and Monod constant might reduce the need for
619 correlations. Another option could be reparametrisations where a the gaussian prior
620 is translated into a uniform prior (using gaussian quantiles transform). Accumulat-
621 ing informations about the actual prior distribution of the parameters, as observed,
622 would inform the best practical choice.

623 *3.9. Applicability to other models*

624 Although VarBUQ was only evaluated on AD models, it should have similar per-
625 formance when applied to models involving kindred mechanisms. Most biochem-
626 ical reaction network models display similar features, relying on a combination of
627 ODEs and algebraic equations, and using similar formulas to infer reaction kinet-
628 ics from the concentration of reactants. For models focusing on microbial commu-
629 nities (*e.g.*, AM2, ADM1, ASM2, models for dark fermentation, etc.), the network

630 usually corresponds to Monod equations in cascade, with corrections for the impact
631 of environmental parameters such as pH or temperature. For cell-centered models
632 (*e.g.*, dynamic metabolic simulation), the same approach is implemented through *e.g.*
633 Michaelis-Menten kinetics which are mathematically analogous to the Monod equa-
634 tion. Thus, it could be considered that all these models form a family with compara-
635 ble non-linearity and differing by their complexity, that is to say the number of rep-
636 resented reactions and model parameters. VarBUQ should display similar advantages
637 and limits for models belonging to this family.

638 4. Conclusion

639 UQ is crucial to ensure that the right level of confidence is given to future model pre-
640 dictions. The Bayesian-inspired methodology outperformed the most commonly used
641 UQ techniques, both regarding parameter recovery and confidence intervals on test
642 predictions. It benefits from inductive bias encoded in the prior, mitigating the risk
643 of overfitting, and improving robustness compared to standard calibration. Its com-
644 putational cost, while important, was still sufficiently small to be used in real world
645 scenario and could still be further improved. The methodology is implemented in a
646 readily-available python package to facilitate future use.

647 E-supplementary data for this work can be found in e-version of this paper online.

648 *Data and code availability*

649 The implementation and datasets used are available on the following github reposi-
650 tory: <https://github.com/BayesianUncertaintyQuantifAnaeroDig/AnaeroDigUQ>.

651 References

- 652 1. P. Alquier, B. Guedj, Simpler PAC-bayesian bounds for hostile data, *Ma-*
653 *chine Learning* 107 (2018) 887–902. URL: [https://doi.org/10.1007/](https://doi.org/10.1007/s10994-017-5690-0)
654 [s10994-017-5690-0](https://doi.org/10.1007/s10994-017-5690-0).

- 655 2. P. Alquier, O. Wintenberger, Model selection for weakly dependent time series
656 forecasting, *Bernoulli* 18 (2012) 883 – 913. URL: [https://doi.org/10.3150/
657 11-BEJ359](https://doi.org/10.3150/11-BEJ359).
- 658 3. D. J. Batstone, J. Keller, I. Angelidaki, S. V. Kalyuzhnyi, S. G. Pavlostathis,
659 A. Rozzi, W. T. M. Sanders, H. Siegrist, V. A. Vavilin, The IWA Anaerobic
660 Digestion Model No 1 (ADM1), *Water Science and Technology* 45 (2002) 65–
661 73. URL: <https://doi.org/10.2166/wst.2002.0292>.
- 662 4. M. J. Beal, Variational algorithms for approximate Bayesian inference, Ph.D.
663 thesis, University of London, University College London (United Kingdom),
664 2003. URL: <https://discovery.ucl.ac.uk/id/eprint/10101435/>.
- 665 5. E. M. L. Beale, Confidence regions in non-linear estimation, *Journal of the*
666 *Royal Statistical Society: Series B (Methodological)* 22 (1960) 41–76. URL:
667 <https://doi.org/10.1111/j.2517-6161.1960.tb00353.x>.
- 668 6. O. Bernard, Z. Hadj-Sadok, D. Dochain, A. Genovesi, J.-P. Steyer, Dynamical
669 model development and parameter identification for an anaerobic wastewater
670 treatment process, *Biotechnology and Bioengineering* 75 (2001) 424–438. URL:
671 <https://doi.org/10.1002/bit.10036>.
- 672 7. K. Beven, *Environmental Modelling*, CRC Press, 2018. URL: [http://dx.doi.
673 org/10.1201/9781482288575](http://dx.doi.org/10.1201/9781482288575). doi:10.1201/9781482288575.
- 674 8. O. Catoni, PAC-bayesian supervised classification: the thermodynamics of
675 statistical learning, *IMS Lecture Notes Monograph Series* 56 (2007). URL:
676 <https://doi.org/10.1214/074921707000000391>.
- 677 9. P. Couto, M. Brustello, R. Albanez, J. Rodrigues, M. Zaiat, R. Ribeiro, Cali-
678 bration of ADM1 using the Monte Carlo Markov Chain for modeling of anaer-

