

THÈSE DE DOCTORAT

UNCERTAINTY QUANTIFICATION IN MULTI-PHYSICS
MODEL FOR WIND TURBINE ASSET MANAGEMENT

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Introduction

Industrial context and motivation

The current challenge of energy transition involves, among other things, reducing the share of fossil fuels in the global electricity mix. In this context, offshore wind energy offers several advantages ([Beauregard et al., 2022](#)). Offshore energy benefits from more consistent winds than onshore, mainly due to the absence of terrain roughness, it also makes possible the installation of larger and more powerful wind turbines. Since the construction of the first offshore wind farm in Vindeby, Denmark, in 1991, the industry has experienced rapid growth, with a total capacity of 56 GW in operation worldwide in 2021. Over time, offshore wind technology has matured, resulting in significant achievements such as securing projects in Europe through “zero-subsidy bids” where the electricity produced is directly sold on the wholesale market ([Beauregard et al., 2022](#)).

However, despite the progress of this sector, scaling limitations and numerous scientific challenges emerge. To meet ambitious national and regional development targets, the wind energy industry must address various scaling issues, including port logistics, the demand for critical natural resources, and sustainable end-of-life processes. Furthermore, the field presents several scientific challenges that often involve coupling data with numerical simulations of physical systems and their surrounding environment. The wind energy community is focused on different objectives, including enhancing the design of floating offshore wind turbines, refining wind resource estimation techniques, and optimizing maintenance operations. In general, several decisions are made throughout the lifespan of a wind turbine by its designer, installer, and operator, all while having only partial knowledge of certain physical phenomena. Therefore, modeling and controlling the various sources of uncertainties associated with offshore wind energy proved to be a key success factor in this highly competitive industry.

Overall, the offshore wind industry needs methods for uncertainty management regarding safety margins and industrial asset management (at the component, wind turbine, and overall wind farm levels) ([Van Kuik et al., 2016](#)). For wind project developers, the primary focus is on improving the wind potential assessment of candidate sites by combining various sources of information and modeling the multivariate distribution of environmental conditions. In the case of floating wind projects, the goal is to incorporate a probabilistic aspect from the design phase

(e.g., of the floaters) to define safer, more robust, and more cost-effective solutions. For wind farm owners, end-of-life management is another significant concern. An owner of a wind farm at the end of its life has three options: extend the operational life of assets, replace current wind turbines with newer models, or decommission and sell the wind farm. The first two options require evaluating the structural reliability and residual lifespan, with quantitative assessments reviewed by certification bodies and insurers to issue operating permits. To provide rigorous risk assessments, the generic methodology of *uncertainty quantification methodology* is a widely accepted approach in industrial sectors facing these types of issues ([de Rocquigny et al., 2008](#)).

Generic methodology for uncertainty quantification

Computer experiment is a discipline that emerged with the advent of informatics. This practice produces numerical models that allow the simulation of complex system behavior based on initial conditions defined by the analyst. Numerical models quickly became essential for the analysis, design, and certification of complex systems in cases where experiments or physical measurements are too costly or even unfeasible. However, such numerical models are mostly deterministic: the reproducible result of a simulation is associated with a fixed input set of parameters. The issue of managing uncertainties associated with these inputs arises when performing analysis with numerical models.

Uncertainty quantification aims at modeling and controlling uncertainties around a numerical model. To do so, a generic methodology has been proposed to quantify and analyze uncertainties between input and output variables of a numerical model ([de Rocquigny et al., 2008](#)). An overview of the mathematical tools used in this field is provided by [Sullivan \(2015\)](#). This approach improves the understanding of a system, ultimately contributing to more robust decision-making. Figure 1 illustrates the main step of the generic uncertainty quantification method, which are briefly summarized hereafter:

- **Step A – Problem specification:** This step involves identifying the system under study and constructing a numerical model capable of precisely simulating its behavior. Specifying the problem also involves the definition of a set of parameters inherent to the numerical model. These parameters include both the input variables and the output variables generated by the simulation. In this document, the numerical model is considered a black box, in contrast to approaches that are integrated within the numerical solution schemes for the system's behavioral equations (referred to as intrusive approaches ([Le Maître and Knio, 2010](#))). Generally, these numerical models are first calibrated against measured data and pass a process of validation and verification to reduce modeling errors ([Oberkampf and Roy, 2010](#)).
- **Step B – Uncertainty modeling:** The objective of the second step is to identify and model all the sources of uncertainty related to the input variables. Most of the time the uncertainty modeling is done in the probabilistic framework.

- **Step C – Uncertainty propagation:** This step consists in propagating the uncertain inputs through the computer model. Consequently, the output of the numerical model (commonly scalar) also becomes uncertain. The goal is to estimate a quantity of interest, which is a statistic related to the studied random output variable. The uncertainty propagation method may differ depending on the quantity of interest targeted (e.g., central tendency, a quantile, a rare event probability, etc.).
- **Step C' – Inverse analysis:** In this additional step, a sensitivity analysis can be performed to study the role allocated to each uncertain input leading to the uncertain output.
- **Metamodeling:** Considering the high computational cost associated with some simulations, statistical approaches emulate these expensive simulators with a limited number of simulations. Uncertainty quantification can then be carried out using a “surrogate model” (or metamodel) for a reduced computational cost. This optional step of statistical learning is not strictly a part of uncertainty quantification, but it often proves to be essential for enabling its practical implementation.

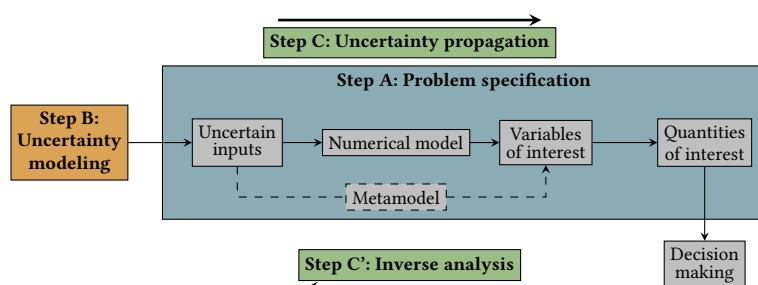


Figure 1 General uncertainty quantification framework ([de Rocquigny et al. \(2008\)](#), adapted by [Ajenjo \(2023\)](#))

Problem statement and outline of the thesis

Risk and uncertainty management in the field of wind energy is a significant concern for the electric utility Électricité de France (EDF). This thesis aims at adapting and applying the generic uncertainty quantification methodology to industrial offshore wind energy studies. As such, this use case raises scientific challenges related to its specific characteristics, described in the following:

- The numerical model exploited in the present work consists of a series of numerical models executed sequentially. This chain is divided into three parts: first, a temporal and stochastic generation of wind and wave velocity fields, followed by the simulation of the coupled hydro-aero-servo-elastic behavior of the wind turbine, and finally a post-processing phase to obtain scalar quantities of interest, aggregated over the temporal outputs.

- The complexity of this simulator, along with the high unit computational cost (about 40 minutes per simulation), requires the use of efficient sampling methods and high-performance computing systems. In addition to the complexity associated with the numerical model, modeling the input uncertainties also represents a challenge. Indeed, the joint distribution associated to environmental conditions present a complex dependence structure. The quality of the inference step is critical as it directly impacts the conclusions of uncertainty propagation.

In order to apply the generic methodology for uncertainty quantification to the offshore wind turbine case, this thesis aims at answering the following questions:

- Q1.** *How to accurately model the dependence structure associated with the joint environmental distribution?* (⇒ Step B)
- Q2.** *How to perform uncertainty propagation through a computationally expensive numerical chain uniquely based on an empirical description (measured data) of input uncertainties?* (⇒ Step C)
- Q3.** *How to estimate rare event probabilities related to the fatigue failure of offshore wind turbine structures?* (⇒ Step C)
- Q4.** *How to assess and analyse the sensitivity of uncertain inputs regarding quantities of interest resulting from structural reliability (i.e., reliability-oriented sensitivity analysis)?* (⇒ Step C')

To propose an answer to these questions, this manuscript is divided into three parts. The first part offers an introduction to uncertainty quantification methods and offshore wind turbine numerical modeling. The second part presents the contributions of this thesis to uncertainty quantification and propagation while the third part describes the contributions to rare event estimation. This manuscript is divided into seven chapters, which are summarized hereafter:

Chapter 1 – Introduction to uncertainty quantification. This chapter gives a brief overview of various topics in uncertainty quantification ([Sullivan, 2015](#)). After a reminder of some mathematical concepts, the model specification step is described, considering a black box and its input and output variables. The different types and sources of uncertainties are then presented, along with their modeling within a probabilistic framework. Uncertainty propagation depends on the estimated quantities of interest, therefore, one section addresses propagation methods for central tendency studies, and another focuses on rare event probability estimation (a statistic related to the tails of output distributions). The section dedicated to central tendency presents numerical integration, sampling, and design of experiments methods ([Fang et al., 2018](#)). The one about rare event probabilities introduces usual methods from the field of structural reliability ([Lemaire et al., 2009; Morio and Balesdent, 2015](#)).

This chapter also covers the main methods for global sensitivity analysis ([Da Veiga et al., 2021](#)). This field divides its methods into two major classes: screening methods and importance

measures. Screening techniques, typically applied in high-dimensional problems, aim to identify variables with low impact on the variability of the output of interest. Importance measures, on the other hand, quantitatively allocate, for each input variable, a share of the output variability, enabling the ranking of variables based on their influence.

Finally, this chapter presents an overview of the families of metamodels commonly used in uncertainty quantification ([Forrester et al., 2008](#)). Special attention is given to the Gaussian process regression, which involves conditioning a Gaussian process on a set of observations from the numerical model. Once conditioned, the Gaussian process provides richer information than other types of metamodels. This method simultaneously offers a surrogate model (mean of the Gaussian process, also called predictor) and an error function (variance of the process). Some iterative methods (called “active”) use this additional information to progressively enrich the metamodel and improve its predictability. These techniques were quite successful in the 1990s for solving optimization problems with expensive functions ([Jones et al., 1998](#)). Since then, their use has expanded to solve problems in structural reliability [Echard et al. \(2011\)](#).

Chapter 2 – Introduction to wind turbine modeling and design. The simulation of an offshore wind turbine involves modeling multiple physical aspects interacting with random environmental conditions. This chapter first introduces spectral methods used to generate wind and wave velocity fields by applying inverse Fourier transforms (e.g., as implemented in the TurbSim tool ([Jonkman, 2009](#))). These simulated wind velocity fields then become the inputs of a multi-physics wind turbines numerical model. Such simulation includes a simplified modeling of the interactions between fluids and structures (using the blade element momentum theory), dynamic modeling of the structure using flexible multibody methods, and modeling of wind turbine control systems [source]. The numerical code studied generates time series of several physical quantities describing the system’s behavior.

This thesis particularly focuses on the probabilistic evaluation of fatigue damage in wind turbine structures. Fatigue damage is a phenomenon that deteriorates the mechanical properties of a material as a result of exposure to many of cyclic, low-amplitude stresses. Currently, standards recommend the use of deterministic safety factors to address this failure mode ([IEC-61400-1, 2019](#); [DNV-ST-0437, 2016](#)). A probabilistic approach enhances the analysis and can sometimes reveal conservative of safety margins. Several recent studies have addressed this topic from different methodological perspectives ([Huchet, 2019](#); [Lataniotis, 2019](#); [Cousin, 2021](#); [Hirvoas, 2021](#); [Petrovska, 2022](#)).

In this context, this chapter enumerates the input parameters of the calculation chain that are considered uncertain. These random variables are grouped into two groups: the random vector related to the environment (e.g., average wind speed, wind speed standard deviation, wind direction, significant wave height, wave period, and wave direction), and the random vector related to the system (e.g., controller wind misalignment error, soil stiffness, fatigue calculation curve parameters).

Chapter 3 – Kernel-based uncertainty quantification. This chapter examines perturbations in environmental conditions within an offshore wind farm induced by wake effects [Larsen et al. \(2008\)](#). A theoretical offshore wind farm off the southern coast of Brittany is considered as a use case, and a simplified numerical model of wake in this wind farm is used. This model provides an analytical prediction of the wind speed deficit and turbulence created by the wake, taking into account the influence of the floaters' positions due to rigid body dynamics.

In a second phase, uncertainty propagation is carried out thought the wake model, considering the joint distribution of ambient environmental conditions as inputs. In the end, an environmental distribution perturbed by the wake is simulated for each wind turbine. A dissimilarity measure between distribution, based of kernels and named the *maximum mean discrepancy* (MMD), is used to compare the distributions perceived by each wind turbine. This measure allows the clustering of wind turbines exposed to similar environmental conditions, resulting in identical structural responses. Given the high computational cost of aero-servo-hydro-elastic simulations for offshore wind turbines, this preliminary study enables reliability analysis at the wind farm scale without repeating the analysis for each turbine. Ultimately, only four classes are selected to represent a wind farm of 25 turbines.

Chapter 4 – Kernel-based central tendency estimation. Chapter four presents the use of the kernel-based dissimilarity measure (MMD) in the context of probability distribution sampling, a method known as "kernel herding" introduced by [Chen et al. \(2010\)](#). This quadrature technique belongs to the family of "Bayesian quadratures" [Briol et al. \(2019\)](#), which can be viewed as a generalization of quasi-Monte Carlo methods [Li et al. \(2020\)](#).

The properties of this method are highlighted through an industrial application dedicated to estimating the mean fatigue damage of a wind turbine structure. Although this quantity is crucial in the design and certification of wind turbines, the methods used to estimated it are known to be suboptimal (i.e., regular grids). The study is conducted on a model of a fixed offshore wind turbine belonging to a farm in the North Sea. Uncertainties in input environmental conditions are inferred from in-situ measured data.

Finally, a numerical comparison with Monte Carlo and quasi-Monte Carlo sampling reveals the performance and practical advantages of kernel herding. This method allows for direct subsampling from a large environmental database without the need for inference (step B).

Chapter 5 – Kernel-based metamodel validation. This chapter proposes the use of kernel-based sampling methods in the context of model validation for machine learning (or surrogate models). Estimating the predictivity of supervised learning models requires an evaluation of the learned surrogate model on a set of test points that were not used during training. The quality of the validation naturally depends on the properties of the test set and the metric used to summarize the prediction error. This contribution first suggests using space-filling sampling methods to "optimally" select a test set, then, it introduces a new predictivity coefficient that weights the observed errors to improve the global error estimation. A numerical comparison between several sampling methods based on geometric approaches ([Shang and Apley, 2020](#)) or

kernel methods [Chen et al. \(2010\)](#); [Mak and Joseph \(2018\)](#) is carried out. Our results show that weighted versions of kernel methods offer superior performance. An application to simulated mechanical loads in an offshore wind turbine model is also presented. This experiment illustrates the practical relevance of this technique as an effective alternative to costly cross-validation techniques.

Chapter 6 – Nonparametric rare event estimation. Estimating rare events probabilities is a common issue in industrial risk management, especially in the field of structural reliability ([Chabridon, 2018](#)). To address this, several techniques have been proposed to overcome the known limitations of the Monte Carlo method. Among them, “subset sampling” ([Au and Beck, 2001](#)) is a technique based on the split of a rare probability into a product of less rare (and thus easier to estimate) conditional probabilities associated with nested failure events. However, this technique relies on conditional simulation using Markov chain Monte Carlo (MCMC) methods. These algorithms, while converging, often produce samples that are not independent and identically distributed (i.i.d.) due to the correlation between the Markov chains. In this chapter another conditional sampling method is proposed, with the advantage of preserving the i.i.d. property. Independent sampling is particularly relevant for reusing these samples in a posterior reliability-oriented sensitivity analysis. The algorithm introduced is based on the non-parametric inference of the conditional joint distribution using kernel density estimation of marginals combined with dependence inference using the empirical Bernstein copula ([Sancetta and Satchell, 2004](#)). The so-called “Bernstein adaptive nonparametric conditional sampling” (BANCS), is compared to the subset sampling method for several structural reliability problems. The initial results are promising, but further investigation is needed to control the estimator’s bias.

Chapter 7 – Sequential reliability oriented sensitivity analysis. This chapter deals with sensitivity analysis for risk measures (e.g., rare event probabilities). Global sensitivity analysis ([Da Veiga et al., 2021](#)) assigns a portion of the global output variability to each variable (or group of variables), often using a functional decomposition of the output variance. However, when studying risk measure (often located in the distributions’ tails), the global sensitivity might be very different to the sensitivity to the risk measure. “Reliability-oriented sensitivity analysis” (ROSA), studies the impact of the inputs in regard to a risk-measure such as a rare event probability (see e.g., [Chabridon \(2018\)](#)). Using the nested subsets obtained with the BANCS algorithm (presented in Chapter 6), the idea of this chapter is to study the ROSA evolution as the subsets get closer to the failure domain. For each subset, a ROSA is carried out with a kernel-based importance measure called the “Hilbert-Schmidt Independence Criterion” adapted to this context ([Marrel and Chabridon, 2021](#)).

Numerical developments

Several implementations developed in this thesis are available on different platforms, allowing the reader to reproduce some numerical results in an open-data approach:

- This Python package generates designs of experiments based on kernel methods such as Kernel Herding and Support Points. A tensorized implementation of the algorithms was proposed, significantly increasing their performances. Additionally, optimal weights for Bayesian quadrature are provided.

- This Python package, developed in collaboration with J.Muré, is available on the platform Pypi and fully documented.

-
- This Python package proposes an implementation of the “Bernstein Adaptive Non-parametric Conditional Sampling” method for rare event estimation.

- bancs²
- This Python package is available on the PyPI platform and is illustrated with examples and analytical benchmarks.

-
- This Python package presents a standardized process to benchmark different sampling methods for central tendency estimation.

- ctbenchmark³
- This Python package is available on a GitHub repository with analytical benchmarks.

-
- This Python package proposes an implementation of a synthetic visualization tool for multivariate distributions.

- copulogram⁴
- This Python package, developed in collaboration with V.Chabridon, is available on the Pypi platform.

¹Documentation: <https://efekhari27.github.io/otkerneldesign/master/>

²Repository: <https://github.com/efekhari27/bancs>

³Repository: <https://github.com/efekhari27/ctbenchmark>

⁴Repository: <https://github.com/efekhari27/copulogram>

Publications and communications

The research contributions in this manuscript are based on the following publications:

Book Chap.	<u>E. Fekhari</u> , B. Iooss, J. Muré, L. Pronzato and M.J. Rendas (2023). "Model predictivity assessment: incremental test-set selection and accuracy evaluation". In: <i>Studies in Theoretical and Applied Statistics</i> , pages 315–347. Springer.
Jour. Pap.	<u>E. Fekhari</u> , V. Chabridon, J. Muré and B. Iooss (2023). "Given-data probabilistic fatigue assessment for offshore wind turbines using Bayesian quadrature". In: <i>Data-Centric Engineering</i> .
Int. Conf.	<u>E. Fekhari</u> , B. Iooss, V. Chabridon, J. Muré (2022). "Numerical Studies of Bayesian Quadrature Applied to Offshore Wind Turbine Load Estimation". In: <i>SIAM Conference on Uncertainty Quantification (SIAM UQ22)</i> , Atlanta, USA. (Talk)
	<u>E. Fekhari</u> , B. Iooss, V. Chabridon, J. Muré (2022). "Model predictivity assessment: incremental test-set selection and accuracy evaluation". In: <i>22nd Annual Conference of the European Network for Business and Industrial Statistics (ENBIS 2022)</i> , Trondheim, Norway. (Talk)
	<u>E. Fekhari</u> , B. Iooss, V. Chabridon, J. Muré (2022). "Efficient techniques for fast uncertainty propagation in an offshore wind turbine multi-physics simulation tool". In: <i>Proceedings of the 5th International Conference on Renewable Energies Offshore (RENEW 2022)</i> , Lisbon, Portugal. (Paper & Talk)
	<u>E. Fekhari</u> , V. Chabridon, J. Muré and B. Iooss (2023). "Bernstein adaptive nonparametric conditional sampling: a new method for rare event probability estimation" ⁵ . In: <i>Proceedings of the 13th International Conference on Applications of Statistics and Probability in Civil Engineering (ICASP 14)</i> , Dublin, Ireland. (Paper & Talk)
	<u>E. Vanem</u> , <u>E. Fekhari</u> , N. Dimitrov, M. Kelly, A. Cousin and M. Guiton (2023). "A joint probability distribution model for multivariate wind and wave conditions". In: <i>Proceedings of the ASME 2023 42th International Conference on Ocean, Offshore and Arctic Engineering (OMAE 2023)</i> , Melbourne, Australia. (Paper)
	<u>A. Lovera</u> , <u>E. Fekhari</u> , B. Jézéquel, M. Dupoirion, M. Guiton and E. Ardillon (2023). "Quantifying and clustering the wake-induced perturbations within a wind farm for load analysis". In: <i>Journal of Physics: Conference Series (WAKE 2023)</i> , Visby, Sweden (Paper)
Nat. Conf.	<u>E. Fekhari</u> , B. Iooss, V. Chabridon, J. Muré (2022). "Kernel-based quadrature applied to offshore wind turbine damage estimation". In: <i>Proceedings of the Mascot-Num 2022 Annual Conference (MASCOT NUM 2022)</i> , Clermont-Ferrand, France (Poster)
	<u>E. Fekhari</u> , B. Iooss, V. Chabridon, J. Muré (2023). "Rare event estimation using nonparametric Bernstein adaptive sampling". In: <i>Proceedings of the Mascot-Num 2023 Annual Conference (MASCOT-NUM 2023)</i> , Le Croisic, France (Talk)
Invited Lec.	Le Printemps de la Recherche 2022, Nantes, France. "Traitement des incertitudes pour la gestion d'actifs éoliens". (Talk)
	Journées Scientifiques de l'Eolien 2024, Saint-Malo, France. "Evaluation probabiliste de la fiabilité en fatigue des structures éoliennes en mer". (Talk)

⁵This contribution was rewarded by the "CERRA Student Recognition Award"

PART I:

INTRODUCTION TO UNCERTAINTY QUANTIFICATION AND WIND ENERGY

Toute pensée émet un coup de dé.