- 679 obic biodigestion of sugarcane vinasse in an AnSBBR, *Chemical Engineering*
680 Research and Design 141 (2019) 425–435. URL: [https://doi.org/10.1016/
681 j.cherd.2018.11.014](https://doi.org/10.1016/j.cherd.2018.11.014).
- 682 10. D. Dochain, P. Vanrolleghem, *Dynamical Modelling and Estimation in*
683 Wastewater Treatment Processes, IWA Publishing, 2001. URL: [https://doi.
684 org/10.2166/9781780403045](https://doi.org/10.2166/9781780403045).
- 685 11. A. Donoso-Bravo, J. Mailier, C. Martin, J. Rodríguez, C. Aceves-Lara,
686 A. Wouwer, Model selection, identification and validation in anaerobic diges-
687 tion: a review, *Water research* 45 (2011) 5347–5364. URL: [https://doi.org/
688 10.1016/j.watres.2011.08.059](https://doi.org/10.1016/j.watres.2011.08.059).
- 689 12. B. Guedj, A primer on PAC-Bayesian learning, in: *Proceedings of the second*
690 congress of the French Mathematical Society, volume 33, 2019, pp. 391–414.
691 URL: <https://arxiv.org/abs/1901.05353>.
- 692 13. M. Haddouche, B. Guedj, Online PAC-bayes learning, *Advances in Neural*
693 Information Processing Systems 35 (2022) 25725–25738. URL: [https://doi.
694 org/10.48550/arXiv.2206.00024](https://doi.org/10.48550/arXiv.2206.00024).
- 695 14. G. E. Hinton, D. Van Camp, Keeping the neural networks simple by min-
696 imizing the description length of the weights, in: *Proceedings of the sixth*
697 annual conference on Computational learning theory, 1993, pp. 5–13. URL:
698 <https://doi.org/10.1145/168304.168306>.
- 699 15. L. Le Cam, *Asymptotic methods in statistical decision theory*, Springer New
700 York, NY, 2012. URL: <https://doi.org/10.1007/978-1-4612-4946-7>.
- 701 16. E. L. Lehmann, G. Casella, *Theory of Point Estimation*, 2nd ed., Springer
702 New York, NY, 1998. URL: <https://doi.org/10.1007/b98854>.