S. MALLARMÉ

Chapter **1**

Uncertainty quantification in computer experiments

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1.1 Introduction

The progress of computer simulation gradually allows the virtual resolution of more complex problems in scientific fields such as physics, astrophysics, engineering, climatology, chemistry, or biology. This domain often provides a deterministic solution to complex problems depending on several inputs. Associating an uncertainty quantification (UQ) analysis with these numerical models is a key element to improving the understanding of the phenomena studied. A wide panel of UQ methods has been developed over the years to pursue these studies for a reasonable computational cost.

This chapter presents the essential tools and methods from the generic UQ framework, including elements partially inspired from [Sullivan \(2015\)](#) and [Chabridon \(2018\)](#). It is structured as follows: Section 1.2 describes the context of the model specification step; Section 1.3 presents a classification of the inputs uncertainties and the probabilistic framework to model them; Section 1.4 and 1.5 introduce various methods to propagate the input uncertainties through the numerical model for different purposes; Section 1.6 presents the main inverse methods to perform sensitivity analysis in our framework; Finally, 1.7 introduces the concept of surrogate models to emulate a model by realizing a statistical learning on a limited dataset.

OpenTURNS¹. Is a high-performance Python library dedicated to UQ ([Baudin et al., 2017](#)). OpenTURNS (“Open source initiative for the Treatment of Uncertainties, Risks’N Statistics”) is developed by industrial researchers from EDF R&D, Airbus Group, PHIMECA Engineering, IMACS and ONERA. It combines high-performance using C++ programming with high-accessibility through a Python API. Overall, this open source library provides tools for various steps of the UQ framework (e.g., uncertainty quantification, uncertainty propagation, surrogate modeling, reliability, sensitivity analysis and calibration). To guaranty software quality, the development follows robust processes such as exhaustive unit testing and multiplatform continuous integration. A dedicated forum hosts an active community, which is helping new users and discussing future developments. Finally, no-code users can benefit from OpenTURNS’s free-download Graphical User Interface software, named [Persalys²](#). In this chapter, the methodological concepts introduced are linked to minimal OpenTURNS implementations examples, available in the Appendix ??.

1.2 Black-box model specification

In our computer experiments context, uncertainty quantification is performed around an input-output numerical simulation model. This numerical model, or code, is hereafter considered as *black-box* since the knowledge of the underlying physics doesn’t inform the UQ methods. Alternatively, one could consider *intrusive* UQ methods, introducing uncertainties within the

¹OpenTURNS installation guide and documentation are available at <https://openturns.github.io/www/>

²Persalys, a free-download graphical user interface available at <https://www.persalys.fr/obtenir.php>

resolution of the equations of the physics (see e.g., [Le Maître and Knio 2010](#)). In practice, numerical models might be a sequence of codes executed in series to obtain a variable of interest.

While simulation models are in most cases deterministic, they may also be qualified as intrinsically stochastic (i.e., two runs of the same model taking the same inputs return different outputs). Additionally, numerical simulation always presents modeling errors. In the following, it will be assumed that the numerical models passed a *validation & verification* phase, to quantify their confidence and predictive accuracy.

Formally, part of the problem specification is the definition of the set of d input variables $\mathbf{x} = (x_1, \dots, x_d)^\top$ considered as uncertain (e.g., wind speed, wave period, etc.). The outputs studied are also defined at this stage, which will only be of scalar type in the present work. UQ methods suited to other types of outputs exist (see e.g., for time series outputs [Lataniotis 2019](#), for functional outputs [Auder et al. 2012](#); [Rollón de Pinedo et al. 2021](#)). Let us then define the following numerical model:

$$\mathcal{M} : \begin{array}{ccc} \mathcal{D}_x \subseteq \mathbb{R}^d & \longrightarrow & \mathcal{D}_y \subseteq \mathbb{R} \\ \mathbf{x} & \longmapsto & y. \end{array} \quad (1.1)$$

Unlike the typical machine learning input-output dataset framework, the UQ analyst can simulate the output image of any inputs (in the input domain), using a numerical model. However, numerical simulations often come with an important computational cost. Therefore, UQ methods should be efficient and require as few simulations as possible. In this context, surrogate models (or metamodels) are statistical approximations of the costly numerical model, that can be used to perform tractable UQ. Surrogate models are built and validated on a limited number of simulations (in a *supervised learning* framework). In practice, note that the model specification step is often associated with the development of a *wrapper* of the code. It is an overlay of code allowing its execution in a parametric way, which is often associated with *high-performance computer* (HPC) deployment. Once the model is specified, a critical step in uncertainty quantification is enumerating the input uncertainties and building their associated mathematical model.

1.3 Enumerating and modeling the uncertain inputs

1.3.1 Sources of the input uncertainties

The analyst should construct a list of uncertain inputs as exhaustive as possible, to ensure a complete risk assessment (e.g., associated with the exploitation of a wind energy asset). Even if these uncertainties might have different origins, they should all be considered jointly in the UQ study. Authors proposed to classify them for practical purposes into two groups:

- **aleatory uncertainty** regroups the uncertainties arising from natural randomness (e.g., wind turbulence). From a risk management point of view, these uncertainties are qualified

as *irreducible* since the industrials facing them will not be able to acquire additional information to reduce them (e.g., additional measures).

- **epistemic uncertainty** gathers the uncertainties resulting from a lack of knowledge (e.g., material properties). Contrarily to the aleatory ones, epistemic uncertainties might be reduced by investigating their origin (often at a certain cost).

[Der Kiureghian and Ditlevsen \(2009\)](#) discuss the relevance of this classification. They affirm that this split is practical for decision-makers to identify possible ways to reduce their uncertainties. However, it should not affect the way of modeling or propagating uncertainties. In the following, the probabilistic framework is introduced to deal with uncertainties.

1.3.2 Modeling uncertain inputs with the probabilistic framework

Uncertainties are traditionally modeled with objects from the probability theory. In this thesis, the *probabilistic framework* is adopted. Alternative theories exist to mathematically model uncertainties. For example, imprecise probability theory allows more general modeling of the uncertainties ([Beer et al., 2013; Schöbi and Sudret, 2017](#)). It becomes useful when dealing with very limited and possibly contradictory information (e.g., expert elicitation). The core probabilistic tools and objects are introduced hereafter.

The *probability space* is a measure space with total measure summing to one, also called probability triple and denoted $(\Omega, \mathcal{A}, \mathbb{P})$. This mathematical concept first includes a sample space Ω , which contains a set of outcomes $\omega \in \Omega$. Note that an *event* is defined as a set of outcomes in the sample space. Then, a σ -algebra \mathcal{A} , also called event space, is a set of events. Finally, a probability function $\mathbb{P} : \mathcal{A} \rightarrow [0, 1]$, is a positive probability measure associated with an event. Most often, the choice of the probability space will not be specified. The main object will be functions defined over this probability space: random variables.

The *random vector X* (i.e., multivariate random variable) is a measurable function defined as:

$$X : \begin{cases} \Omega & \longrightarrow \mathcal{D}_x \subseteq \mathbb{R}^d \\ \omega & \longmapsto X(\omega) = x. \end{cases} \quad (1.2)$$

In the following, the random vector X will be considered to be a squared-integrable function against the measure \mathbb{P} (i.e., $\int_{\Omega} |X(\omega)|^2 d\mathbb{P}(\omega) < \infty$). Moreover, the present thesis deals with continuous random variables.

The *probability distribution* of the random vector X is the pushforward measure of \mathbb{P} by X . Which is a probability measure on $(\mathcal{D}_x, \mathcal{A})$, denoted \mathbb{P}_X and defined by:

$$\mathbb{P}_X(B) = \mathbb{P}(X \in B) = \mathbb{P}(\omega \in \Omega : X(\omega) \in B), \quad \forall B \in \mathcal{A}. \quad (1.3)$$

The *cumulative distribution function* (CDF) is a common tool to manipulate random variables. It is a function $F_{\mathbf{X}} : \mathcal{D}_{\mathbf{x}} \rightarrow [0, 1]$ defined for all $\mathbf{x} \in \mathcal{D}_{\mathbf{x}}$ as:

$$F_{\mathbf{X}}(\mathbf{x}) = \mathbb{P}(\mathbf{X} \leq \mathbf{x}) = \mathbb{P}(X_1 \leq x_1, \dots, X_d \leq x_d) = \mathbb{P}_{\mathbf{X}}([-\infty, x_1] \times \dots \times [-\infty, x_d]). \quad (1.4)$$

The CDF is a positive, increasing, right-continuous function, which tends to 0 as \mathbf{x} tends to $-\infty$ and to 1 as \mathbf{x} tends to $+\infty$. In the continuous case, one can also define a corresponding *probability density function* (PDF) $f_{\mathbf{X}} : \mathcal{D}_{\mathbf{x}} \rightarrow \mathbb{R}_+$ with $f_{\mathbf{X}}(\mathbf{x}) = \frac{\partial^d F_{\mathbf{X}}(\mathbf{x})}{\partial x_1 \dots \partial x_d}$.

The expected value of a random vector $\mathbb{E}[\mathbf{X}]$, also called first moment, is a vector defined as:

$$\mu_{\mathbf{X}} = \mathbb{E}[\mathbf{X}] = \int_{\Omega} \mathbf{X}(\omega) d\mathbb{P}(\omega) = \int_{\mathcal{D}_{\mathbf{x}}} \mathbf{x} f_{\mathbf{X}}(\mathbf{x}) d\mathbf{x} = (\mathbb{E}[X_1], \dots, \mathbb{E}[X_d])^\top. \quad (1.5)$$

In addition, considering two random variables X_i and X_j , with $i, j \in \{1, \dots, d\}$, one can write their respective variance:

$$\text{Var}(X_i) = \mathbb{E}[X_i - \mathbb{E}[X_i]], \quad (1.6)$$

and a covariance describing their joint variability:

$$\text{Cov}(X_i, X_j) = \mathbb{E}[(X_i - \mathbb{E}[X_i])(X_j - \mathbb{E}[X_j])]. \quad (1.7)$$

The *standard deviation* $\sigma_{X_j} = \sqrt{\text{Var}(X_j)}$ and *coefficient of variation* $\delta_{X_j} = \frac{\text{Var}(X_j)}{|\mathbb{E}[X_j]|}$ are two quantities directly associated to the two first moments.

1.3.3 Joint input probability distribution

This section introduces various techniques to model and infer a joint probability distribution (or multivariate distribution). It will first define the *copula*, a mathematical tool used to model the dependence structure of a joint distribution. Then, a few methods to fit a joint distribution over a dataset will be mentioned. Finally, a panel of tools to evaluate the goodness of fit between a probabilistic model and a dataset will be recalled.

In general, the single effects of multivariate distributions tend to be well modeled. However, modeling the dependence structure underlying in a joint distribution is often overlooked. To illustrate the importance of this step, Fig. 1.1 represents three i.i.d samples from three bivariate distributions sharing the same single effects (e.g., here two exponential distributions) but different dependence structures. Judging from this example, one can assume that the joint distribution results from the composition of the single effects, also called marginals, and an application governing the dependence between them.

An empirical way of isolating the dependence structures from this example is to transform the samples in the ranked space. Let us consider an n -sized sample $\mathbf{X}_n = \{\mathbf{x}^{(1)}, \dots, \mathbf{x}^{(n)}\} \in \mathcal{D}_{\mathbf{x}}^n$. The corresponding ranked sample is defined as: $\mathbf{R}_n = \{\mathbf{r}^{(1)}, \dots, \mathbf{r}^{(n)}\}$, where³ $r_j^{(i)} = \sum_{l=1}^n \mathbb{1}_{\{x_j^{(l)} \leq x_j^{(i)}\}}$, $\forall j \in \{1, \dots, d\}, i \in \{1, \dots, n\}$. Ranking a multivariate dataset allows us to isolate the dependence

³The *indicator function* is defined such that $\mathbb{1}_{\{\mathcal{A}\}}(x) = 1$ if $x \in \mathcal{A}$ and is equal to zero otherwise.

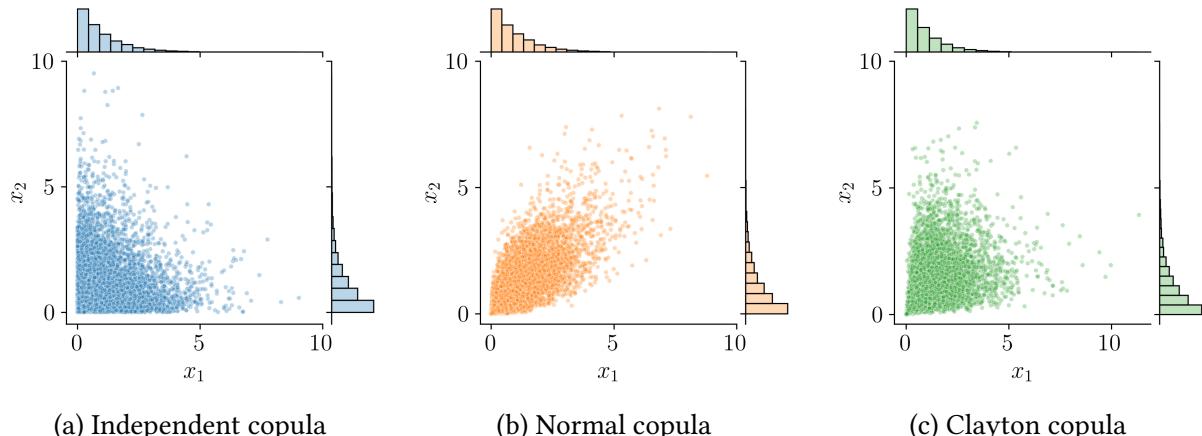


Figure 1.1 Samples of three joint distributions with identical marginals and different dependence structures

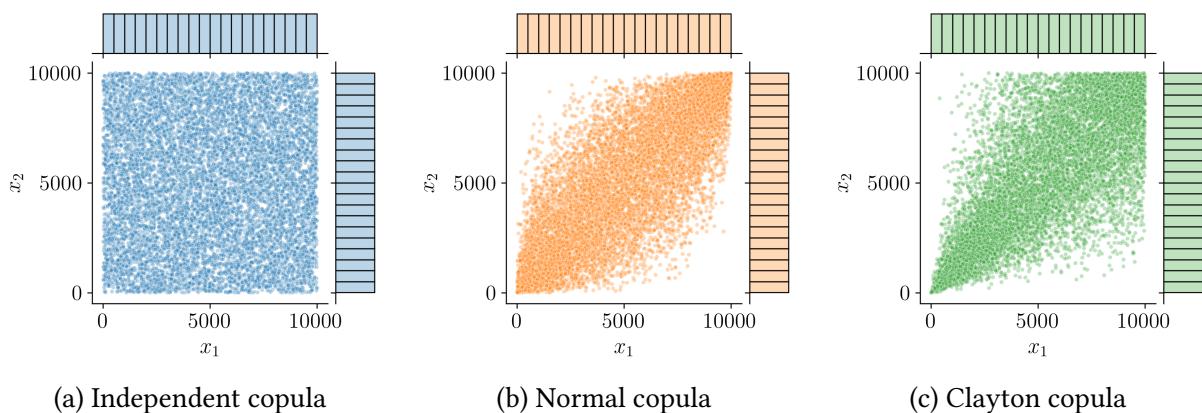


Figure 1.2 Ranked samples represented in the Fig. 1.1

structure witnessed empirically (Saporta, 2006). Fig. 1.2 shows the same three samples from Fig. 1.1 in the ranked space. One can first notice that the marginals are uniform since each rank is uniformly distributed. Then, the scatter plot from the distribution with independent copula (left plot) is uniform while the two others present different patterns.

A theorem states that the multivariate distribution of any random vector can be broken down into two objects (Joe, 1997). First, a set of univariate marginal distributions describing the behavior of the individual variables; Second, a function describing the dependence structure between all variables: a copula.

Theorem 1 (Sklar's theorem). *Let $\mathbf{X} \in \mathbb{R}^d$ be a random vector and its joint CDF $F_{\mathbf{X}}$ with marginals $\{F_{X_j}\}_{j=1}^d$, there exists a copula $C : [0, 1]^d \rightarrow [0, 1]$, such that:*

$$F_{\mathbf{X}}(x_1, \dots, x_d) = \mathbb{P}(X_1 \leq x_1, \dots, X_d \leq x_d) = C(F_{X_1}(x_1), \dots, F_{X_d}(x_d)). \quad (1.8)$$

If the marginals F_{X_i} are continuous, then this copula is unique. If the multivariate distribution has a PDF $f_{\mathbf{X}}$, it can also be expressed:

$$f_{\mathbf{X}}(x_1, \dots, x_d) = c(F_{X_1}(x_1), \dots, F_{X_d}(x_d)) \times f_{X_1}(x_1) \times \dots \times f_{X_d}(x_d), \quad (1.9)$$

where c is the density of the copula, sometimes also called copula by misuse of language. The reader might refer to [Durante and Sempi \(2015\)](#) for three different mathematical proofs.

Theorem 1 expresses the joint CDF by combining marginal CDFs and a copula, which is practical for sampling joint distributions. Conversely, the copula can be defined by using the joint CDF and the marginal CDFs:

$$C(u_1, \dots, u_d) = F_{\mathbf{X}}(F_{X_1}^{-1}(u_1), \dots, F_{X_d}^{-1}(u_d)) \quad (1.10)$$

This equation allows us to extract a copula from a joint distribution by knowing its marginals. Additionally, copulas are invariant under increasing transformations. This property is important to understand the use of rank transformation to display the copula without the marginal effects.

Identically to the univariate continuous distributions, a large catalog of families of copulas exists (e.g., independent, Normal, Clayton, Frank, Gumbel copula, etc.). Note that the independent copula Π implies that the distribution is defined as the product of its marginals $\Pi = \prod_{j=1}^d u_j$. In an inference context, this theorem divides the fitting problem into two independent problems: fitting the marginals and fitting the copula. Provided a dataset, this framework allows the potential combination of a parametric (or nonparametric) fit of marginals with a parametric (or nonparametric) fit of the copula.

To infer a joint distribution over a dataset, the analyst should determine a fitting strategy. Appropriate data visualization helps to choose the fitting methods susceptible to be relevant to the problem. In practice, the following points can be asked at this early stage:

- Is the distribution unimodal? If not, mixtures methods or nonparametric models might be required;
- Is the validity domain restrictive? If so, specific families of parametric distributions can be chosen or truncation can be applied;
- Is there a dependence structure? Does it concern all the variables together or only some groups of variables?
- Is the dependence structure complex? Transforming the dataset in the ranked space gives an empirical description of the dependence.

To ease the reading, a few techniques for estimating marginal distributions are available in Appendix ???. In addition, two nonparametric methods are introduced in Chapter ?? to infer a copula: the “empirical Bernstein copula” and the “Beta copula”. The adequation between a fitted probabilistic model and a dataset should be validated, therefore, Appendices ?? recall visual and quantitative tools for univariate goodness-of-fit evaluation.

OpenTURNS 1 (Bivariate distribution). The Python code available in Appendix ?? proposes a minimalistic OpenTURNS example of a probabilistic uncertainty modeling. Figures illustrating the present section may be reproduced, using the OpenTURNS scripts available on GitHub⁴.

1.4 Uncertainty propagation for central tendency study

The previous section aimed at building a probabilistic model of the uncertainties considering the knowledge available. This one introduces diverse methods for forward propagation of the input uncertainties through a numerical model. In the present section, uncertainty propagation is dedicated to the “central tendency” as its goal is to study the mean and variance of the output distribution. This approach contrasts with the uncertainty propagation committed to rare event probability estimation, which will be introduced in Section 1.5 (e.g., used to assess reliability).