- 703 17. A. Leurent, R. Moscoviz, Modeling a propionate-oxidizing syntrophic coculture
704 using thermodynamic principles, *Biotechnology and Bioengineering* 119 (2022)
705 2423–2436. URL: <https://doi.org/10.1002/bit.28156>.
- 706 18. C. Martin, E. Ayesa, An integrated Monte Carlo methodology for the cali-
707 bration of water quality models, *Ecological Modelling* 221 (2010) 2656–2667.
708 URL: <https://doi.org/10.1016/j.ecolmodel.2010.08.008>.
- 709 19. C. Martin, C. de Gracia, E. Ayesa, Bayesian calibration of the disintegration
710 process in WWTP sludge digesters, 8th IWA Symposium on Systems Analysis
711 and Integrated Assessment (WaterMatex) (2011).
- 712 20. D. A. McAllester, Some PAC-Bayesian theorems, *Machine Learning* 37 (1999)
713 355–363. URL: <https://doi.org/10.1023/A:1007618624809>.
- 714 21. M. D. Morris, Factorial sampling plans for preliminary computational experi-
715 ments, *Technometrics* 33 (1991) 161–174. URL: [https://doi.org/10.1080/](https://doi.org/10.1080/00401706.1991.10484804)
716 [00401706.1991.10484804](https://doi.org/10.1080/00401706.1991.10484804).
- 717 22. V. Pastor-Poquet, S. Papirio, J. Harmand, J.-P. Steyer, E. Trably, R. Escudiá,
718 G. Esposito, Assessing practical identifiability during calibration and cross-
719 validation of a structured model for high-solids anaerobic digestion, *Water*
720 *Research* 164 (2019) 114932. URL: [https://doi.org/10.1016/j.watres.](https://doi.org/10.1016/j.watres.2019.114932)
721 [2019.114932](https://doi.org/10.1016/j.watres.2019.114932).
- 722 23. J. Quinonero-Candela, M. Sugiyama, A. Schwaighofer, N. D. Lawrence,
723 Dataset shift in machine learning, Mit Press, 2008. URL: [https://mitpress.](https://mitpress.mit.edu/9780262545877/dataset-shift-in-machine-learning/)
724 [mit.edu/9780262545877/dataset-shift-in-machine-learning/](https://mitpress.mit.edu/9780262545877/dataset-shift-in-machine-learning/).
- 725 24. L. Rieger, S. Gillot, G. Langergraber, T. Ohtsuki, A. Shaw, I. Takacs,
726 S. Winkler, Guidelines for using activated sludge models, IWA publishing,

- 727 2012. URL: <https://www.iwapublishing.com/books/9781843391746/>
728 [guidelines-using-activated-sludge-models](https://www.iwapublishing.com/books/9781843391746/guidelines-using-activated-sludge-models).
- 729 25. C. Rosén, U. Jeppsson, Aspects on ADM1 implementation within the BSM2
730 framework, Department of Industrial Electrical Engineering and Automation,
731 Lund University, Lund, Sweden (2006) 1–35.
- 732 26. M. Seeger, PAC-Bayesian generalisation error bounds for gaussian process
733 classification, *Journal of machine learning research* 3 (2002) 233–269. URL:
734 <https://www.jmlr.org/papers/volume3/seeger02a/seeger02a.pdf>.
- 735 27. Y. Seldin, F. Laviolette, N. Cesa-Bianchi, J. Shawe-Taylor, P. Auer, PAC-
736 Bayesian inequalities for martingales, *IEEE Transactions on Information*
737 *Theory* 58 (2012) 7086–7093. URL: [https://doi.org/10.1109/TIT.2012.](https://doi.org/10.1109/TIT.2012.2211334)
738 [2211334](https://doi.org/10.1109/TIT.2012.2211334).
- 739 28. L. Sordo Vieira, R. C. Laubenbacher, Computational models in systems biol-
740 ogy: standards, dissemination, and best practices, *Current Opinion in Biotech-*
741 *nology* 75 (2022) 102702. URL: [https://doi.org/10.1016/j.copbio.2022.](https://doi.org/10.1016/j.copbio.2022.102702)
742 [102702](https://doi.org/10.1016/j.copbio.2022.102702).
- 743 29. A. Tolessa, N. J. Goosen, T. M. Louw, Probabilistic simulation of biogas pro-
744 duction from anaerobic co-digestion using Anaerobic Digestion Model No. 1: A
745 case study on agricultural residue, *Biochemical Engineering Journal* 192 (2023)
746 108810. URL: <https://doi.org/10.1016/j.bej.2023.108810>.
- 747 30. A. Tsigkinopoulou, S. M. Baker, R. Breitling, Respectful modeling: Address-
748 ing uncertainty in dynamic system models for molecular biology, *Trends*
749 *in Biotechnology* 35 (2017) 518–529. URL: [https://doi.org/10.1016/j.](https://doi.org/10.1016/j.tibtech.2016.12.008)
750 [tibtech.2016.12.008](https://doi.org/10.1016/j.tibtech.2016.12.008).

Table 1: Assessment of UQ methods for parameters estimation

	Bootstrap	FIM	Beale	VarBUQ (λ)	VarBUQ (2λ)	VarBUQ (8λ)
AM2 LN	0.0 ($< 1.2\text{e-}2$)	0.0	5.0e-9	0.91	n.a.	n.a.
AM2 HN	0.0 ($< 1.2\text{e-}2$)	3.9e-4	5.6e-4	0.87	n.a.	n.a.
AM2 LF	0.0 ($< 1.2\text{e-}2$)	1.9e-2	0.34	0.90	n.a.	n.a.
AM2 HF	3.1e-2 ($< \mathbf{5.6\text{e-}2}$)	2.5e-2	3.8e-4	0.91	n.a.	n.a.
ADM1 LN	n.a.	0.0	3.3e-11	2.5e-6	5.2e-4	0.56
ADM1 HN	n.a.	0.0	0.0	0.22	0.48	0.89
ADM1 LF	n.a.	0.0	1.1e-3	0.0	7.1e-9	3.7e-3
ADM1 HF	n.a.	0.0	0.0	0.0	2.5e-8	4.1e-3

p-values in bold imply that the true set of parameters was inside the 95% confidence region. For the Bootstrap method, the upper bound given in parenthesis is valid with probability at least 0.95. Since datasets LVN (resp. LVF) share its training data and true parameter with dataset LN (resp. LF), the performance of the uncertainty quantification routines are identical.

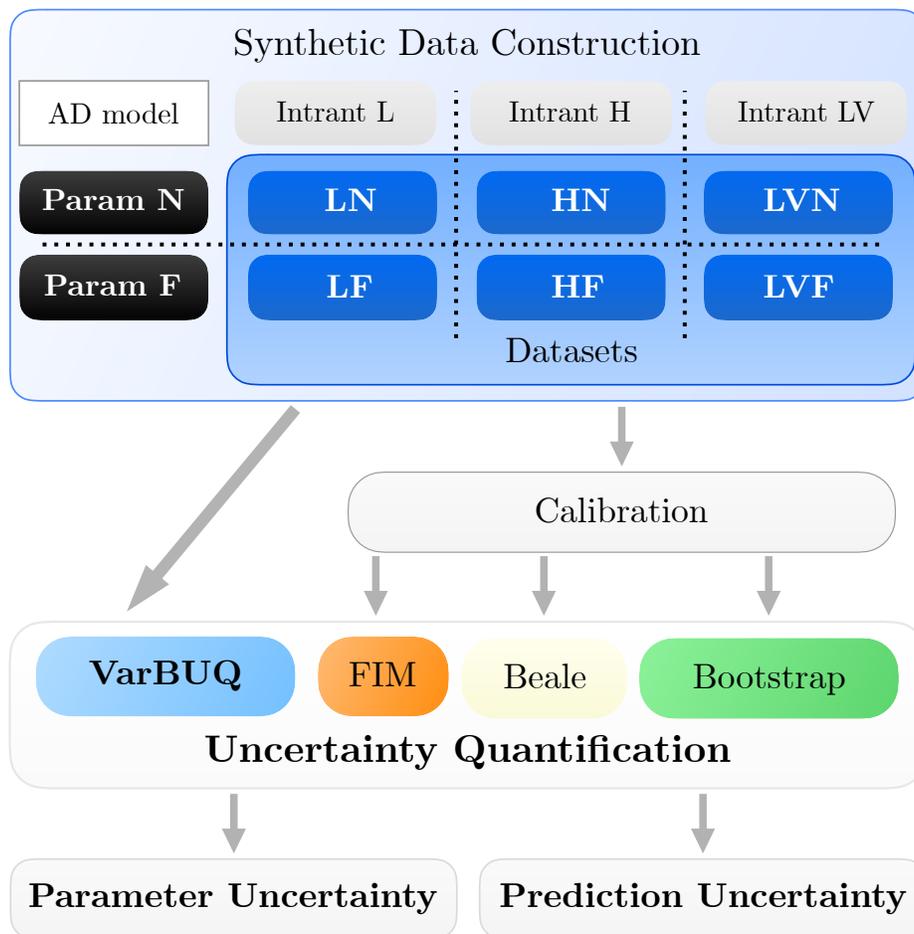


Figure 1: UQ analysis methodology. For each AD model, six datasets are evaluated, spanning a choice of two parameters and three intrans descriptions. After calibration, three ad-hoc UQ methods are assessed and compared to VarBUQ's joint calibration and UQ, both on their ability to encompass the true set of parameter values and to quantify uncertainty on the predictions.