The difficulties related to any uncertainty propagation mostly arise from the practical properties of the numerical model. Its potential high dimension, irregularity and nonlinearity each represent a challenge. Such studies rely on a finite number of observations of the numerical model, depending on the computational budget affordable. Uncertainty propagation is at the end of generic UQ approach (step C), however, it is affected by the “garbage in, garbage out” concept. Meaning that its conclusions depend on the accuracy of the inputs’ uncertainty modeling.

This section introduces the main methods of global uncertainty propagation, outlining the links between numerical integration (i.e., Lebesgue integration or central tendency estimation) and numerical design of experiments.

1.4.1 Numerical integration

Forward uncertainty propagation aims at integrating a measurable function $g : \mathcal{D}_X \rightarrow \mathbb{R}$ with respect to a probability measure \mathbb{P}_X . Numerical integration provides algorithmic tools to help the resolution of this probabilistic integration (i.e., Lebesgue integration). Note that the measurable function g , in the context of computer experiments, becomes the numerical model \mathcal{M} introduced in Eq. (1.1).

In practice, this integral is approximated by summing a finite n -sized set of realizations $y_n = \{g(x^{(1)}), \dots, g(x^{(n)})\}$ from a set of input samples $X_n = \{x^{(1)}, \dots, x^{(n)}\}$. A *quadrature* establishes a rule selecting the input samples X_n (also called nodes), and an associated set of weights

⁴https://github.com/efekhari27/thesis/blob/main/numerical_experiments/chapter1/copulas.ipynb

$\mathbf{w}_n = \{w_1, \dots, w_n\} \in \mathbb{R}^n$. The approximation given by a quadrature rule is defined as a weighted arithmetic mean of the realizations:

$$I_{\mathbb{P}_X}(g) := \int_{\mathcal{D}_X} g(\mathbf{x}) d\mathbb{P}_X(\mathbf{x}) \approx \sum_{i=1}^n w_i g(\mathbf{x}^{(i)}). \quad (1.11)$$

For a given sample size n , the goal is to find a set of tuples $\{\mathbf{x}^{(i)}, w_i\}_{i=1}^n$ (i.e., quadrature rule), giving the best approximation of our quantity. Ideally, the approximation quality should be fulfilled for a wide class of integrands. Most quadrature rules only depend on the measure space $(\Omega, \mathcal{A}, \mathbb{P}_X)$, regardless of the integrand values. In the context of a costly numerical model, this property allows the analyst to massively distribute the calls to the numerical model.

This section aims at presenting the main multivariate integration techniques. These methods encompass different properties: some are deterministic and some are aleatory; some are sequential (i.e., nested) some are not; some are victims of the curse of dimensionality and some are not.

Classical multivariate deterministic quadrature

Historically, quadrature methods have been developed for univariate integrals. The Gaussian rule and the Fejér-Clebschaw-Curtis rule are two univariate deterministic quadratures that will be briefly introduced (see [Sullivan 2015](#) for further elements).

Gaussian quadrature is a powerful univariate quadrature building together a set of irregular nodes and a set of weights. The computed weights are positive, which ensures a numerically stable rule even for large sample sizes.

Different variants of Gaussian rules exist, the most common being the Gauss-Legendre quadrature. In this case, the function g to be integrated with respect to the uniform measure on $[-1, 1]$ is approximated by Legendre polynomials. Considering the Legendre polynomial of order n , denoted l_n , the quadrature nodes $x^{(i)}_{i=1}^n$ are given by the polynomial roots. The respective weights are given by the following formula:

$$w_i = \frac{2}{\left(1 - (x^{(i)})^2\right) (l'_n(x^{(i)}))^2}. \quad (1.12)$$

Gauss-Legendre quadrature guarantees a very precise approximation provided that the integrand is well-approximated by a polynomial of degree $2n - 1$ or less on $[-1, 1]$. This rule is deterministic but not sequential, meaning that two rules with sizes n_1 and n_2 , $n_1 < n_2$ will not be nested. However, a sequential extension is proposed by the Gauss-Kronrod rule ([Laurie, 1997](#)), at the expense of a slightly lower accuracy.

To overcome this practical drawback, Fejér then Clebschaw with Curtis proposed a nested rule with mostly equivalent accuracy as Gaussian quadratures. This method is usually presented to integrate a function with respect to the uniform measure on $[-1, 1]$ and starts with a change

of variables:

$$\int_{-1}^1 g(x) dx = \int_0^\pi g(\cos(\theta)) \sin(\theta) d\theta. \quad (1.13)$$

This expression can be written as an expansion of the integrand using cosine series. Therefore, knowing that cosine series are closely related to the Chebyshev polynomials of the first kind. Fejér's "first rule" (Trefethen, 2008) uses the Chebyshev polynomials roots as nodes $x^{(i)} = \cos(\theta^{(i+1/2)})$, associated with the following weights:

$$w_i = \frac{2}{n} \left(1 - 2 \sum_{j=1}^{\lfloor n/2 \rfloor} \frac{1}{4j^2 - 1} \cos(j\theta^{(2i+1)}) \right). \quad (1.14)$$

These two univariate integration schemes are both very efficient on a wide panel of functions. Yet, Fejér-Clebsch-Curtis is sequential and offers easy implementations, benefitting from powerful algorithms such as the *fast Fourier transform*. Fig. 1.3 illustrates the nested properties of Fejér-Clebsch-Curtis quadrature by representing the nodes of quadrature rules with increasing size.

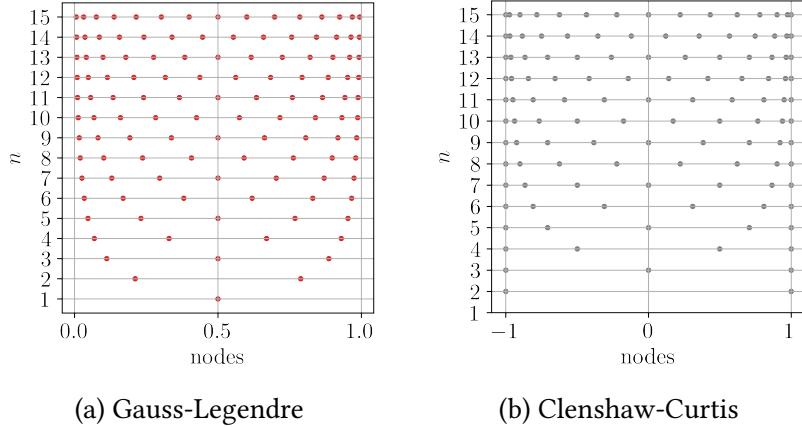


Figure 1.3 Univariate quadrature nodes for increasing sizes ($1 \leq n \leq 15$)

Uncertainty quantification problems are rarely unidimensional, but one can directly build a multivariate quadrature rule by defining the tensor product (also called full grids) of univariate rules. This exhaustive approach quickly shows its practical limits as the problem's dimension increases. In Fig. 1.4, the left plot represents a two-dimensional tensor product of identical Gauss-Legendre quadratures. Alternatively, sparse multivariate quadratures (i.e., Smolyak sparse grid) explore the joint domain more efficiently. Using the Smolyak recursive formula (see e.g., Sullivan 2015), two univariate quadratures can be combined as illustrated on the right of Fig. 1.4.

Monte Carlo methods

Monte Carlo methods were initially developed in the 1940s to solve problems in neutronics. Ever since, this frequentist technique has been applied to the resolution of the Lebesgue integral.

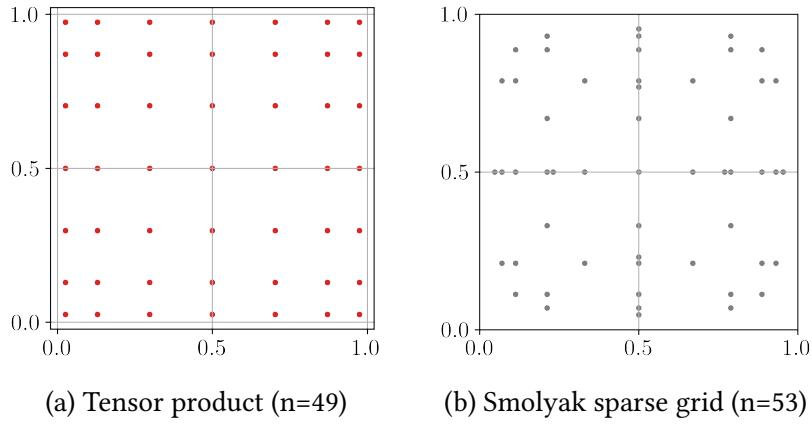


Figure 1.4 Two identical univariate Gauss-Legendre quadratures combined as a tensor product (left) and a Smolyak sparse grid (right).

To integrate a function g against a measure \mathbb{P}_X , it randomly generates points following the input measure. The integral is estimated by taking the uniform arithmetic mean of the nodes' images obtained by this random process.

This aleatory method requires to be able to generate points following a given distribution. To do so, the most common approach is to first uniformly generate a sequence of random points on $[0, 1]$. These sequences mimic actual randomness but are in fact generated by deterministic algorithms, also called pseudorandom number generators. Pseudorandom algorithms generate a sequence of numbers with a very large, but finite length. This sequence can be exactly repeated by fixing the same initial point, also called *pseudorandom seed*. Most programming languages use the Mersenne-Twister pseudorandom generator (Matsumoto and Nishimura, 1998), offering a very long period (around 4.3×10^{6001} iterations).

Formally, the “Vanilla” Monte Carlo (sometimes called “crude” Monte Carlo) method uses a set of i.i.d samples $\mathbf{X}_n = \{\mathbf{x}^{(1)}, \dots, \mathbf{x}^{(n)}\}$ following the joint distribution of \mathbb{P}_X . The Monte Carlo estimator of the integral is given by:

$$I_{\mathbb{P}_X}(g) \approx \bar{y}_n^{\text{MC}} = \frac{1}{n} \sum_{i=1}^n g(\mathbf{x}^{(i)}). \quad (1.15)$$

By construction, the law of large numbers makes this estimator unbiased, however, it converges relatively slowly. Considering the images of the sample \mathbf{X}_n , one can also estimate the variance of the output random variable $\hat{\sigma}_Y^2$. The variance of the Monte Carlo estimator results from a manipulation of the central limit theorem:

$$\text{Var}\left(\bar{y}_n^{\text{MC}}\right) = \frac{1}{\sqrt{n}} \text{Var}(g(\mathbf{X})). \quad (1.16)$$

This estimator also comes with theoretical confidence intervals at $\alpha\%$, regardless of the output distribution:

$$I_{\mathbb{P}_X}(g) \in \left[\bar{y}_n^{\text{MC}} - q_\alpha \frac{\text{Var}(g(\mathbf{X}))}{\sqrt{n}}, \bar{y}_n^{\text{MC}} + q_\alpha \frac{\text{Var}(g(\mathbf{X}))}{\sqrt{n}} \right], \quad (1.17)$$

where q_α is the α -quantile of the standard normal distribution. Monte Carlo presents the advantage of being a universal method, with no bias and strong convergence guarantees. Moreover, it is worth noting that its convergence properties do not depend on the dimension of the input domain. Unlike the previous multivariate deterministic quadrature, it doesn't suffer from the curse of dimensionality. The main limit of crude Monte Carlo is its convergence speed, making it intractable for most practical cases. More recent methods aim at keeping the interesting properties of this technique while making it more efficient. Among the *variance reduction* methods, let us mention importance sampling, stratified sampling (e.g., Latin hypercube sampling), control variates and multi-level Monte Carlo. For further details, the reader may refer to Chapters 8, 9 and 10 from [Owen \(2013\)](#) and [\(Giles, 2008\)](#).

Quasi-Monte Carlo and Koksma-Hlawka inequality

Among the methods presented so far, classical deterministic quadratures are subject to the curse of dimension while Monte Carlo methods deliver contrasted performances. Quasi-Monte Carlo is a deterministic family of numerical integration schemes with respect to the uniform measure on $[0, 1]$. It offers powerful performances with strong guarantees by choosing nodes according to *low discrepancy* sequences.

The discrepancy of a set of nodes (or a design) can be seen as a metric of its uniformity. The lowest the discrepancy of a design is, the “closest” it is to uniformity.

The Koksma-Hlawka theorem ([Morokoff and Caflisch, 1995](#); [Leobacher and Pillichshammer, 2014](#)) is a fundamental result for understanding the role of the discrepancy in numerical integration.

Theorem 2 (Koksma-Hlawka). *If $g : [0, 1]^d \rightarrow \mathbb{R}$ has a bounded variation (i.e., its total variation is finite), then for any design $\mathbf{X}_n = \{\mathbf{x}^{(1)}, \dots, \mathbf{x}^{(n)}\} \in [0, 1]^d$:*

$$\left| \int_{[0,1]^d} g(\mathbf{x}) d\mathbf{x} - \frac{1}{n} \sum_{i=1}^n g(\mathbf{x}^{(i)}) \right| \leq V(g) D^*(\mathbf{X}_n). \quad (1.18)$$

Where $D^*(\mathbf{X}_n)$ is the star discrepancy of the design \mathbf{X}_n , while $V(g)$ quantifies the complexity of the integrand, which is related to its total variation. The reader might refer to [Leobacher and Pillichshammer \(2014\)](#) Section 3.4 for further mathematical proof.

The function's variation $V(g)$ in Eq. (1.18) can be formally defined as the Hardy-Klause variation:

$$V(g) = \sum_{u \subseteq \{1, \dots, p\}} \int_{[0,1]^u} \left| \frac{\partial^u g}{\partial \mathbf{x}^u}(\mathbf{x}_u, 1) \right| d\mathbf{x}_u. \quad (1.19)$$

In which the L_p star discrepancy of a design \mathbf{X}_n is defined as the L_p -norm of the difference between the empirical CDF of the design $\widehat{F}_{\mathbf{X}_n}$ and the CDF of the uniform distribution F_U :

$$D_p^*(\mathbf{X}_n) = \|\widehat{F}_{\mathbf{X}_n} - F_U\|_p = \left(\int_{[0,1]^d} |\widehat{F}_{\mathbf{X}_n}(\mathbf{x}) - F_U(\mathbf{x})|^p d\mathbf{x} \right)^{1/p}. \quad (1.20)$$

Additionally, the L_∞ star discrepancy can be defined from a geometric point of view. Let us first consider the number of elements from a design \mathbf{X}_n , falling in a subdomain $[\mathbf{0}, \mathbf{x})$ as $\#(\mathbf{X}_n \cap [\mathbf{0}, \mathbf{x}))$. Then, if this empirical quantification is compared with the volume of the rectangle $[\mathbf{0}, \mathbf{x})$, denoted by $\text{vol}([\mathbf{0}, \mathbf{x}))$, the star discrepancy is expressed as:

$$D^*(\mathbf{X}_n) = \sup_{\mathbf{x} \in [0,1]^d} \left| \frac{\#(\mathbf{X}_n \cap [\mathbf{0}, \mathbf{x}))}{n} - \text{vol}([\mathbf{0}, \mathbf{x})) \right|. \quad (1.21)$$

Let us point out that this star discrepancy is equivalent to the Kolmogorov-Smirnov statistic, verifying whether the design follows a uniform distribution.

One can notice how the Koksma-Hlawka inequality dissociates the quadrature performance into a contribution from the function complexity and one from the repartition of the quadrature nodes. Knowing that the complexity of the studied integrand is fixed, this property explains the motivation to generate low-discrepancy quadratures in numerical integration.

Note that the design can also be considered as a discrete distribution (uniform sum of Dirac distributions). The discrepancy can then be expressed as a probabilistic distance between this discrete distribution and the uniform distribution. A generalized discrepancy between distributions called *maximum mean discrepancy* is introduced in the Appendix ?? and used for efficient sampling in Chapter ?? of this manuscript.

Some famous low-discrepancy sequences (e.g., van der Corput, Halton, Sobol', Faure, etc.) can offer a bounded star discrepancy $D^*(\mathbf{X}_n) \leq \frac{C \log(n)^d}{n}$, with the constant C depending on the sequence. Therefore, using these sequences as a quadrature rule with uniform weights provides the following absolute error upper bound:

$$\left| \int_{[0,1]^d} g(\mathbf{x}) d\mathbf{x} - \frac{1}{n} \sum_{i=1}^n g(\mathbf{x}^{(i)}) \right| \leq \frac{V(g) \log(n)^d}{n}. \quad (1.22)$$

The generation of such sequences does not necessarily require more effort than pseudo-random sampling. Chapter 15 in [Owen \(2013\)](#) offers an extended presentation of the ways to generate different low-discrepancy sequences. For example, the van der Corput and Halton sequences rely on congruential generators.

Halton sequences in medium dimension, unfortunately introduce pathological patterns when looking at their subprojections. To overcome these limits, digital nets such as the famous Sobol' or Faure sequences were developed. Sobol' sequences are in base two and have the advantage of being extensible in dimension. Note that by construction, these sequences offer significantly lower discrepancies for specific size values. Typically, designs with sizes equal to powers of two or power of prime numbers will be favorable. To illustrate the different repartition and properties of the methods, Fig. 1.5 represents the three Monte Carlo and quasi-Monte Carlo designs (with size $n = 256$). Each is split into the first 128 points (in red) and the following 128 points (in black) to show the nested properties of the QMC sequences.

Crude Monte Carlo estimators provide a confidence associated to the estimate. This complementary information is essential to deliver an end-to-end uncertainty quantification, which

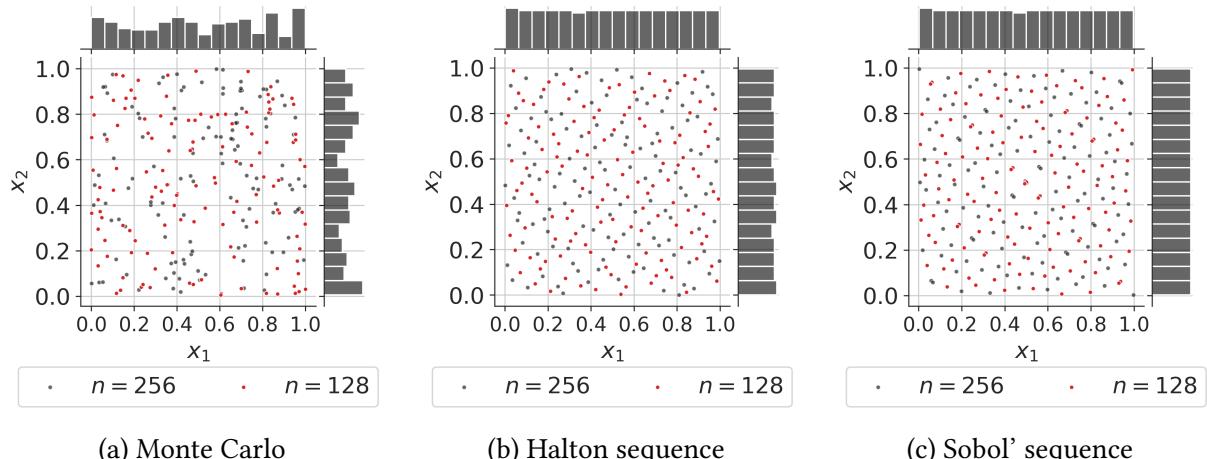


Figure 1.5 Nested Monte Carlo and quasi-Monte Carlo designs ($n = 256$)

misses in deterministic QMC methods. *Randomized quasi-Monte Carlo* (RQMC) is a method introducing some randomness in QMC in order to compute confidence intervals while benefiting from a low variance. A specific review of the randomized (also called “scrambled”) QMC is proposed by L’Ecuyer (2018). Various authors recommend the use of RQMC by default instead of QMC as a good practice. Recent works aim at exploring the use of these methods to estimate different quantities of interest, such as an expected value (Gobet et al., 2022) or a quantile (Kaplan et al., 2019).

Ultimately, quasi-Monte Carlo methods generate powerful integration schemes. The Koksma-Hlawka inequality associates an upper bound and a convergence rate to most integrals. A randomization overlay fades the deterministic property of these designs, allowing to compute confidence intervals. In the following, sampling techniques are presented from the numerical *design of experiments* point of view. Even if the goal might look different from numerical integration, these two topics shares many methods and concepts.

OpenTURNS 2 (Numerical integration). The Python code available in Appendix ?? proposes a minimalistic OpenTURNS example to build multivariate quadrature rules. Figures illustrating the present section may be reproduced, using the OpenTURNS scripts available on GitHub⁵.

1.4.2 Numerical design of experiments

Numerical design of experiments aim at uniformly exploring the input domain, e.g., to build a learning set for a regression model, or to initialize a multi-start optimization strategy. A design of experiment (also simply called design) is qualified as *space-filling* when it uniformly covers a domain. As well as in integration, a design is used to propagate uncertainties through a numerical model (or a physical experiment). However, a difference comes from the fact that

⁵https://github.com/efekhari27/thesis/blob/main/numerical_experiments/chapter1/integration.ipynb

this community often works with designs of very limited size. Users of designs of experiments also consider various properties.

- Some might be interested in the sequentiality of a sampling method, to eventually add new points as they get their computational budget extended.
- Some might request a sampling method conserving its properties in any subdomains. This second property can be useful to reduce the problem's dimension by dropping a few unimportant variables (see the following Section 1.6 on global sensitivity analysis).

Different metrics are commonly used to quantify how space-filling a design of experiments is. The previously introduced of discrepancies are an example of space-filling metrics. Other types of space-filling metrics rely on purely geometrical considerations.

This section will first define a few space-filling metrics. Secondly, the *Latin hypercube sampling* (LHS) will be introduced as a variance-reduction method that became popular the UQ community. Finally, a general discussion on uncertainty propagation with respect to non-uniform measures will be presented.

Space-filling metrics and properties

Space-filling criteria are key to evaluating designs and are often used to optimize their performances. In the previous section, the star discrepancy was introduced as a distance of a finite design to uniformity. However, the L_∞ star discrepancy is hard to estimate, fortunately, [Warnock \(1972\)](#) elaborated an explicit expression specific to the L_2 star discrepancy:

$$[D_2^*(\mathbf{X}_n)]^2 = \frac{1}{9} - \frac{2}{n} \sum_{i=1}^n \prod_{l=1}^d \frac{(1-x_l^{(i)})}{2} + \frac{1}{n^2} \sum_{i,j=1}^n \prod_{l=1}^d \left[1 - \max(x_l^{(i)}, x_l^{(j)}) \right]. \quad (1.23)$$

One can notice that this expression is similar to the Cramér-von Mises test statistic. Even if this expression is tractable, [Fang et al. \(2018\)](#) detailed its limits: the star L_2 discrepancy generates designs that are not robust to projections in sub-spaces; it is not an invariant metric by rotation and reflection; and finally, by construction, L_p discrepancies give a disproportionate role to the point $\mathbf{0}$ by anchoring the box $[\mathbf{0}, \mathbf{x}]$.

Two improved criteria were proposed by [Hickernell \(1998\)](#) with the *centered L_2 discrepancy* and the *wrap-around L_2 discrepancy*. Those are widely used in practice since they solve the previous limits while satisfying the Koksma-Hlawka inequality with a modification of the total variation. Let us introduce the explicit formula of the centered L_2 discrepancy:

$$\begin{aligned} CD_2^*(\mathbf{X}_n) = & \left(\frac{13}{12} \right)^d - \frac{2}{n} \sum_{i=1}^n \prod_{l=1}^d \left(1 + \frac{1}{2} |x_l^{(i)} - 0.5| - \frac{1}{2} |x_l^{(i)} - 0.5|^2 \right) \\ & + \frac{1}{n^2} \sum_{i,j=1}^n \prod_{l=1}^d \left(1 + \frac{1}{2} |x_l^{(i)} - 0.5| + \frac{1}{2} |x_l^{(j)} - 0.5| - \frac{1}{2} |x_l^{(i)} - x_l^{(j)}| \right). \end{aligned} \quad (1.24)$$

As an alternative to discrepancies, many geometrical criteria exist to assess a space-filling design. The most common way to do so is to maximize the minimal distance among the pairs of Euclidian distances between the points of a design. The criterion to maximize is then simply called the *minimal distance* of a design (denoted ϕ_{\min}). For numerical reasons, the ϕ_p criterion is often used instead of the minimal distance. The following ϕ_p criterion converges towards the minimum distance as $p \geq 1$ tends to infinity:

$$\phi_{\min}(\mathbf{X}_n) = \min_{i \neq j} \|\mathbf{x}^{(i)} - \mathbf{x}^{(j)}\|_2, \quad \phi_p(\mathbf{X}_n) = \sum_{i=1}^j \sum_{j=1}^n \left(|x^{(i)} - x^{(j)}|^{-p} \right)^{\frac{1}{p}}. \quad (1.25)$$

More space-filling criteria are reviewed in [Abtini \(2018\)](#) and in the Appendix A from [Da Veiga et al. \(2021\)](#). Further relations between some mathematical objects related to space-filling are developed in [Pronzato and Müller \(2012\)](#). These space-filling metrics are widely used to optimize a different sampling technique.

Latin hypercube sampling

Latin hypercube sampling is a method introduced in 1979 ([Mckay et al., 1979](#)), initially for numerical integration. In a bounded domain, this stratified sampling technique forces the distribution of each sub-projection to be as uniform as possible. To do so, for an n -sized design, each marginal domain is divided into n identical segments. This creates a regular grid of n^d squared cells over the domain.

Then, a Latin hypercube design (LHD) does not allow more than one point within a segment. That way, new LHDs can be built as a permutation of the marginals of an existing LHD. Inside each selected cell from the grid, the point can be placed at the center or randomly.

Various contributions proposed a variance, and a central limit theorem to LHS ([Koehler and Owen, 1996](#)). Similarly to the Monte Carlo variance in Eq. (1.16), LHS variance can be expressed as:

$$\text{Var}\left(\bar{y}_n^{\text{LHS}}\right) = \frac{1}{\sqrt{n}} \text{Var}(g(\mathbf{X})) - \frac{C}{n} + o\left(\frac{1}{n}\right). \quad (1.26)$$

Where C is a positive constant, showing that the LHS usually reduces the variance for numerical integration. Because of its stratified structure, LHS can generate poor designs from a space-filling point of view (see e.g., the illustration in Fig. 1.6a). The following section presents various methods aiming at optimizing LHDs.

Optimized Latin hypercube sampling

To improve the space-filling property of LHD, it is common to add an optimization step. The goal of this optimization is to improve a space-filling criterion by generating LHD from permutations of an initial LHD. [Damblin et al. \(2013\)](#) reviews LHS optimization using different discrepancy criteria and subprojection properties. This optimization can be performed by different algorithms, such as the stochastic evolutionary algorithm or simulated annealing. The results from

this work show that LHD optimized by L_2 centered or wrap-around discrepancies offer strong robustness to two-dimensional projections. It also shows that these designs keep this property for dimensions larger than 10, while scrambled Sobol' sequences lose it. Fig. 1.6 illustrates two LHD, optimized by the L_2 centered discrepancy and the geometrical ϕ_p . The space-filling difference is not obvious in two dimensions, and they both spread uniformly.

More recent work developed different ways to optimize LHD. Among them, let us mention the maximum projection designs from Joseph et al. (2015) which relies on the optimization of a geometrical criterion and delivers interesting performances. In the same vein, the uniform projection designs from Sun et al. (2019) is also a method to optimize LHS, this time based on a criterion averaging discrepancies between each pairs of marginals.

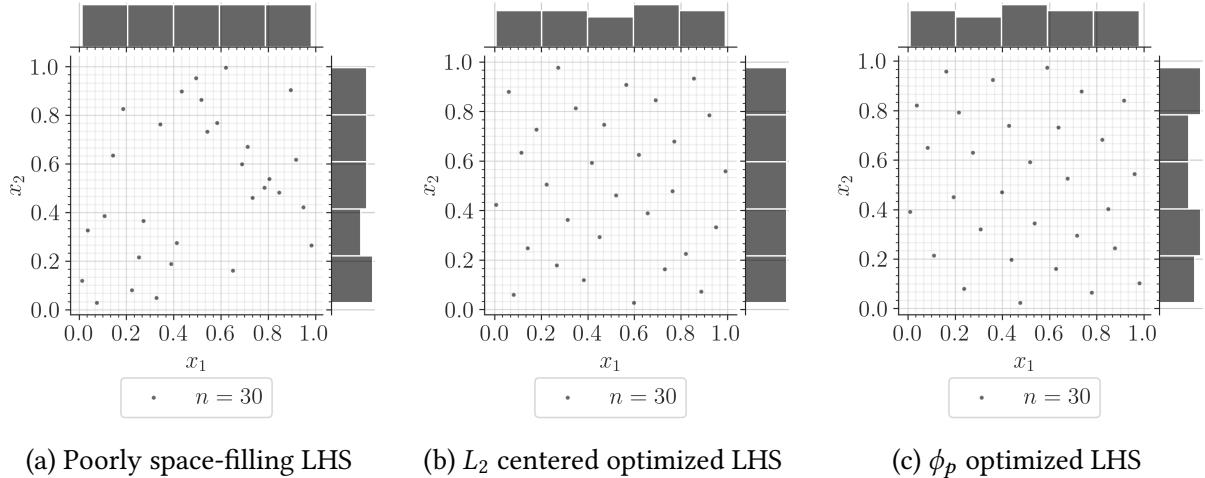


Figure 1.6 Latin hypercube designs with poor and optimized space-filling properties ($n = 8$)

OpenTURNS 3 (Design of experiments). The Python code available in Appendix ?? proposes a minimalistic OpenTURNS example to build an LHS and an LHS optimized w.r.t. to a space-filling metric (here the L2-centered discrepancy) using the simulated annealing algorithm. Figures illustrating the present section may be reproduced, using the OpenTURNS scripts available on GitHub⁶.

1.4.3 Summary and discussion

A wide panel of sampling techniques exists for numerical integration or design of experiments purposes. In both cases, the studied domain is bounded and the targeted measure is uniform. However, uncertainty propagation is often performed on complex input distributions, with possibly unbounded domains. In uncertainty quantification, this step might be referred to as the estimation of the output random variable's central tendency (i.e., its mean and variance). Central tendency estimation is a numerical integration with respect to any input distribution,

⁶https://github.com/efekhari27/thesis/blob/main/numerical_experiments/chapter1/designofexperiments.ipynb

sometimes called *probabilistic integration* (Briol et al., 2019) as part of *probabilistic numerics* (Oates and Sullivan, 2019).

To generate i.i.d samples following any distribution (i.e., non-uniform), one may use *inverse transform* sampling. After generating samples in the unit hypercube, the inverse CDF function (i.e., quantile function) is applied on marginals. Finally, possible dependence effects may be added using the Sklar theorem Eq. (1).

One may wonder if the properties from the uniform design are conserved after this nonlinear transformation. Li et al. (2020) explores this question from a discrepancy point of view. The authors find correspondences between discrepancies with respect to uniformity and discrepancy with respect to the target distribution. However, this result show practical limits, sometimes making the interpretation of the last discrepancy easier. This question will be further discussed in the [Chapter 4], using a more general framework.

Let us also remark that, depending on the distribution, defining the inverse CDF is not always possible. For example, samples following truncated distributions or mixture distributions might sometime be generated with a different technique. The *acceptance-rejection* method offers a versatile generation only based on the PDF f_x . Assuming that a well-known proposal PDF f_x^* exists such that $f_x \leq c \times f_x^*, c \in [1, +\infty]$. One may generate a sample according to $c \times f_x^*$ and only retain from this sample the points under the PDF f_x . Note that some sampling methods, such as QMC, are not well suited with acceptance-rejection since their structure gets perturbed.

In this section, many methods were presented to propagate input uncertainties against a deterministic function. The propagation with the three following goals and contexts were introduced:

- building a quadrature rule for numerical integration against a uniform distribution,
- creating a space-filling design of experiments to uniformly explore the space, often in a small data context (e.g., to build the learning set of a surrogate model),
- generating a design for central-tendency estimation, which is simply a numerical integration against a nonuniform density.

These three objectives have been explored in different communities, but they actually share similar methods. They all have in common the general analysis (i.e., global behavior) of the output random variable. However, some studies require to shift the focus towards specific areas of the output random variables. When using uncertainty propagation to perform risk analysis, the events studied are often contained in the tails of the output distribution. In this case, dedicated uncertainty propagation methods will significantly improve the estimation of the associated statistical quantities.

1.5 Uncertainty propagation for rare event estimation

This section aims at presenting another type of uncertainty propagation. In the context of a risk analysis applied to the engineering field, the reliability of a system needs to be assessed. Most often, a risk measure associated with a failure mode of the studied system is estimated.

Since most systems studied in risk analysis must be highly reliable, the occurrence of such event is qualified as rare. Only a small amount of extreme input conditions or an unlikely unfavorable combinations of inputs lead to the failure of the system. Hence, the usage of the equivalent terms *reliability analysis* and *rare event estimation*. The notion of risk associated with an event is often decomposed as a product of its likelihood and its consequences. The failure of a system might be very rare, but its consequences can be severe (e.g., civil engineering structures, nuclear infrastructure, telecommunication networks, electrical grid, railway signalling, etc.).

Different risk measures (i.e., quantities of interest related to the tail of the distributions) can be studied depending on the type of risk analysis. Quantiles are a first conservative measure, widely used for risk analysis. The α -quantile q_α of the output random variable Y is defined as:

$$q_\alpha = \inf_{y \in \mathbb{R}} \{F_Y(y) \geq \alpha\}, \quad \alpha \in [0, 1]. \quad (1.27)$$

As an alternative, one can define a scalar safety threshold y_{th} that should not be exceeded to keep the system safe. Then, a second risk measure is the probability of exceeding this safety threshold, also called *failure probability*:

$$p_f = \mathbb{P}(Y \geq y_{\text{th}}), \quad y_{\text{th}} \in \mathbb{R}. \quad (1.28)$$

To illustrate this quantity, Fig. 1.7 shows the one-dimensional propagation of a normal distribution (represented by the PDF on the left), through a function $g(\cdot)$. The probability of exceeding a given threshold y_{th} is represented by the area in red under the output PDF on top. An interesting reflection on the use and the interpretation of risk measures including measures from the finance domain such as the *conditional value-at-risk* (also called superquantile) is presented in [Rockafellar and Royset \(2015\)](#).

In the following section, the formalism for reliability analysis problems will be first presented, then the main methods solving this specific problem will be introduced. Note however that the present work will not address the problems of time-dependent reliability analysis tackled in [Hawchar et al. \(2017\)](#).

1.5.1 Problem statement

Following to the UQ methodology, the behavior of the system is modeled by $M(\cdot)$. Considering the problem of exceeding a safety threshold in Eq. (1.28), the system's performance is commonly defined as the difference between the model's output and the safety threshold $y_{\text{th}} \in \mathbb{R}$. Formally,

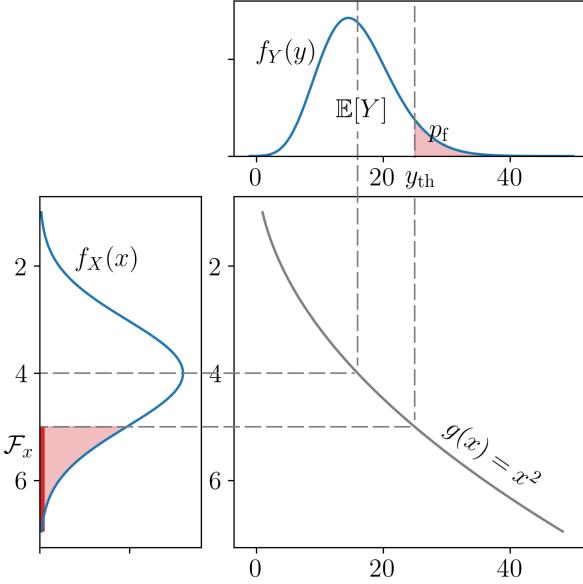


Figure 1.7 One-dimensional reliability analysis example

the *limit-state function* (LSF) is a deterministic function $g : \mathbb{R} \rightarrow \mathbb{R}$ quantifying this performance:

$$g(\mathbf{x}) = y_{\text{th}} - \mathcal{M}(\mathbf{x}). \quad (1.29)$$

Depending on the sign of its images, this function splits the inputs space into two disjoint and complementary domains called the *failure domain* \mathcal{F}_x , and the *safe domain* \mathcal{S}_x which are defined as:

$$\mathcal{F}_x = \{\mathbf{x} \in \mathcal{D}_x \mid g(\mathbf{x}) \leq y_{\text{th}}\}, \quad \mathcal{S}_x := \{\mathbf{x} \in \mathcal{D}_x \mid g(\mathbf{x}) > y_{\text{th}}\}. \quad (1.30)$$

The border between these two domains is a hypersurface called *limit-state surface* (LLS), defined by $\mathcal{F}_x^0 := \{\mathbf{x} \in \mathcal{D}_x \mid g(\mathbf{x}) = 0\}$. Similarly to any UQ study using a numerical model, this problem may require to be resolved using a limited number of calls to a black-box simulator. The difficulties in a reliability problem come from the properties of the LSF: nonlinear, costly to evaluate or with a multimodal failure domain. Additionally, note that the reliability problem can be the composition of multiple reliability problems, often modeled as system of problems in series and parallel.

A rare event estimation results from a particular uncertainty propagation through the LSF. Considering the output variable of interest $g(\mathbf{X})$, its probability of being negative (i.e., in the failure domain) is a common risk measure. The so-called *failure probability*, denoted by p_f , is the quantity of interest for reliability analysis considered in this work. This quantity is formally written⁷:

$$p_f = \mathbb{P}(Y \geq y_{\text{th}}) = \mathbb{P}(g(\mathbf{X}) \leq 0) = \int_{\mathcal{F}_x} f_X(\mathbf{x}) d\mathbf{x} = \int_{\mathcal{D}_x} \mathbb{1}_{\mathcal{F}_x}(\mathbf{x}) f_X(\mathbf{x}) d\mathbf{x}, \quad (1.31)$$

⁷Note that this probabilistic integration is usually written using the PDF $f_X(\cdot)$, but it could identically be expressed in terms of probability measure by taking $f_X(\mathbf{x}) d\mathbf{x} = d\mathbb{P}_X(\mathbf{x})$, $\forall \mathbf{x} \in \mathcal{D}_x$.

were the indicator function applied to the failure domain returns $\mathbb{1}_{\{\mathcal{F}_X\}}(x) = 1$ if $x \in \mathcal{F}_X$ and $\mathbb{1}_{\{\mathcal{F}_X\}}(x) = 0$ otherwise. Rare event estimation implies both contour finding (i.e., characterizing the LSF) and an estimation strategy targeting the failure domain (often with a limited number of simulations). Note that failure events are qualified as rare when their failure probability has an order of magnitude between $10^{-2} \leq p_f \leq 10^{-9}$ (see e.g., [Lemaire et al. 2009](#)).

Instead of directly performing a reliability analysis in the physical space (i.e., \mathbf{x} -space), these problems are usually solved in the *standard normal space* (i.e., \mathbf{u} -space). Working in the standard space reduces numerical issues caused by potentially unscaled or asymmetric marginals. Moreover, a larger panel of methods can be applied in the standard space since the random inputs become independent. The bijective mapping between these two spaces is called an “iso-probabilistic transformation”, denoted by $T : \mathcal{D}_X \subseteq \mathbb{R}^d \rightarrow \mathbb{R}^d$, $\mathbf{x} \mapsto T(\mathbf{X}) = \mathbf{u} = (u_1, \dots, u_d)^\top$. When considering any random vector $\mathbf{X} = (X_1, \dots, X_d)^\top$ and the independent standard Gaussian vector $\mathbf{U} = (U_1, \dots, U_d)^\top$, the following equalities hold:

$$\mathbf{U} = T(\mathbf{X}) \Leftrightarrow \mathbf{X} = T^{-1}(\mathbf{U}). \quad (1.32)$$

A reliability problem can be expressed in the standard normal space. Let us first consider the transformed limit-state function \check{g} defined as:

$$\check{g} : \begin{array}{ccc} \mathbb{R}^d & \longrightarrow & \mathbb{R} \\ \mathbf{u} & \longmapsto & \check{g}(\mathbf{u}) = (g \circ T^{-1})(\mathbf{u}). \end{array} \quad (1.33)$$

Since this transformation is a diffeomorphism⁸, one can apply the change of variable $\mathbf{x} = T(\mathbf{u})$ to express the reliability problem from Eq. (1.31) in the standard space:

$$p_f = \mathbb{P}(\check{g}(\mathbf{U}) \leq 0) = \int_{\mathcal{F}_u} \varphi_d(\mathbf{u}) d\mathbf{u} = \int_{\mathbb{R}^d} \mathbb{1}_{\mathcal{F}_u}(\mathbf{u}) \varphi_d(\mathbf{u}) d\mathbf{u}, \quad (1.34)$$

with the transformed failure domain denoted by $\mathcal{F}_u = \{\mathbf{u} \in \mathbb{R}^d \mid \check{g}(\mathbf{u}) \leq 0\}$, and the d -dimensional standard Gaussian PDF $\varphi_d(\mathbf{u}) = \frac{1}{(2\pi)^{d/2}} \exp\left(-\frac{\|\mathbf{u}\|_2^2}{2}\right)$. The fact that the failure probability is invariant by this transformation allows the analyst to estimate this quantity in both spaces.