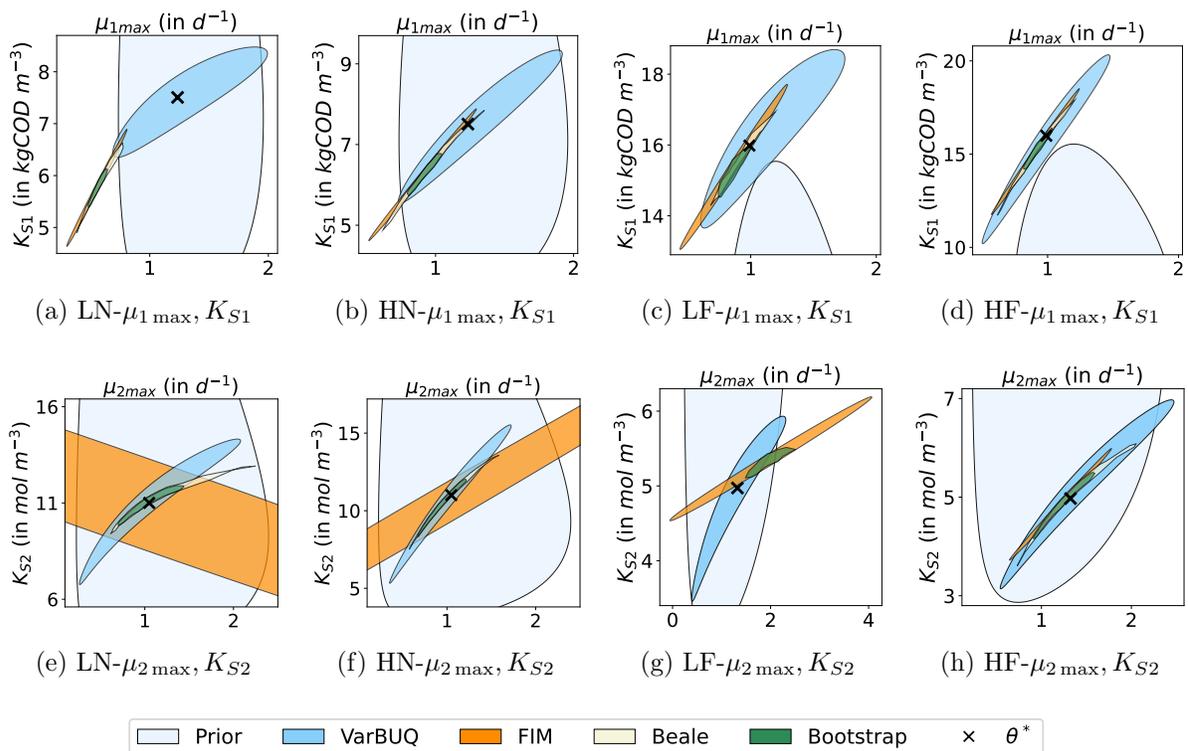


Figure 2: 95% Confidence regions for AM2. The prior distribution is in light blue, the posterior in blue, FIM in orange, Beale in beige and Bootstrap in green. The true parameter is represented by a black cross. VarBUQ was the only methodology able to recapture the true sets of parameters in all settings. The methodology can benefit from the prior’s inductive bias (figs. 2a, 2b and 2g), but is also able to adapt to cases where the parameter is outside the boundary of the prior’s confidence region (figs. 2c and 2d). Those confidence regions are shaped as ellipses in log-space. The ellipsoidal confidence regions obtained through FIM tend to englobe those constructed through Beale’s or Bootstrap methods. They suffer from some instability as exhibited in figs. 2e and 2f, englobing negative values. The confidence regions obtained through Beale’s method tend to englobe those constructed through the Bootstrap method. Both methods regions with similar curvatures and an overall direction coherent with FIM’s confidence regions, except for fig. 2e. All UQ methods responded to the limited identifiability of the maximum growth rate and Monod constant (i.e. the fact that those parameters can compensate for one another) by constructing confidence regions which are squeezed along an axis.