Different types of transformations exist, such as the Rosenblatt or the generalized Nataf transformation introduced by [Lebrun \(2013\)](#). In practice, the transformation choice depends on the properties of the input distribution studied. For example in OpenTURNS, depending on the three following cases, different types of transformations are applied:

- for elliptical distributions, a linear Nataf transformation is applied;
- for distributions with an elliptical copula, the generalized Nataf transformation is used;
- otherwise, the Rosenblatt transformation is used.

⁸Considering two manifolds A and B , a transformation $T : A \rightarrow B$ is called a diffeomorphism if it is a differentiable bijection with a differentiable inverse $T^{-1} : B \rightarrow A$.

1.5.2 Rare event estimation methods

The main risk measure chosen for rare event estimation in this work is the previously introduced failure probability. Therefore, let us recall that the goal is to build an efficient estimation (or approximation) of the following d -dimensional integral:

$$p_f = \int_{\mathcal{D}_x} \mathbb{1}_{\mathcal{F}_x}(\mathbf{x}) f_x(\mathbf{x}) d\mathbf{x} \quad (1.35)$$

In the context of rare event estimation using costly to evaluate numerical models, the simulation budget is often limited to n runs with $p_f \ll \frac{1}{n}$. Which explains the need for specific methods offering approximations or simulations targeting the unknown failure domain. Two types of rare event estimation methods are classically presented: first, using approximation approaches, second, using sampling techniques. This section introduced the commonly used rare event methods, see [Morio and Balesdent \(2015\)](#) for a more exhaustive review.

First and second order reliability methods (FORM/SORM)

The well-known first and second order reliability methods (FORM and SORM) both rely on a geometric approximation to estimate a failure probability ([Lemaire et al., 2009](#)). They extrapolate a local approximation of the LSF built in the vicinity of a *most-probable-failure-point* (MPFP), also called *design point*.

Working in the standard space, the methods first look for this MPFP, denoted P^* , with coordinates \mathbf{u}^* . To find it, one can solve the following quadratic optimization problem:

$$\mathbf{u}^* = \arg \max_{\mathbf{u} \in \mathbb{R}^d} (\mathbb{1}_{\mathcal{F}_u}(\mathbf{u}) \varphi_d(\mathbf{u})). \quad (1.36)$$

Using the properties of the standard space allows us to rewrite it as:

$$\mathbf{u}^* = \arg \max_{\mathbf{u} \in \mathbb{R}^d} \frac{1}{(2\pi)^{d/2}} \exp\left(-\frac{\mathbf{u}^\top \mathbf{u}}{2}\right) \quad \text{s.t.} \quad \mathbf{u} \in \mathcal{F}_u \quad (1.37)$$

$$= \arg \min_{\mathbf{u} \in \mathbb{R}^d} \mathbf{u}^\top \mathbf{u} \quad \text{s.t.} \quad \check{g}(\mathbf{u}) \leq 0. \quad (1.38)$$

This problem then becomes a quadratic optimization under nonlinear constraint. It is classically solved by gradient decent algorithms (e.g., Abdo-Rackwitz algorithm [Abdo and Rackwitz, 1991](#)) but can also use gradient-free techniques (e.g., Cobyla algorithm [Powell, 1994](#)). This point defines the smallest Euclidian distance between the LSS and the origin of the standard space. To understand its role in the reliability problem, let us recall that the density of the standard normal present an exponential decay in its radial and tangential direction. Then, P^* is the point with the biggest contribution to the failure probability (see the illustration in Fig. 1.8).

This distance between the origin and P^* is another risk measure, defined as the *Hasofer-Lind reliability index* (Lemaire et al., 2009), $\beta \in \mathbb{R}$ such that:

$$\beta = \|\mathbf{u}^*\|_2 = \boldsymbol{\alpha}^\top \mathbf{u}^*, \quad \text{s.t.} \quad \boldsymbol{\alpha} = \frac{\nabla_{\mathbf{u}} \check{g}(\mathbf{u})}{\|\nabla_{\mathbf{u}} \check{g}(\mathbf{u})\|_2}. \quad (1.39)$$

The vector $\boldsymbol{\alpha}$ is the unit vector pointing at P^* from the origin point.

Then, FORM aims at approximating the limit-state function $\check{g}(\cdot)$ by its first-order Taylor expansion around the MPFP, denoted $\check{g}_1(\mathbf{u}^*)$:

$$\begin{aligned} \check{g}(\mathbf{u}) &= \check{g}_1(\mathbf{u}^*) + o\left(\|\mathbf{u} - \mathbf{u}^*\|_2^2\right) \\ &= \check{g}(\mathbf{u}^*) + \nabla_{\mathbf{u}} \check{g}(\mathbf{u}^*)^\top (\mathbf{u} - \mathbf{u}^*) + o\left(\|\mathbf{u} - \mathbf{u}^*\|_2^2\right) \\ &= \|\nabla_{\mathbf{u}} \check{g}(\mathbf{u})\|_2 (\boldsymbol{\alpha}^\top \mathbf{u}^* - \boldsymbol{\alpha}^\top \mathbf{u}) + o\left(\|\mathbf{u} - \mathbf{u}^*\|_2^2\right) \end{aligned} \quad (1.40)$$

Using $\check{g}_1(\cdot)$ as an approximation of the LSF, the failure probability can be approximated as:

$$p_f \approx p_f^{\text{FORM}} = \mathbb{P}(-\boldsymbol{\alpha}^\top \mathbf{u} \leq -\beta) = \Phi(-\beta), \quad (1.41)$$

with $\Phi(\cdot)$ the CDF of the standard Gaussian. Depending on the properties of the LFS, this approximation will be more or less accurate. Note that for a purely linear LFS, $p_f = p_f^{\text{FORM}}$. When the function is nonlinear, adding a quadratic term to the Taylor expansion can help the approximation. The approximation method is then called SORM for *second order reliability method*. However, this added complexity implies the computation of Hessian matrices, which can be complicated (see the Chapter 1 from Bourinet 2018 for their estimation).

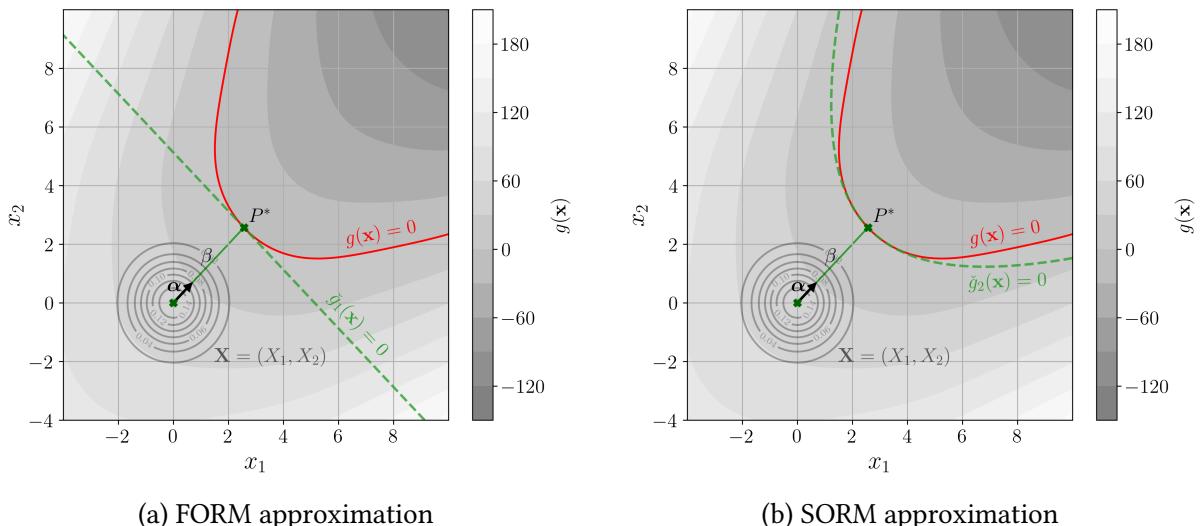


Figure 1.8 FORM and SORM approximation on a two-dimensional reliability problem

When the MPFP is not unique, the application of these methods might lead to important errors. From a geometrical point of view, having more than one MPFP means that more than one failure zones are at the same euclidean distance of the origin. Applying a FORM or SORM resolution in this particular case leads to the estimation of only one of the failure areas. The

muti-FORM algorithm (see [Der Kiureghian and Dakessian \(1998\)](#)) prevents this situation by applying successive FORM. Once the first MPFP $P^{*(1)}$ found, the LSS is modified by removing a nudge to find to following MPFP $P^{*(2)}$, positioned at a similar distance but in a different direction.

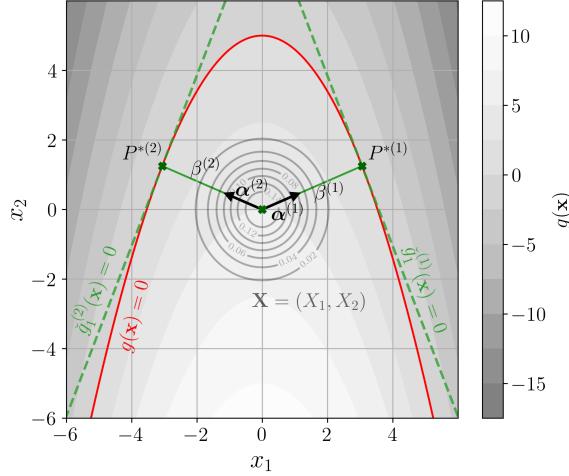


Figure 1.9 Multi-FORM approximation on an example with two MPFPs

Overall, FORM and SORM methods deliver a very efficient approximation of small probabilities for relatively simple problems (in terms of linearity and dimension). For this reason, they have been widely used in the practical context of limited simulation budget. [Straub \(2014\)](#) illustrates the efficiency of FORM approaches on industrial cases such as probabilistic fatigue damage. However, these methods present serious limits as the dimension increases (see the discussion in the Chapter 1 from [Chabridon 2018](#)). Additionally, their main drawback is the lack of complementary information concerning the confidence of the results. The textbook example illustrated in Fig. 1.9 shows that the method might miss some important areas of the failure domain, leading to poor estimations. As an alternative to approximation methods, simulation-based methods often provide to the analyst an assessment of the estimation's confidence.

Monte Carlo

Crude Monte Carlo sampling is a universal and empirical method for uncertainty propagation. As introduced earlier, it relies on the pseudo-random generation of i.i.d. samples $\{\mathbf{x}^{(i)}\}_{i=1}^n \stackrel{\text{i.i.d.}}{\sim} f_{\mathbf{X}}$. Only the estimator is now written using the indicator function applied to the LSF:

$$p_f \approx \hat{p}_f^{\text{MC}} = \frac{1}{n} \sum_{i=1}^n \mathbb{1}_{\mathcal{F}_{\mathbf{x}}}(\mathbf{x}^{(i)}). \quad (1.42)$$

Provided that the failure probability is bounded, this estimator converges towards it almost surely according to the LLN. Once again, Monte Carlo offers an unbiased estimator, regardless of the problem's dimension or the regularity of the function $g(\cdot)$. Additionally, the variance of

this estimator is fully known:

$$\text{Var}(\widehat{p}_f^{\text{MC}}) = \frac{1}{n} p_f(1 - p_f). \quad (1.43)$$

The variance of this estimator can be used to build its confidence interval according to the central limit theorem (similarly to the ones from Eq. (1.17)). Because of the small scale of the quantities manipulated in rare event estimation, the estimator's coefficient of variation is also widely used:

$$\delta_{\widehat{p}_f^{\text{MC}}} = \frac{\sqrt{\text{Var}(\widehat{p}_f^{\text{MC}})}}{\mathbb{E}[\widehat{p}_f^{\text{MC}}]} = \sqrt{\frac{1 - p_f}{np_f}}. \quad (1.44)$$

In theory, Monte Carlo estimation presents multiple advantages for rare event estimation. First, this method can be applied directly in the physical space, without transformation (which is practical for complex input distributions). Second, it does not suffer from the curse of dimensionality. Third, it is qualified as embarrassingly parallel method since each of the numerical simulations are independent. Finally, it offers strong convergence guarantees and complementary information on the estimation confidence. These properties often make Monte Carlo the reference method in rare event estimation benchmarks.

However, the advantages of this estimator are shadowed by its slow convergence. To estimate a target failure probability $p_f = 10^{-\alpha}$, a Monte Carlo estimation with a convergence level $\delta_{\widehat{p}_f^{\text{MC}}} = 0.1$ famously requires $n = 10^{\alpha+2}$ simulations.

In the context of rare event estimation, Monte Carlo needs a number of simulation that is often prohibitive in practice. This excessive simulation budget comes from the fact that the vast majority of the samples drawn from the input distribution are not in the failure domain.

Importance sampling

Importance sampling (IS) is a variance reduction method, aiming at improving the performances of crude Monte Carlo sampling. In the context of rare event estimation, the main idea is to deliberately introduce a bias in the sampled density, shifting it towards the failure domain. If this shift actually goes towards the failure domain, it allows drawing more points in it, leading to a better estimate of our quantity.

The challenge in importance sampling is to pick a relevant *instrumental* distribution h_X (also called *auxiliary* distribution) to replace the distribution f_X . Then, by introducing the fully known *likelihood ratio* $w_X(x) = \frac{f_X(x)}{h_X(x)}$, one can rewrite $f_X(x) = w_X(x)h_X(x)$ and inject it in the failure probability expression:

$$p_f = \int_{\mathcal{D}_X} \mathbb{1}_{\mathcal{F}_X}(x) f_X(x) dx = \int_{\mathcal{D}_X} \mathbb{1}_{\mathcal{F}_X}(x) w_X(x) h_X(x) dx. \quad (1.45)$$

This simple writing trick allows us to integrate against the auxiliary distribution. With a Monte Carlo method, this task should be easier than integrating directly against the initial distribution.

The importance sampling estimator of the failure probability is defined for a sample drawn on the auxiliary distribution $\{\mathbf{x}^{(i)}\}_{i=1}^n \stackrel{\text{i.i.d.}}{\sim} h_{\mathbf{X}}$:

$$\hat{p}_f^{\text{IS}} = \frac{1}{n} \sum_{i=1}^n \mathbb{1}_{\mathcal{F}_{\mathbf{x}}}(\mathbf{x}^{(i)}) w_{\mathbf{X}}(\mathbf{x}^{(i)}). \quad (1.46)$$

Similarly to Monte Carlo, this estimator is unbiased, however, its variance is defined as:

$$\text{Var}(\hat{p}_f^{\text{IS}}) = \frac{1}{n} \left(\mathbb{E}_h \left[\left(\mathbb{1}_{\mathcal{F}_{\mathbf{x}}}(\mathbf{X}) \frac{f_{\mathbf{X}}(\mathbf{X})}{h_{\mathbf{X}}(\mathbf{X})} \right)^2 \right] - p_f^2 \right). \quad (1.47)$$

The quality of the variance reduction associated to this technique fully depends on the choice of the instrumental distribution. In fact, importance sampling can lead to higher variance than crude Monte Carlo when the instrumental distribution is poorly chosen (Owen and Zhou, 2000). However, an optimal instrumental distribution h_{opt} theoretically gives the smallest variance by setting it equal to zero in Eq. (1.47):

$$h_{\text{opt}}(\mathbf{x}) = \frac{\mathbb{1}_{\mathcal{F}_{\mathbf{x}}}(\mathbf{x}) f_{\mathbf{X}}(\mathbf{x})}{p_f}. \quad (1.48)$$

The optimal expression above is unfortunately not usable in practice since it includes the targeted quantity p_f . Considering this framework, various techniques intend to define instrumental distributions as close as possible to this theoretical result. An important review of the use of importance sampling in the context of reliability analysis was proposed by Tabandeh et al. (2022).

The most immediate solution is to combine the information provided by the results of FORM with importance sampling, simply called FORM-IS. In practice, the instrumental distribution is defined as the initial distribution centered on the design point resulting from FORM. Fig. 1.10 illustrates on the same two-dimensional case, the estimation by Monte Carlo and importance sampling centered on the design point. The points in red reached the failure domain and their number seem insufficient for Monte Carlo. Note that comparing the results from FORM and FORM-IS allows to assess the nonlinearity of the LSF in the vicinity of the design point. This strategy is simple to implement, but it inherits the main drawbacks of FORM, such as the limits related to multiple failure areas (see the example illustrated in Fig. 1.9). Finally, other importance sampling schemes integrate adaptive mechanisms, progressively leading the sampling towards the failure domain (Bugallo et al., 2017).

Adaptive importance sampling by cross-entropy

The *cross-entropy-based adaptive importance sampling* (CE-AIS) is an adaptive strategy, optimizing the IS variance reduction by searching the best instrumental distribution within a parametric

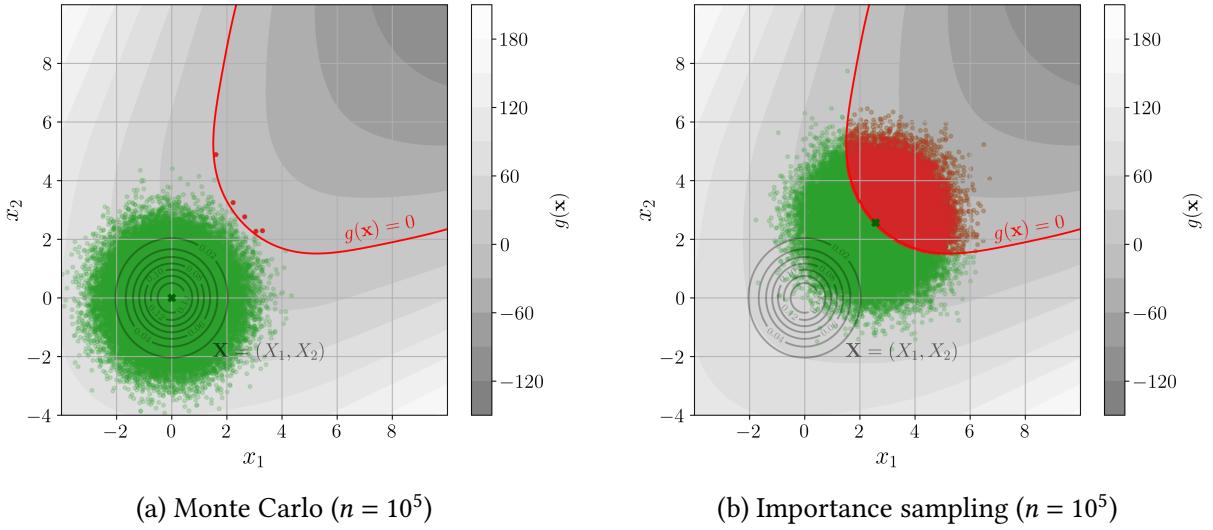


Figure 1.10 Illustration of a rare event estimation.

family. Let us consider the distribution h_λ , belonging to the parametric family \mathcal{H}_λ , defined as:

$$\mathcal{H}_\lambda = \left\{ \mathbf{x} \mapsto h_{\mathbf{X}}(\mathbf{x}|\boldsymbol{\lambda}) = h_\lambda(\mathbf{x}), \quad \boldsymbol{\lambda} = (\lambda_1, \dots, \lambda_p) \in \mathcal{D}_\lambda \subseteq \mathbb{R}^p \right\}. \quad (1.49)$$

The early work of [Bucher \(1988\)](#) only included normal distributions to minimize the IS variance w.r.t. the parameter $\boldsymbol{\lambda}$, using Eq. (1.47) the optimization simplifies as:

$$\boldsymbol{\lambda}^* = \arg \min_{\boldsymbol{\lambda} \in \mathcal{D}_\lambda} \mathbb{E}_{h_\lambda} [\mathbb{1}_{\mathcal{F}_x}(\mathbf{X}) w_{\mathbf{X}}(\mathbf{X})^2]. \quad (1.50)$$

However, this optimization strategy requires sampling with respect to the instrumental distribution at each optimization iteration, which was overcome by a different approach.

The “cross-entropy” (CE) method uses Kullback-Leibler (KL) divergence to optimize importance sampling. KL divergence is a dissimilarity measure between distributions, expressed between the parametric instrumental distribution h_λ and the optimal one h_{opt} :

$$D_{\text{KL}}(h_{\text{opt}} || h_\lambda) = \int_{\mathcal{D}_x} \log \left(\frac{h_{\text{opt}}(\mathbf{x})}{h_\lambda(\mathbf{x})} \right) h_{\text{opt}}(\mathbf{x}) d\mathbf{x} \quad (1.51a)$$

$$= \int_{\mathcal{D}_x} \log(h_{\text{opt}}(\mathbf{x})) h_{\text{opt}}(\mathbf{x}) d\mathbf{x} - \int_{\mathcal{D}_x} \log(h_\lambda(\mathbf{x})) h_{\text{opt}}(\mathbf{x}) d\mathbf{x}. \quad (1.51b)$$

[Rubinstein and Kroese \(2004\)](#) symplify the expression of the optimization problem minimizing the KL divergence, which is most often convex and differentiable w.r.t. $\boldsymbol{\lambda}$:

$$\boldsymbol{\lambda}^* = \arg \min_{\boldsymbol{\lambda} \in \mathcal{D}_\lambda} D_{\text{KL}}(h_{\text{opt}} || h_\lambda). \quad (1.52)$$

By injecting the expression in Eq. (1.51b), the optimization problem simply becomes function of an expected value over the initial density f_X :

$$\lambda^* = \arg \max_{\lambda \in \mathcal{D}_\lambda} \int_{\mathcal{D}_x} \log(h_\lambda(\mathbf{x})) h_{\text{opt}}(\mathbf{x}) d\mathbf{x} = \arg \max_{\lambda \in \mathcal{D}_\lambda} \mathbb{E}_{f_X} [\mathbb{1}_{\mathcal{F}_X}(\mathbf{X}) \log(h_\lambda(\mathbf{X}))]. \quad (1.53)$$

To directly estimate this expected value, the failure probability p_f should not be too rare, which allows to use an empirical estimator of the expected value:

$$\lambda^* = \arg \max_{\lambda \in \mathcal{D}_\lambda} \sum_{i=1}^n \mathbb{1}_{\mathcal{F}_X}(\mathbf{x}^{(i)}) \log(h_\lambda(\mathbf{x}^{(i)})), \quad \{\mathbf{x}^{(i)}\}_{i=1}^n \stackrel{\text{i.i.d.}}{\sim} f_X. \quad (1.54)$$

Eventually, this optimization can be solved by cancelling the gradient:

$$\sum_{i=1}^n \mathbb{1}_{\mathcal{F}_X}(\mathbf{x}^{(i)}) [\nabla \log(h_{\lambda^*})](\mathbf{x}^{(i)}) = \mathbf{0}. \quad (1.55)$$

According to [Rubinstein and Kroese \(2004\)](#), this system of equations has a unique analytical solution when assuming that the instrumental distribution belongs to the “natural exponential family”.

However, when dealing with rare probabilities, the empirical estimation does not draw enough points in the failure domain to get an accurate estimate. The adaptive version of this technique, called *multilevel cross-entropy*, gradually builds a set of intermediate levels, decreasing towards the failure level (equal to zero). By working on a set of individually less rare events, the empirical estimation in Eq. (1.53) is made possible.

The algorithm starts by generating and evaluating an initial sample $\{g(\mathbf{X}_{[1]}^{(i)})\}_{i=1}^n$, on which a threshold level $q_{[1]}^{p_0}$ is computed as the empirical p_0 -quantile. Using the samples below the first threshold $q_{[1]}^{p_0}$, a first instrumental distribution $h_{\lambda_{[1]}^*}$ is optimized. At the next steps $k \in \{1, \dots, k_{\#}\}$, the sample $\{\mathbf{X}_{[k]}^{(i)}\}_{i=1}^n$ is generated from the density $h_{\lambda_{[k-1]}^*}$ and the rest of the process repeats until the estimated threshold level becomes negative, $q_{[k_{\#}]}^{p_0} \leq 0$.

The final instrumental density $h_{\lambda_{[k_{\#}]}^*}$ is then considered for importance sampling as defined in Eq. (1.46):

$$\hat{p}_f^{\text{CE-AIS}} = \frac{1}{n} \sum_{i=1}^n \mathbb{1}_{\{g(\mathbf{x}) \leq 0\}} \frac{f_X(\mathbf{x}_{[k_{\#}]}^{(i)})}{h_{\lambda_{[k_{\#}]}^*}(\mathbf{x}_{[k_{\#}]}^{(i)})}, \quad \{\mathbf{X}_{[k_{\#}]}^{(i)}\}_{i=1}^n \stackrel{\text{i.i.d.}}{\sim} h_{\lambda_{[k_{\#}]}^*}. \quad (1.56)$$

CE-AIS is widely used in rare event estimation, as it develops an adaptive technique while conserving the explicit IS variance given in Eq. (1.47). According to [Rubinstein and Kroese \(2004\)](#), the successive instrumental distributions $h_{\lambda_{[k]}^*}$ converge towards h_{opt} under a few hypotheses. The most important one is that the optimal density must belong to the parametric family considered, which should offer enough flexibility to describe a wide range of distributions.

When failure domain is composed of multiple regions, different improvements of the CE-AIS were proposed. [Kurtz and Song \(2013\)](#) proposed to optimize h_{λ^*} among a mixture of Gaussian distributions. This method was further studied by [Wang and Song \(2016\)](#) and [Papaioannou et al. \(2019\)](#) using advanced mixtures in the standard space. However, when using mixtures, the optimization problem does not have an analytical expression anymore ([Geyer et al., 2019](#)).

In the parametric framework, the family choice leads to a complicated trade-off between optimization complexity and flexibility allowed by the family. A similar mechanism is used by other importance sampling methods, inferring the optimal instrumental density by applying kernel density estimation to the points in the failure domain.

Nonparametric adaptive importance sampling

The use of multivariate kernel density estimation (KDE) to approximate the importance sampling optimal density h_{opt} was introduced in the context of structural reliability by [Ang et al. \(1992\)](#), latter followed by [Zhang \(1996\)](#). Let us first present the nonparametric importance sampling from [Zhang \(1996\)](#), considering the instrumental density $h_{[0]}$ (for now, $h_{[0]} \neq f_x$), on which a sample $\{\mathbf{x}_{[1]}^{(i)}\}_{i=1}^n$ is generated. A first failure probability can be roughly estimated, assuming that enough samples lead to the failure domain:

$$\widehat{p}_{f[1]} = \frac{1}{n} \sum_{i=1}^n \mathbb{1}_{\{g(\mathbf{x} \leq 0)\}} \left(\mathbf{x}_{[1]}^{(i)} \right) \frac{f_x \left(\mathbf{x}_{[1]}^{(i)} \right)}{h_{[0]} \left(\mathbf{x}_{[1]}^{(i)} \right)} = \frac{1}{n} \sum_{i=1}^n \mathbb{1}_{\{g(\mathbf{x}) \leq 0\}} \left(\mathbf{x}_{[1]}^{(i)} \right) w_{[1]}^{(i)}. \quad (1.57)$$

On this biased sample, another density can be fitted using KDE, using the previously defined $\widehat{p}_{f[1]}$ as a normalization term:

$$\widehat{h}_{[1]}(\mathbf{x}) = \frac{\det(\mathbf{H}_{[1]})^{-1/2}}{n \widehat{p}_{f[1]}} \sum_{i=1}^n \mathbb{1}_{\{g(\mathbf{x}) \leq 0\}} \left(\mathbf{x}_{[1]}^{(i)} \right) w_{[1]}^{(i)} K \left(\mathbf{H}_{[1]}^{-1/2} (\mathbf{x} - \mathbf{x}_{[1]}^{(i)}) \right). \quad (1.58)$$

Where the kernel K is commonly taken as the multivariate Gaussian centered density with the covariance matrix \mathbf{H} . The tuning of \mathbf{H} is usually done by minimizing an asymptotic mean integrated squared error (AMISE) criterion ([Glad et al., 2007](#)). In the previous expression, the normalization constant insures to build a probability density while the weights $w_{[1]}^{(i)}$, defined above, reflect the contribution of each point to $\widehat{p}_{f[1]}$. After performing this KDE, the estimated density can be used as instrumental density in Eq. (1.46).

As for the CE-IS methods, the risk is that barely any points sampled from the instrumental density $h_{[0]}$ hit the failure domain, leading to poor estimates. [Zhang \(1996\)](#) proposed to couple an adaptive mechanism with a nonparametric inference of the optimal density. This method is further referred to as NAIS for *nonparametric adaptive importance sampling*. Later, the NAIS method was adapted by [Morio \(2011\)](#) to the reliability analysis problem, using a similar mechanism to the CE-AIS method.

In this framework, a series of intermediate threshold are computed as empirical p_0 -quantiles $q_{[1]}^{p_0} > \dots > q_{[k_\#]}^{p_0}$ of the successive importance sampling steps. This algorithm is initiated by setting $h_{[0]} = f_X$ and stops at the step $k_\#$, when $q_{[k_\#]}^{p_0} < 0$.

At the step k , the intermediate normalization constant is written as:

$$\widehat{p}_f[k] = \frac{1}{kn} \sum_{j=1}^k \sum_{i=1}^n \mathbb{1}_{\{g(\mathbf{x}) \leq q_{[j]}^{p_0}\}} \left(\mathbf{x}_{[j]}^{(i)} \right) \frac{f_X \left(\mathbf{x}_{[j]}^{(i)} \right)}{\widehat{h}_{[j-1]} \left(\mathbf{x}_{[j]}^{(i)} \right)} = \frac{1}{kn} \sum_{j=1}^k \sum_{i=1}^n \mathbb{1}_{\{g(\mathbf{x}) \leq q_{[j]}^{p_0}\}} \left(\mathbf{x}_{[j]}^{(i)} \right) w_{[j]}^{(i)}, \quad (1.59)$$

with $\left\{ \mathbf{x}_{[j]}^{(i)} \right\}_{i=1}^n \stackrel{\text{i.i.d.}}{\sim} h_{[j-1]}$. Then, an intermediate instrumental density is inferred by KDE on the samples exceeding the threshold $q_{[k]}^{p_0}$ such that:

$$\widehat{h}_{[k+1]}(\mathbf{x}) = \frac{\det(\mathbf{H}_{[k]})^{-1/2}}{kn \widehat{p}_f[k]} \sum_{j=1}^k \sum_{i=1}^n \mathbb{1}_{\{g(\mathbf{x}) \leq q_{[j]}^{p_0}\}} \left(\mathbf{x}_{[j]}^{(i)} \right) w_{[j]}^{(i)} K \left(\mathbf{H}_{[k]}^{-1/2} (\mathbf{x} - \mathbf{x}_{[j]}^{(i)}) \right). \quad (1.60)$$

The last instrumental density $\widehat{h}_{[k_\#]}$ is finally considered as an approximation of the optimal density for importance sampling introduced in Eq. (1.46):

$$\widehat{p}_f^{\text{NAIS}} = \frac{1}{n} \sum_{i=1}^n \mathbb{1}_{\{g(\mathbf{x}) \leq 0\}} \frac{f_X \left(\mathbf{x}_{[k_\#]}^{(i)} \right)}{\widehat{h}_{[k_\#]} \left(\mathbf{x}_{[k_\#]}^{(i)} \right)}, \quad \left\{ \mathbf{x}_{[k_\#]}^{(i)} \right\}_{i=1}^n \stackrel{\text{i.i.d.}}{\sim} h_{k_\#}. \quad (1.61)$$

Overall, the NAIS offers more flexibility to infer the optimal importance sampling density. This property might suit problems presenting highly nonlinear limit state function. Then, relying on importance sampling still provides an expression of the estimator's variance, by adapting Eq. (1.47) to the recurrent mechanism in NAIS. Because this approach depends on KDE, it inherits its drawbacks. As discussed in [Morio \(2011\)](#), tuning the KDE can create numerical issues and KDE famously suffers from the curse of dimension. In practice, the performances of NAIS seriously decrease for problems in dimension larger than ten.

Subset sampling

Although the concept of splitting already existed, the name of *subset sampling* (SS) was first introduced by [Au and Beck \(2001\)](#) in the structural reliability community. This concept was generalized as a sequential Monte Carlo method under the name of “adaptive multilevel splitting”, as reviewed by [Cérou et al. \(2019\)](#).

Subset sampling splits the failure event \mathcal{F}_x into an intersection of $k_\#$ intermediary events $\mathcal{F}_x = \cap_{k=1}^{k_\#} \mathcal{F}_{[k]}$. Each are nested such that $\mathcal{F}_{[1]} \supset \dots \supset \mathcal{F}_{[k_\#]} = \mathcal{F}_x$. The failure probability is then expressed as a product of conditional probabilities:

$$p_f = \mathbb{P}(\mathcal{F}_x) = \mathbb{P}(\cap_{k=1}^{k_\#} \mathcal{F}_{[k]}) = \prod_{k=1}^{k_\#} \mathbb{P}(\mathcal{F}_{[k]} | \mathcal{F}_{[k-1]}). \quad (1.62)$$

From a practical point of view, the analyst tunes the algorithm⁹ by setting the intermediary probabilities $\mathbb{P}(\mathcal{F}_{[k]} | \mathcal{F}_{[k-1]}) = p_0, \forall k \in \{1, \dots, k_{\#}\}$. Then, the corresponding quantiles $q_{[1]}^{p_0} > \dots > q_{[k_{\#}]}^{p_0}$ are estimated for each conditional subset samples $\mathbf{X}_{[k],N}$ of size N . Note that the initial quantile is estimated by crude Monte Carlo sampling on the input PDF f_X . Following conditional subset samples are generated by *Monte Carlo Markov Chain* (MCMC) sampling of $f_X(\mathbf{x} | \mathcal{F}_{[k-1]})$, using as seeds initialization points the $n = Np_0$ samples given by $\mathbf{A}_{[k],n} = \{\mathbf{X}_{[k-1]}^{(i)} \subset \mathbf{X}_{[k-1],N} | g(\mathbf{X}_{[k-1]}^{(i)}) > \hat{q}_{[k-1]}^{p_0}\}_{i=1}^n$. This process is repeated until an intermediary quantile becomes negative: $\hat{q}_{[k_{\#}]}^{p_0} < 0$. Finally, the failure probability is estimated by:

$$\hat{p}_f^{\text{SS}} = p_0^{k_{\#}-1} \frac{1}{N} \sum_{i=1}^n \mathbb{1}_{\{g(\mathbf{x}) \leq 0\}}(\mathbf{X}_{[k_{\#}],N}^{(i)}). \quad (1.63)$$

In practice, the subset sample size should be large enough to properly estimate intermediary quantiles, leading to the usual recommendation of $p_0 = 0.1$. Fig. 1.11 illustrates the consecutive subset samples moving towards the failure domain. At each step of the algorithm (corresponding to a color), a subset is generated and an intermediate quantile estimated.

[Au and Beck \(2001\)](#) also provide bounds to the coefficient of variation of \hat{p}_f^{SS} . The first one results from a first order Taylor expansion of Eq. (1.63) and is often considered as an upper bound. While the second assumes the estimations of the conditional probabilities to be independent, and tends to underestimate the coefficient of variation.

As discussed in ([Papaioannou et al., 2015](#)), the efficiency of the SS method depends on the choice and tuning of the MCMC algorithm. The Metropolis–Hastings (MH) algorithm is widely used as MCMC algorithm for subset sampling, however, it quickly becomes inefficient as the dimension increases. Different improvements of the MH are made possible by working in the standard space, such as the “component-wise” (or “modified M–H”). More recently, alternative MCMC methods including physical system dynamics (e.g., Hamiltonian MCMC) showed promising results in high-dimension reliability problems ([Papakonstantinou et al., 2023](#)).

The subset sampling is a versatile method, presenting consistent performances even for rare probabilities. Its flexibility allows dealing with highly nonlinear LSF, but its drawbacks arise from the use of MCMC sampling. The convergence of MCMC is complex to control and depends on its tuning, in addition, the MCMC samples are dependent. Unlike the methods derived from importance sampling, the variance of \hat{p}_f^{SS} is only approximated.

1.5.3 Summary and discussion

This section introduced the generic formulation and the main methods for rare event estimation. Even if the problem is generic rare event estimation requires tailored solutions. Depending on the properties of the problem tackled, some methods might outperform others. Beyond the one introduced previously, many more methods are worth mentioning in the field of reliability analysis, such as the *directional sampling* [Bjerager \(1988\)](#), or *line sampling* ([Koutsourelakis](#),

⁹An algorithmic presentation of the generic subset sampling method is given in Appendix ??.

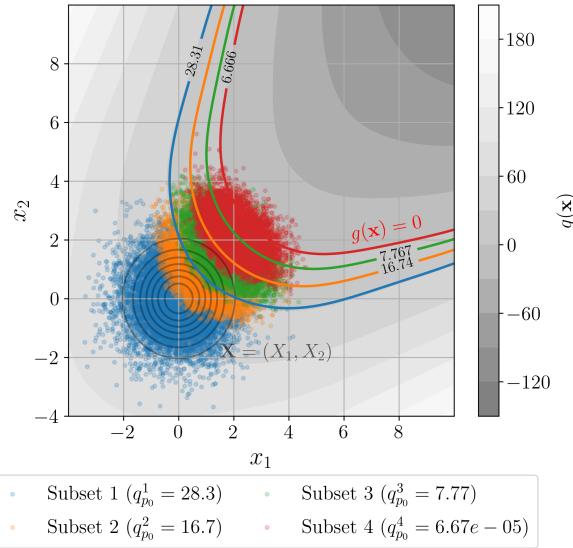


Figure 1.11 Illustration of a rare event estimation by subset sampling ($n = 4 \cdot 10^4, p_0 = 0.1$).

2004), *moving particles* (Walter, 2015). Morio and Balesdent (2015) compares the advantages and drawbacks of the most commonly used one, with corresponding algorithmic descriptions and numerical benchmarks.

Overall, the main properties increasing the complexity of reliability problems are related to:

- the computational cost of the limit-state function evaluation;
- the strong nonlinearity of the limit-state function;
- the rareness of the failure event.

In regard to the methods, the estimation is made easier by algorithms with simple tuning or allowing to work in the physical space (avoiding a possibly complex iso-probabilistic transform). Considering all these elements the analyst may set up a sampling strategy, possibly coupled with the use of a surrogate model (further discussed in Section 1.7).

Nevertheless, the unified formulation of reliability analysis problems (see 1.31) is an opportunity for the community to share standardized benchmark problems. Following the well-accepted benchmark platform for optimization “Comparing Continuous Optimizers” (COCO) (Hansen et al., 2021), an equivalent initiative was proposed for structural reliability. In 2019, the “black-box reliability challenge”, was organized as a hackathon by the Dutch organization for applied scientific research (TNO) (Rozsas and Slobbe, 2019). This platform proposed a large catalog of reliability problems with their respective solutions. Most of them were encapsulated as a Python package called `otbenchmark`¹⁰ (Fekhari et al., 2021), based on core OpenTURNS objects.

When working with computationally expensive numerical models, the direct use of rare event estimation methods is most often intractable. Many contributions were dedicated to the coupling of surrogate models with sampling methods for rare event estimation. Moustapha et al.

¹⁰<https://github.com/mbaudin47/otbenchmark/>

(2022) presented the results of a wide benchmark on the challenge from TNO, obtained by using surrogate models for reliability developed in the UQLab software (Marelli and Sudret, 2014).

In any case, risk assessment analysts should favor the methods offering convergence guarantees over punctual performance demonstrations. Finally, the robustness of the failure probability to the input uncertainty model is a major question, which was studied from probabilistic (Lemaître et al., 2015) and extra-probabilistic (Ajenjo et al., 2022) frameworks.

OpenTURNS 4 (Rare event estimation). The Python code available in Appendix ?? proposes a minimalistic OpenTURNS example to estimate rare event probabilities. Figures illustrating the present section may be reproduced, using the OpenTURNS scripts available on GitHub¹¹.

1.6 Global sensitivity analysis

The aim of sensitivity analysis (SA) is to determine the impact of a single (or a group of random inputs) on a random output(s). As described earlier, this step is qualified as an inverse analysis in the general UQ framework (illustrated in Fig. 1), in opposition with the forward uncertainty propagation step. In fact, the analyst studies the effect of the inputs at different scales, hence the distinction between “local” and “global” SA. Local SA focuses on the impact of small perturbations around nominal values of the inputs (i.e., derivative-based approaches), while global sensitivity analysis (GSA), typically studies the general variability (e.g., the variance) of the output. Two types of GSA methods exist in the literature, either proposing qualitative and quantitative approaches:

- *screening methods*: determines the non-influential variables in a UQ study (qualitative);
- *importance measures*: assess the contribution of inputs in the global variability of the output (quantitative).

Screening methods are typically used in a statistical learning process, to drop the irrelevant variables to the learning. In this context, *feature selection* serves the same purpose with a slight difference. Screening methods usually assume the inputs to be independent while feature selection does not. Moreover, feature selection not only looks for the irrelevant features to the learning but also the redundant features (Fan and Lv, 2010).

The global sensitivity of an output can be explained by different elements: the single variability of the inputs, their dependence, and their interactions. Two variables present interactions when their simultaneous effect on an output is not additive. Note that SA on dependent inputs is an active field of research and the inputs will mostly be considered as independent in the following.