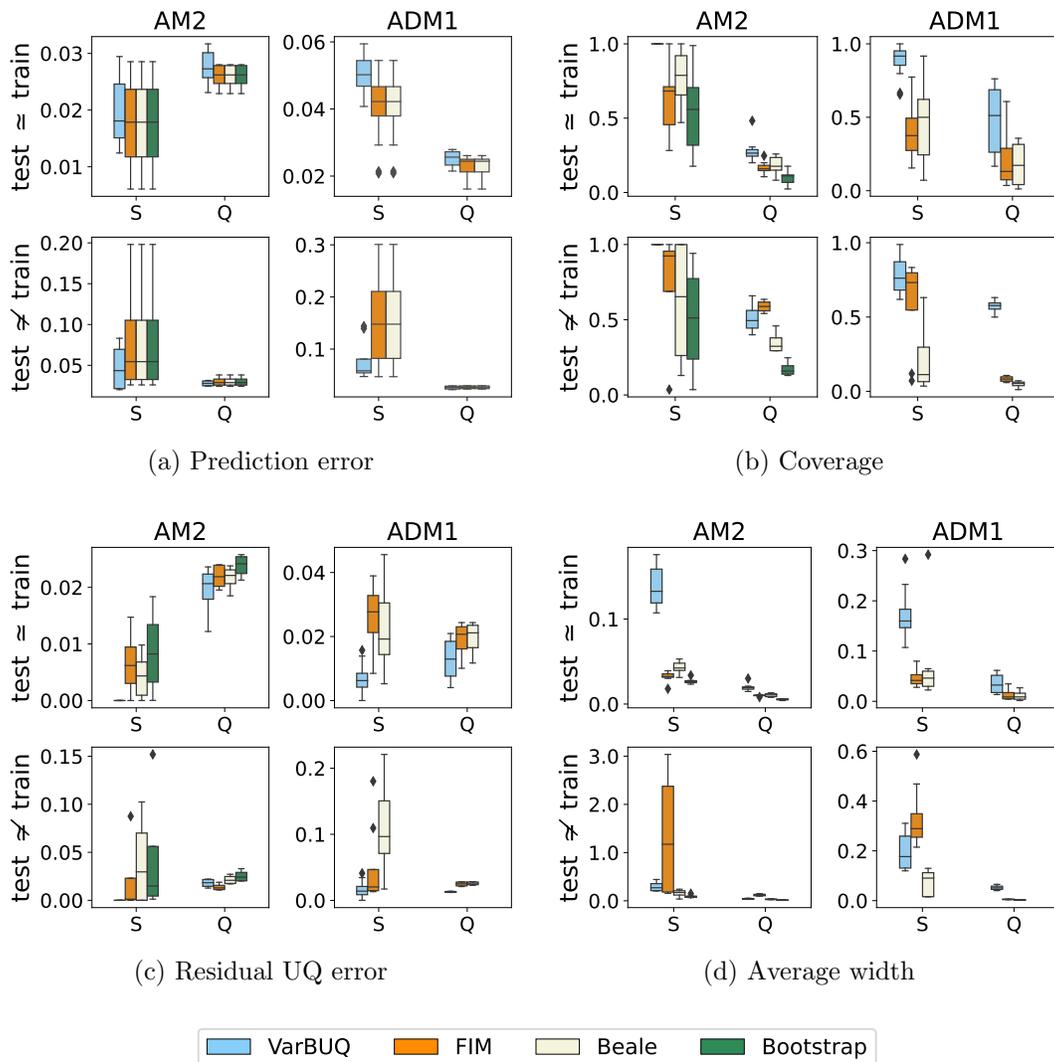


Figure 3: Performances of UQ methods on predictions (VarBUQ in blue, FIM in orange, Beale in beige and Bootstrap in green). Types of predictions are grouped depending on whether they are soluble compounds (S) or gas flows (Q). VarBUQ obtained slightly larger test error when the test dataset is similar to the train dataset, but noticeably lower test error when the test dataset exhibit distribution shift (fig. 3a). The coverage of VarBUQ’s confidence intervals on the predictions was globally higher than those of the remaining methods - achieving systematically 100% coverage for soluble compounds for AM2 (fig. 3b). The coverage and residual projection on the confidence intervals are globally coherent with the width of the confidence intervals, with the notable exception of FIM’s behavior for soluble compounds under distribution shift, where the higher width of the confidence intervals does not result in higher coverage or smaller residual errors compared VarBUQ.