¹¹https://github.com/efekhari27/thesis/blob/main/numerical_experiments/chapter1/reliability.ipynb

1.6.1 Screening methods

Many UQ methods suffer from the curse of dimensionality, thankfully, high-dimensional problems often only depend on a few variables. This observation was formalized with the concept of *effective dimension* introduced by [Owen \(2003\)](#). Screening methods allow to discriminate the non-influential variables, which can be considered afterwards as determinist to simplify the problem.

Morris method

The Morris method ([Morris, 1991](#)) is a screening method historically used in engineering applications. It starts by mapping the input domain \mathcal{D}_X into a unit hypercube $[0, 1]^d$, which is discretized as a regular grid with step $\Delta \in \mathbb{R}$. The algorithm computes local elementary sensitivity by building “one at a time” (OAT) local trajectories over the regular grid. Each OAT design starts at a random node $\mathbf{x}^{(t)} = (x_1^{(t)}, \dots, x_j^{(t)}, \dots, x_d^{(t)})$ of the grid, and moves only in one direction by an increment equal to the elementary step such that: $\mathbf{x}^{(t)} + \Delta_j = (x_1^{(t)}, \dots, x_j^{(t)} + \Delta, \dots, x_d^{(t)})$. The elementary effect in the direction of the variable i from a OAT trajectory t is expressed as a finite difference:

$$\text{EE}_j^{(t)} = \frac{g(\mathbf{x}^{(t)}) - g(\mathbf{x}^{(t)} + \Delta_j)}{\Delta}. \quad (1.64)$$

The Morris method generates $T \in \mathbb{N}$ OAT trajectories and computes theirs respective elementary effects in each direction i . To assess the global sensitivity of the function, the mean $\overline{\text{EE}}_j$ and variance $\widehat{\text{Var}}(\text{EE}_j)$ of the elementary effects are computed:

$$\overline{\text{EE}}_j = \frac{1}{n} \sum_{t=1}^T |\text{EE}_j^{(t)}|, \quad \widehat{\text{Var}}(\text{EE}_j) = \frac{1}{n-1} \sum_{t=1}^T \left(\text{EE}_j^{(t)} - \overline{\text{EE}}_j \right)^2. \quad (1.65)$$

It allows to divide the variables into three categories, regardless of any regularity hypothesis on the function: (i) negligible effects; (ii) linear effects without interaction; and (iii) nonlinear effects with possible interactions. This method is very intuitive but quickly shows its limits as the dimension increases since it relies on a discretization of the space by a regular grid. Another disadvantage of this method is that it does not distinguish interactions and nonlinear effects of inputs.

Derivative-based global sensitivity measures

The Derivative-based global sensitivity measures (DGSM) are a GSA method introduced in [Sobol and Gresham \(1995\)](#) and further studied in [Kucherenko et al. \(2009\)](#). As the Morris method, they study the mean value of local derivatives of the model output with regard to the inputs:

$$v_j = \int_{\mathcal{D}_X} \left(\frac{\partial g(\mathbf{x})}{\partial x_j} \right)^2 f_X(\mathbf{x}) d\mathbf{x} = \mathbb{E} \left[\left(\frac{\partial g(\mathbf{X})}{\partial X_j} \right)^2 \right]. \quad (1.66)$$

This continuous formulation does not require using OAT designs, which was proven to be more efficient when exploiting sampling methods such as quasi-Monte Carlo. The efficiency of the DGSMs for screening purposes was outlined in many papers (e.g., [Kucherenko and Iooss \(2017\)](#)). Since their value depends on the probability distribution of the input, a normalized version was developed. The connections between DGSM and variance-based GSA measures (i.e., Sobol' indices introduced hereafter), revealed bounding properties between DGSMs and Sobol' total indices ([Lamboni et al., 2013](#)).

1.6.2 Variance-based importance measures

Screening methods determine the non-influential variables in a UQ problem. Beyond this information, importance measures quantify the influence of inputs, allowing to rank the inputs according to their contribution to the output variability.

Functional variance decomposition and Sobol' indices

Sobol' indices are the most popular importance measure in GSA. Their universality comes from the functional decomposition of the output's variance, attributing variance share to the inputs. Considering a squared-integrable and measurable function $g(\cdot)$ and an independent random vector \mathbf{X} . The output random variable $Y = g(\mathbf{X})$ can be decomposed, according to [Hoeffding \(1948\)](#), as:

$$Y = g(\mathbf{X}) = g_0 + \sum_{j=1}^d g_j(X_j) + \sum_{j < l}^d g_{jl}(X_j, X_l) + \dots + g_{1\dots d}(\mathbf{X}), \quad (1.67)$$

with the previous terms defined according this recurrence:

$$g_0 = \mathbb{E}[g(\mathbf{X})] \quad (1.68a)$$

$$g_j(X_j) = \mathbb{E}[g(\mathbf{X})|X_j] - g_0 \quad (1.68b)$$

$$g_{jl}(X_j, X_l) = \mathbb{E}[g(\mathbf{X})|X_j, X_l] - g_j(X_j) - g_l(X_l) - g_0 \quad (1.68c)$$

$$\dots \quad (1.68d)$$

Sobol in [Sobol' \(1993\)](#) proved that this decomposition is unique by exploiting the orthogonality of the terms of the decomposition. Therefore, this decomposition can be transposed in terms of functional decomposition of variance (also called functional analysis of variance or FANOVA):

$$\text{Var}(Y) = \sum_{j=1}^d V_j(Y) + \sum_{j < l}^d V_{jl}(Y) + \dots + V_{1\dots d}(Y), \quad (1.69)$$

where the previous terms are defined in a recurrent way, in the same fashion as Eq. (1.68): $V_j(Y) = \text{Var}(\mathbb{E}[Y|X_j])$, $V_{jl}(Y) = \text{Var}(\mathbb{E}[Y|X_j, X_l]) - V_j(Y) - V_l(Y)$, and so on for higher order interaction

terms. The Sobol' indices of different order are defined as normalized shares of variance. The *first-order Sobol' index* S_j quantifies the share of variance of the output only explained by the marginal X_j (also called main effect). Second order S_{jl} (or higher order) Sobol' indices quantify the effect of the interactions between a group of marginals.

$$S_j = \frac{V_j(Y)}{\text{Var}(Y)} = \frac{\text{Var}(\mathbb{E}[Y|X_j])}{\text{Var}(Y)} \quad (1.70a)$$

$$S_{jl} = \frac{V_{jl}(Y)}{\text{Var}(Y)} = \frac{\text{Var}(\mathbb{E}[Y|X_j, X_l]) - V_j(Y) - V_l(Y)}{\text{Var}(Y)} \quad (1.70b)$$

$$\dots \quad (1.70c)$$

The generic definition of the Sobol' sensitivity indices associated to a subset of inputs $A \in \mathcal{P}_d$, with \mathcal{P}_d the set of all possible subsets of $\{1, \dots, d\}$, is given by:

$$S_A = \frac{V_A(Y)}{\text{Var}(Y)} = \frac{\sum_{B \subset A} (-1)^{|A|-|B|} \text{Var}(\mathbb{E}[Y|X_B])}{\text{Var}(Y)}. \quad (1.71)$$

By using the functional decomposition of variance in Eq. (1.69), one can show that the Sobol' indices add up to one:

$$\sum_{A \in \mathcal{P}_d} S_A = 1. \quad (1.72)$$

The so-called *closed Sobol' index* associated to a subset of inputs $A \in \mathcal{P}_d$ (equivalent to the first-order Sobol' index of A) is defined as:

$$S_A^{\text{clos}} = \sum_{A' \subset A} S_{A'} = \frac{\text{Var}(\mathbb{E}[Y|X_A])}{\text{Var}(Y)}. \quad (1.73)$$

Assessing Sobol' indices for every order becomes complex in medium to high dimension. The *total Sobol' index* S_j^T associated with the variable j , see Saltelli et al. (2008), quantifies the share of output variance which is explained by all the interactions of the variable X_j :

$$S_j^T = 1 - \frac{\text{Var}(\mathbb{E}[Y|X_{-j}])}{\text{Var}(Y)} = \frac{\mathbb{E}[\text{Var}(Y|X_{-j})]}{\text{Var}(Y)}, \quad (1.74)$$

where X_{-j} represents all the marginals from X but X_j . This definition can also be generalized for a subset of inputs $A \in \mathcal{P}_d$, such that:

$$S_A^T = 1 - S_{A^C}^{\text{clos}} = 1 - \frac{\text{Var}(\mathbb{E}[Y|X_{A^C}])}{\text{Var}(Y)}, \quad A^C = \mathcal{P}_d \setminus A \quad (1.75)$$

By analyzing jointly the first and total Sobol' indices, one can get an indication on the decomposition between the marginal and interaction effects. Note that the total indexes are only equal to the first indexes when the model does not present interactions (i.e., purely additive model).

Estimating Sobol' indices can be achieved in various ways, even if historically the *pick-freeze* scheme was the most popular. This method is based on two samples, but it often requires a prohibitive number of evaluations of the function. Many estimators using the pick-freeze generic scheme were developed to estimate Sobol' indices (e.g., Saltelli's, Jansen's, Martinez's etc.), see further details in the Chapter 3 of Da Veiga et al. (2021). Alternatively, the surrogate models were exploited to estimate such sensitivity measure. Using an input-output dataset, the analyst may build a *polynomial chaos expansion* (PCE) surrogate model, which gives an explicit expression of the Sobol' indices (Sudret, 2008). Authors such as Marrel et al. (2009) also studied the use of Gaussian processes for this purpose.

In the case of independent inputs, the first and total Sobol' indices is a complete tool for GSA. The main advantage of this approach is the quantitative nature of its results, allowing to objectively compare the effect of input variables. When the inputs present a dependence structure, it becomes complicated to distinguish its effects from possible interactions. However, many authors tried to adapt the Sobol's indices to this context. Chapter 5 of Da Veiga et al. (2021) reviews four of these approaches. For example, Mara and Tarantola (2012) proposed two extra Sobol' indices, called "full indices", detecting the contributions associated with the inputs' dependence. Note that the interpretation and estimation of this solution becomes complicated. Moreover, unlike the independent case, the four Sobol' indices do not divide the output variance between the inputs. Beyond Sobol' indices, another important GSA method was adapted from the theory of Shapley values by Owen (2014), allowing to work with dependent inputs.

OpenTURNS 5 (Sobol' indices). The Python code available in Appendix ?? gives a minimalist OpenTURNS implementation of the Sobol' indices to assess global sensitivity analysis on the Ishigami analytical problem. Further scripts are also available on GitHub¹².

Shapley effects

Shapley effects are an adaptation to GSA by Owen (2014) of the Shapley values from the cooperative games' theory (Shapley et al., 1953). This method is an alternative to the Sobol' indices in the case of dependent inputs, for which the natural interpretation of single interaction effects no longer holds. In the game theory, Shapley values act as a rule on how to share the value created by a team between its members (players). The Shapley value allocated to the player X_j is given considering the indices $\{1, \dots, d\} \setminus \{j\}$:

$$\varsigma_j = \sum_{A \subset \{1, \dots, d\} \setminus \{j\}} \binom{d-1}{\text{card}(A)}^{-1} (\text{val}(A \cup \{j\}) - \text{val}(A)), \quad (1.76)$$

where the value (or cost) function is denoted by $\text{val}(A)$, and A is a subset of $\{1, \dots, d\}$ with cardinality $\text{card}(A)$. The Shapley effects adapted this concept to perform a GSA by considering

¹²https://github.com/efekhari27/thesis/blob/main/numerical_experiments/chapter1/sensitivity_analysis.ipynb

the variables as players and the closed Sobol' indices for the value function:

$$Sh_j = \sum_{A \subset -\{j\}} \binom{d-1}{|A|}^{-1} \left(S_{A \cup \{j\}}^{\text{clos}} - S_A^{\text{clos}} \right). \quad (1.77)$$

Conceptually, this expression compares a performance defined by a cost function with or without the variable X_j , and averages it over all the possible combinations of inputs. This importance measure offers the following decomposition:

$$\sum_{j=1}^d Sh_j = 1. \quad (1.78)$$

In the case of independent inputs, the Shapley effects present properties related to the Sobol' indices. The following equation (see proof in [Owen \(2014\)](#)) reveal that the Shapley effects equally divide the interaction effects between the implicated variable:

$$S_j \leq Sh_j \leq S_j^T, \quad Sh_j = \sum_{A \in \mathcal{P}_d, j \in A} \frac{S_A}{\text{card}(A)}. \quad (1.79)$$

Unlike the Sobol' indices, Shapley effects are a nonnegative allocation of output variance with equitable division of the interaction effects. This method presents an interesting alternative in the dependent case, however, estimating Shapley effects creates computational difficulties. The reader may refer to the permutation-based algorithm from [Song et al. \(2016\)](#). Surrogate models were also coupled to estimate Shapley effects, using Gaussian processes in [Benoumechiara and Elie-Dit-Cosaque \(2019\)](#) and random forests in [Bénard et al. \(2022\)](#).

Shapley effects are a promising importance measure based on variance allocation. However, in some cases the variance of the output distribution does not represent well its variability (e.g., multimodal distribution). The following section introduces another family of GSA methods based on distances between distributions.

1.6.3 Moment-independent importance measures

Beyond variance-based GSA, many types of distances between distributions have been used to evaluate the dependence between the input and output distributions. Comparing the entire distributions instead of their moments might be more robust in some cases (e.g., when the variance is a poor indicator of the variability). The tools used to do so are generally called *dissimilarity measures* between distributions. Appendix ?? briefly introduces two families of dissimilarity measures: the class of f -Csiszár divergences (e.g., the Kullback-Leibler divergence, total variation distance) and the class of integral probability metrics (IPM) (e.g., Wasserstein distance, total variation distance, maximum mean discrepancy).

Considering the probability measures \mathbb{P}_{X_j} and \mathbb{P}_Y (associated with the random variables X_j and Y) and a dissimilarity measure $\Delta(\cdot, cdot)$, one can define two formulations for GSA:

- directly using a dissimilarity measure to assess $\Delta(\mathbb{P}_Y, \mathbb{P}_{Y|X_j})$;
- building a *dependence measures* evaluating $\Delta(\mathbb{P}_{(X_j, Y)}, \mathbb{P}_{X_j} \otimes \mathbb{P}_Y)$.

The first approach was studied in association with f -divergences in Da Veiga (2015); Rahman (2016). However, some f -divergences introduce estimation issues, and the resulting importance measures do not propose a functional decomposition of variance (also called FANOVA). Using kernel-based IPMs such as the maximum mean discrepancy (MMD), an alternative importance measure was proposed. The following section presents the *Hilbert-Schmidt Independence Criterion* (HSIC), which was initially introduced by Gretton et al. (2006) for dependence testing, and later adapted as a dependence measure in GSA by Da Veiga (2015).

Hilbert-Schmidt independence criterion

Let us first recall the definition of the maximum mean discrepancy (further discussed in Appendix ??). This distance between two probability distributions π and ζ can be defined as the worst-case error for any function within a unit ball of a function space \mathcal{H} :

$$\text{MMD}(\pi, \zeta) := \sup_{\|g\|_{\mathcal{H}(k)} \leq 1} \left| \int_{\mathcal{D}_X} g(\mathbf{x}) d\pi(\mathbf{x}) - \int_{\mathcal{D}_X} g(\mathbf{x}) d\zeta(\mathbf{x}) \right| \quad (1.80)$$

This quantity is a distance in the RKHS by taking a characteristic kernel (e.g., the Gaussian or Matérn kernel). After a calculation developed in Appendix ??, an unbiased one-sample estimator of the squared-MMD was proposed by Gretton et al. (2006), with a convergence rate of $O(n^{-1/2})$ in probability. Considering the two-samples $\{\pi^{(i)}\}_{i=1}^n \sim \pi$ and $\{\zeta^{(j)}\}_{j=1}^n \sim \zeta$:

$$\widehat{\text{MMD}}^2(\pi, \zeta) = \frac{1}{n(n-1)} \sum_{i=1}^n \sum_{j \neq i}^n k(\pi^{(i)}, \pi^{(j)}) - k(\pi^{(i)}, \zeta^{(j)}) - k(\zeta^{(i)}, \pi^{(j)}) + k(\zeta^{(i)}, \zeta^{(j)}), \quad (1.81)$$

In the context of GSA, a first option is to directly use this dissimilarity measure to define the unnormalized index:

$$S_j^{\text{MMD}} = \text{MMD}(\mathbb{P}_Y, \mathbb{P}_{Y|X_j}). \quad (1.82)$$

da Veiga (2021) remarked that the unnormalized first order Sobol' indices are recovered by taking the linear kernel on the output $k_Y(y, y') = yy'$. Using this non-characteristic kernel (see the definition in Appendix ??) brings us back to a moment-dependent importance measure.

Alternatively, the second option considers a couple of random variables (X_j, Y) , with probability distributions \mathbb{P}_{X_j} and \mathbb{P}_Y , and assumes the RKHS \mathcal{H} induced by the tensor product kernel $k((x_j, y), (x'_j, y')) = k_{X_j}(x_j, x'_j)k_Y(y_j, y'_j)$. The *Hilbert-Schmidt independence criterion* (HSIC) measures the dependence between \mathbb{P}_{X_j} and \mathbb{P}_Y by expressing the MMD between $\mathbb{P}_{(X_j, Y)}$ and $\mathbb{P}_{X_j} \otimes \mathbb{P}_Y$:

$$\text{HSIC}(X_j, Y) = \text{MMD}^2(\mathbb{P}_{(X_j, Y)}, \mathbb{P}_{X_j} \otimes \mathbb{P}_Y). \quad (1.83)$$

This technique showed very good results for screening, and corresponding independence tests were studied for screening in [De Lozzo and Marrel \(2016\)](#).

[da Veiga \(2021\)](#) proposed the functional decomposition of the two indices defined in Eq. (1.82) and Eq. (1.83), allowing to develop their respective normalized versions. Note that the HSIC decomposition requires a specific hypothesis on the structure of the kernel associated to the inputs.

1.6.4 Summary and discussion

This section introduced the GSA methods commonly used in uncertainty quantification. Either to reduce the dimension of a problem (screening) or to quantify the influence of inputs (with importance measures), GSA improves the understanding of an uncertainty quantification study. As for other steps of the generic UQ methodology, SA is made more complicated for computationally costly simulation models, hence the use of surrogates models. Additionally, the dependence between inputs still represents an important limit to interpret GSA results.

Alongside rare event estimation, a literature is dedicated to the influence of the random inputs on such tail statistics. The sensitivity is no more qualified as “global” but becomes “goal-oriented”. In the field of structural reliability, an overview of the reliability-oriented sensitivity analysis methods is presented in [Chabridon \(2018\)](#). Several techniques derive from rare event estimation (e.g., the FORM importance factors [Papaioannou and Straub \(2021\)](#)), or were adapted from GSA, like Sobol’ indices ([Ehre et al., 2020](#)), Target-HSIC ([Marrel and Chabridon, 2021](#)), or Shapley effects ([Demange-Chryst et al., 2023](#)).

Finally, sensitivity analysis may describe the effects of random inputs on the variation of the output, however, this study is done considering by assuming a model on the input uncertainties. The role of a regulatory agency auditing an uncertainty quantification approach for certification (i.e., a nuclear safety authority), might be to challenge the way to model the uncertainties on the inputs. In this case, various tools for *robustness analysis* exist to quantify the impact of misspecifying the random inputs on the quantity of interest studied. Among the methods to perturbate uncertainty models, some remain in the probabilistic framework, such as the “perturbed-law based indices” (PLI) ([Lemaître et al., 2015](#)), or on extra-probabilistic methods ([Ajenjo et al., 2022](#)).

1.7 Surrogate modeling

1.7.1 Common framework

The aim of *surrogate modeling* (or metamodeling) is to build a cheap-to-call statistical model, denoted by $\widehat{g}_n(\cdot)$, replacing a costly numerical model $g(\cdot)$ over the input domain \mathcal{D}_X . To do so, a statistical learning is performed on a finite number of observations of the costly function g . When manipulating computationally expensive simulations, its size can be limited (i.e.,

small-data context). This n -sized set is usually called *learning set* written:

$$\{\mathbf{X}_n, \mathbf{y}_n\} = \left\{ \mathbf{x}^{(i)}, y^{(i)} \right\}_{i=1}^n = \left\{ \mathbf{x}^{(i)}, g(\mathbf{x}^{(i)}) \right\}_{i=1}^n. \quad (1.84)$$

A very large catalog of regression methods exist, here is a list of the most encountered ones in the field of UQ: generalized linear regression, polynomial chaos expansion (PCE) (Soize and Ghanem, 2004; Blatman and Sudret, 2011), support vector machine (SVM) (Cortes and Vapnik, 1995), Gaussian processes (GP) (Rasmussen and Williams, 2006), low-rank tensor approximations (Grasedyck et al., 2013), and artificial neural network (ANN) (Hastie et al., 2009). The following section will provide a short focus on Gaussian process regression.