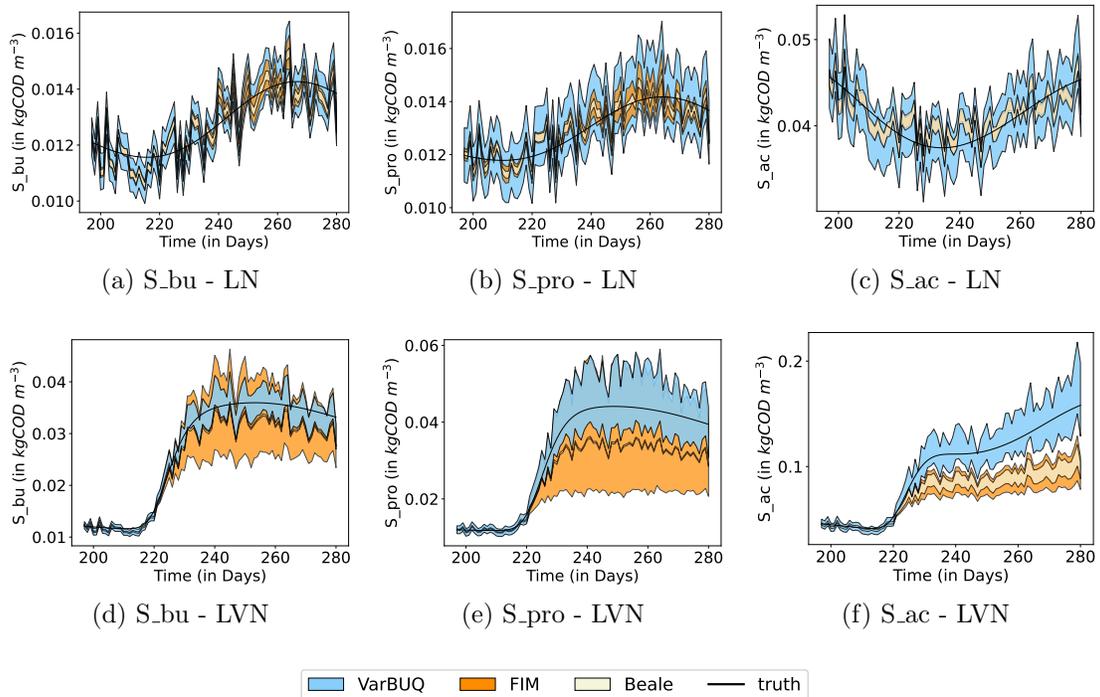


Figure 4: 95% Confidence intervals on predictions for the main three VFAs for LN (first row) and LVN (second row) datasets. The confidence intervals from all methods include high frequencies absent from the true signal, due to the noisy intransit description used. When the test set is similar to the training set, the bayesian calibration has wider confidence intervals, mitigating the impact of the intransit noise (figs. 4a to 4c). Under distribution shift, FIM’s confidence intervals widen considerably, englobing the true signal for both butyrate and propionate concentration, while Beale’s confidence interval remains centered tightly around the inadequate mean prediction (figs. 4d and 4e). Both FIM and Beale’s confidence intervals are unable to account for the increase of acetate production, contrary to VarBUQ’s calibration (fig. 4f). Figures for the remaining datasets are available on the github repository <https://github.com/BayesianUncertaintyQuantifAnaeroDig/AnaeroDigUQ>.