Validating the accuracy and precision of a surrogate model is an important step to guaranty its fidelity with regard to the numerical model. When an m -sized input-output set is dedicated to validating the surrogate model, independently of the learning set, it is called *test set* and denoted by $\{\mathbf{X}_m, \mathbf{y}_m\} = \left\{ \mathbf{x}^{(i)}, g(\mathbf{x}^{(i)}) \right\}_{i=1}^m$. Note that the analyst may work in two different frameworks, affecting the regression and validation method's choice:

- Given-data context: only using a fixed input-output dataset to build and validate the surrogate model.
- Computer experiment context: allowing to generate simulated data points (often at a certain cost).

Validating surrogate models in small-data context appears to be an important challenge. Different validation criteria and techniques exist. The *coefficient of validation*, denoted by R^2 , is a first validation metric that can be directly computed on the learning set:

$$R^2(\hat{g}_n) = 1 - \frac{\sum_{i=1}^n (y(\mathbf{x}^{(i)}) - \hat{g}(\mathbf{x}^{(i)}))^2}{\sum_{i=1}^n (y(\mathbf{x}^{(i)}) - \bar{y}_n)^2}, \quad (1.85)$$

where $\bar{y}_n = (1/n) \sum_{i=1}^n y^{(i)}$ denotes the empirical mean of the observations in the test sample. However, such metrics are not relevant for every regression method (typically, interpolant method have an $R^2 = 1$). The *predictivity coefficient* is an alternative defined as a normalized *integrated square error* (ISE):

$$Q^2(\hat{g}_n) = 1 - \frac{\text{ISE}(\hat{g}_n)}{\text{Var}(g(\mathbf{X}))}, \quad (1.86)$$

where

$$\text{ISE}(\hat{g}_n) = \int_{\mathcal{D}_X} (g(\mathbf{x}) - \hat{g}(\mathbf{x}))^2 d\mathbf{x}, \quad \text{Var}(g(\mathbf{X})) = \int_{\mathcal{D}_X} \left(g(\mathbf{x}) - \int_{\mathcal{D}_X} g(\mathbf{x}) d\mathbf{x}' \right)^2 d\mathbf{x}. \quad (1.87)$$

This quantity can be estimated on a test set $\{\mathbf{X}_m, \mathbf{y}_m\}$:

$$\widehat{Q}^2(\hat{g}_n) = 1 - \frac{\sum_{i=1}^m (y(\mathbf{x}^{(i)}) - \hat{g}(\mathbf{x}^{(i)}))^2}{\sum_{i=1}^m (y(\mathbf{x}^{(i)}) - \bar{y}_m)^2}. \quad (1.88)$$

Note that for either criteria, the higher the value, the better the quality of the fit.

Validating a surrogate model with an independent test-set is sometimes called *holdout* validation. In a small-data context, dedicating an independent test set to validation might be impossible. Then, *cross-validation* is a generic estimation strategy allowing to use only one sample for learning and testing. The most common cross-validation method is the *k-fold* validation, illustrated in Fig. 1.12. The idea is first to split the n -sized dataset in several equal parts, called folds. A first surrogate can be fitted on all the dataset but the first fold, on which a validation criterion is estimated (i.e., performance metric). The operation is repeated for each fold, providing a virtual validation on the entire dataset. Leave-One-Out validation (LOO) is an extreme case of *k*-fold cross-validation, for which $k = n - 1$. Note that multiple variations of these methods exist, for example by adding a permutation or shuffling step. The “bagging” validation method (for “bootstrap aggregating”) consists of a shuffled cross-validation repeated many times (Breiman, 1996).

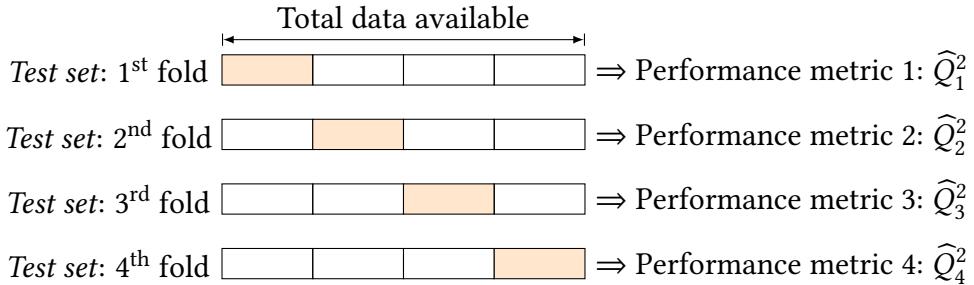


Figure 1.12 Illustration of a k -fold cross-validation (with $k = 4$)

1.7.2 General purposes surrogate model

In this section, a particular focus is dedicated to Gaussian process (GP) regression (also called kriging after the geostatistician D.G. Krige). Gaussian processes are a widely used regression method in UQ for their performance, flexibility and their associated confidence model. In a small-data context, the way of placing the few points forming the surrogate’s learning set is critical. Intuitively, to build a versatile surrogate model, the learning set should collect information over the entire domain uniformly. Which is why space-filling designs of experiments are commonly used to build learning sets. In practice, QMC and optimized LHS design introduced in Section 1.4 are widely used.

Gaussian process regression

Considering a learning set \mathbf{X}_n , the goal is to approximate the function $g(\cdot)$ by a scalar Gaussian process conditioned on a set of observations $\mathbf{y}_n = \left\{ g\left(\mathbf{x}^{(i)}\right) \right\}_{i=1}^n$. Let us first define a prior structure G on the function approximated $g(\cdot)$, taken as a Gaussian process with a mean function $m(\cdot)$ and covariance function $k(\cdot, \cdot)$:

$$G \sim \text{GP}(m(\cdot), k(\cdot, \cdot)), \quad (1.89)$$

with a:

- *trend model*: $m(\mathbf{x}) = \mathbf{f}(\mathbf{x})^\top \boldsymbol{\beta}$, composed of a functional basis $\mathbf{f} = (f_1, \dots, f_d)^\top$ and a vector of coefficients $\boldsymbol{\beta} = (\beta_1, \dots, \beta_d)^\top$,
- *covariance model*: $k(\mathbf{x}, \mathbf{x}')$, usually taken stationary, such that $k(\mathbf{x}, \mathbf{x}') = \sigma^2 k_s(\mathbf{x} - \mathbf{x}', \boldsymbol{\theta})$ with $\sigma^2 > 0$ and $\boldsymbol{\theta} \in \mathcal{D}_X$.

The trend model of a GP defines its general tendency, while the covariance model influences its regularity. Gaussian process regression takes different names depending on the knowledge of the trend model. It is called “simple kriging” when the trend is fully known, “ordinary kriging”, when the trend is unknown but supposed constant and “universal kriging” otherwise. Note that [Schobi et al. \(2015\)](#) introduced a hybrid method named PC-Kriging setting a PCE as the trend of a kriging model.

To ease the presentation, let us first consider the hyperparameters $\sigma, \boldsymbol{\theta}$ fully known and a zero trend $\boldsymbol{\beta} = \mathbf{0}$. At a given point $\mathbf{x} \in \mathcal{D}_b X$ the realization of the GP is a Gaussian random variable $G(\mathbf{x}) \sim \mathcal{N}(m(\mathbf{x}), k(\mathbf{x}, \mathbf{x}))$. Working with Gaussian variables allows to easily write conditioning formulas between $G(\mathbf{x})$ and the observations \mathbf{y}_n . This Gaussian variable $G(\mathbf{x})$ conditioned on the observations \mathbf{y}_n is sometimes called conditional posterior $G_n(\mathbf{x}) := (G(\mathbf{x}) | \mathbf{y}_n) \sim \mathcal{N}(\eta_n(\mathbf{x}), s_n^2(\mathbf{x}))$. The well-known “Kriging equations” (see e.g., [Rasmussen and Williams 2006](#)) offer its explicit expression:

$$\begin{cases} \eta_n(\mathbf{x}) &:= \mathbf{k}^\top(\mathbf{x}) \mathbf{K}^{-1} \mathbf{y}_n \\ s_n^2(\mathbf{x}) &:= k(\mathbf{x}, \mathbf{x}) - \mathbf{k}^\top(\mathbf{x}) \mathbf{K}^{-1} \mathbf{k}(\mathbf{x}) \end{cases} \quad (1.90)$$

where $\mathbf{k}(\mathbf{x})$ is the column vector of the covariance kernel evaluations $[k(\mathbf{x}, \mathbf{x}^{(1)}), \dots, k(\mathbf{x}, \mathbf{x}^{(n)})]$ and \mathbf{K} is the $(n \times n)$ variance-covariance matrix such that the (i, j) -element is $\{\mathbf{K}\}_{i,j} = k(\mathbf{x}^{(i)}, \mathbf{x}^{(j)})$.

In practice the surrogate model is defined by the *predictor* function $\eta_n(\cdot)$. This regression model provides an important complementary information with the *kriging variance* $s_n^2(\mathbf{x})$, reaching zero at the learning points. Let us remark that the kriging variance fully depends on the covariance model (defined by its parametric structure and hyperparameters). In practice, the hyperparameters are unknown, therefore, their estimation is a key step in the construction of a kriging model. This estimation can be done using different approaches, most commonly using maximum likelihood estimation or a cross-validation.

The illustration in Fig. 1.13 is a typical one-dimensional representation of an ordinary kriging model. The mean of the conditioned process is plotted in red while its variability is represented by the many trajectories drawn on the process. In the simplest framework, the kriging model exactly interpolate the observations (black crosses).

Associated with kriging models, another validation criterion is relevant to evaluate the kriging variance $s_n^2(\mathbf{x})$. The predictive variance adequation (PVA) has been introduced by [Bachoc \(2013\)](#) to confirm that the kriging variance is reliable. For a validation performed by holdout,

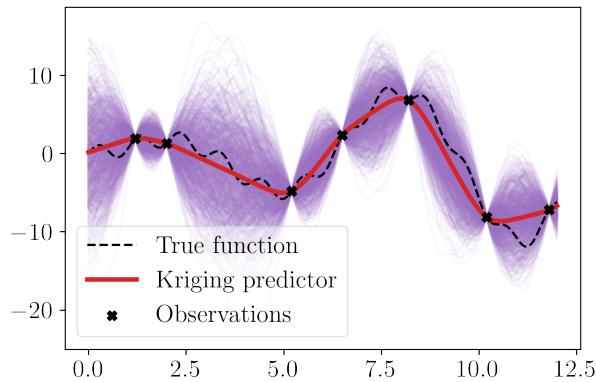


Figure 1.13 Illustration of an ordinary kriging model fitted on a limited set of observations ($n = 7$). The predictor is represented in and several trajectories of the conditioned Gaussian process are drawn represented in purple.

and using an independent m -sized test set, the PVA is defined as:

$$\text{PVA} = \left| \log \left(\frac{1}{m} \sum_{i=1}^m \frac{(y(\mathbf{x}^{(i)}) - \hat{g}(\mathbf{x}^{(i)}))^2}{s_n^2(\mathbf{x}^{(i)})} \right) \right|. \quad (1.91)$$

The smaller this quantity get, the better the quality of the kriging variance.

Gaussian process regression is an elegant solution, offering a lot of flexibility and an associated error model (i.e., the kriging variance). However, well known numerical issues appear during the estimation of the hyperparameters, especially as the learning size increases. More specifically, the computation and memory allocation for the variance-covariance matrix is a recurrent issue. Multiple techniques solve this issue by applying compression schemes on this matrix, e.g., based on sparse approximations (e.g., Hierarchical Matrices Geoga et al. 2020).

This section introduced a general purpose surrogate model, uniformly approximating a function on a domain, however surrogates are often used for specific purposes (e.g., contour finding for reliability analysis).

OpenTURNS 6 (Gaussian process regression). The Python code available in Appendix ?? proposes a minimalistic OpenTURNS example to fit an ordinary kriging model and active learning models. Figures illustrating the present section may be reproduced, using the OpenTURNS scripts available on GitHub^{13,14}.

1.7.3 Goal-oriented active surrogate model

Surrogates are often fitted for a specific purpose, requiring an accurate approximation over a limited subdomain only. In these cases, a more efficient approach might be to circumscribe

¹³https://github.com/efekhari27/thesis/blob/main/numerical_experiments/chapter1/surrogates.ipynb

¹⁴https://github.com/efekhari27/thesis/blob/main/numerical_experiments/chapter1/active_learning.ipynb

the learning to this subdomain (i.e., *goal-oriented learning*), rather than uniformly over the entire domain. For example, to fit a surrogate model for contour finding in reliability analysis, one should concentrate the learning set around the limit-state function. Similarly, to build a surrogate for a global optimization problem, one should focus the learning set around the optimum(s). Unfortunately, the area(s) of interest is usually unknown before evaluating the true function. *Active learning* is a general concept, aiming at iteratively increasing the learning set w.r.t. a *learning criterion* (also called “acquisition function”) depending on the surrogate’s goal to enhance the surrogate in the area(s) of interest. An exploration–exploitation trade-off arises in active learning, mostly sorted by the learning criterion.

Remark 1. This section introduces active learning methods in the computer experiment context, where the true function can be evaluated anywhere for a given computational cost. However, the “active learning” term is also used to handle big data frameworks in the machine learning community (Qiu et al., 2016). When datasets become so large that learning methods do not scale in practice, the analyst needs to select a relevant subset on which the learning is performed.

Active kriging for optimization

In the field of black-box optimization, many methods rely on approximating the function by a surrogate. The use of Gaussian processes as probabilistic surrogates for optimization was popularized by the *efficient global optimization* (EGO) algorithm (Jones et al., 1998). Ever since, many related methods were developed under the generic name of *Bayesian optimization*. The main idea is to exploit the uncertainty model from the GP to direct the point selection. Factually, the learning criterion depends on the Gaussian process variance model. Numerous reviews of this field were proposed by Shahriari et al. (2015); Gramacy (2020) and numerical benchmarks presented in Le Riche and Picheny (2021).

The generic black-box optimization problem tackled is defined as:

$$\mathbf{x}^* = \arg \min_{\mathbf{x} \in \mathcal{D}_X} g(\mathbf{x}) \approx \arg \min_{\mathbf{x} \in \mathcal{D}_X} \hat{g}(\mathbf{x}). \quad (1.92)$$

To illustrate Bayesian optimization, let us present the EGO algorithm, defined by its specific learning criterion: the “expected improvement”. Considering an initial learning set $\{\mathbf{X}_n, \mathbf{y}_n\}$ built on a space-filling input design \mathbf{X}_n to explore the domain. A first surrogate $G_n(\mathbf{x}) \sim \mathcal{N}(\eta_n(\mathbf{x}), s_n^2(\mathbf{x}))$ is fitted using Eq. (1.90). The expected improvement, to be maximized, is then written as:

$$\mathcal{A}^{EI}(\mathbf{x}; \mathbf{y}_n) = \mathbb{E}[\max(g_{\min} - G_n(\mathbf{x}))] \quad (1.93)$$

$$= (g_{\min} - \eta_n(\mathbf{x})) \Phi\left(\frac{g_{\min} - \eta_n(\mathbf{x})}{s_n(\mathbf{x})}\right) + s_n(\mathbf{x}) \phi\left(\frac{g_{\min} - \eta_n(\mathbf{x})}{s_n(\mathbf{x})}\right), \quad (1.94)$$

where $g_{\min} = \min(\mathbf{y}_n)$, ϕ and Φ respectively stand for the PDF and the CDF of the standard Gaussian distribution. This learning criterion is relatively inexpensive and allows to progressively enhance the Gaussian process to solve the optimization problem with a limited number of calls to the true function.

Three iterations of the EGO algorithm are represented in Fig. 1.14 to minimize a function (dashed line), knowing a few observations (black crosses). After fitting an initial kriging model (in red), the corresponding expected improvement function is represented underneath it (green line). This learning criterion determines the location of the observation to be added to the learning set to enhance the surrogate w.r.t. to the optimization problem.

Bayesian optimization is an active research field, with different open problems such as constrained Bayesian optimization ([Petit, 2022](#)), or Bayesian optimization on stochastic functions ([Gramacy, 2020](#)). Similarly, active learning was also adapted for structural reliability problems.

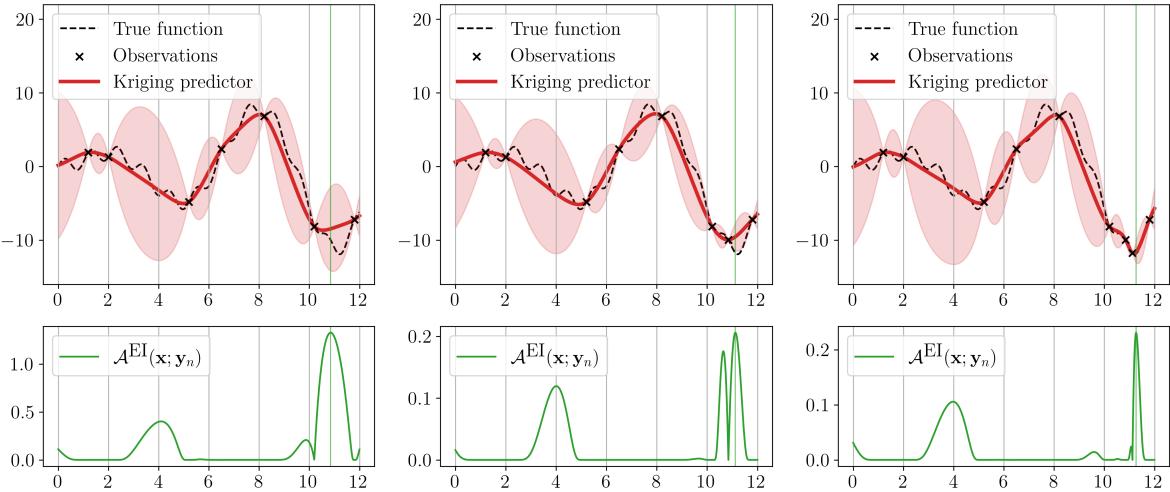


Figure 1.14 Illustration of the expected improvement learning criterion

Active kriging for reliability analysis

Rare event estimation often requires large amounts of evaluations of the limit-state function (becoming intractable for costly numerical models). Emulating this function by a surrogate model can drastically limit the number of calls to the LSF. This surrogate approximates the contour (i.e., border) of the failure domain. However, in most cases, the failure domain represents a very restricted area of the input domain. Active learning methods were proposed to iteratively concentrate the learning set around this border.

For rare event estimation, the surrogate only needs to be accurate near the limit state function. In other words, it should accurately discriminate the points leading to the safe domain from those leading to the failure domain. In fact, this problem can be seen as a binary classification. For example, active learning procedure using SVM classifiers were adapted to this specific goal ([Bourinet, 2018](#)).

The following paragraph introduces the most popular kriging-based learning criterion: the “deviation number” U ([Echard et al., 2011](#)). The reader may refer to [Morio and Balesdent \(2015\)](#) for further active learning techniques dedicated to rare event estimation. More recently, [Teixeira et al. \(2021\)](#) and [Moustapha et al. \(2022\)](#) reviewed this topic with the presentation of wide numerical benchmarks.

Considering an initial learning set $\{\mathbf{X}_n, \mathbf{y}_n\}$ built on a space-filling input design \mathbf{X}_n to explore the domain. A first Gaussian process $G_n(\mathbf{x}) \sim \mathcal{N}(\eta_n(\mathbf{x}), s_n^2(\mathbf{x}))$ is fitted using Eq. (1.90). The deviation number U is looking for points close to the limit-state function while presenting a high kriging variance. This criterion to be minimized, is defined as:

$$\mathcal{A}^U(\mathbf{x}; \mathbf{y}_n) = \frac{|y_{\text{th}} - \eta_n(\mathbf{x})|}{s_n^2(\mathbf{x})}, \quad (1.95)$$

where $y_{\text{th}} \in R$ is a threshold defining the failure domain.

Fig. 1.15 reuses the same one-dimensional function as in Fig. 1.14 to create a rare event problem. In this case, the failure domain is defined for output values below the threshold y_{th} . Once again, three iterations of the AK algorithm are illustrated, with the corresponding learning criterion U (to minimize). In this simple case, the LSF is defined by the two intersections of the function with the threshold. Therefore, the AK method selects points near these intersections.

Unlike optimization problems, the surrogate is used for uncertainty propagation, meaning that the rare event estimation is the result of the approximation of the LSF (i.e., contour finding) and a sampling techniques. AK methods were coupled with most sampling techniques introduced in Section 1.5 (e.g., AK-MCS, AK-IS, AK-SS, etc.). As an agnostic strategy, [Moustapha et al. \(2022\)](#) recommend to start by applying an AK method (using the learning function U) paired with a subset sampling (taking an intermediary probability $p_0 = 0.2$).

The AK methods present the advantages to be easily implemented and interpreted, however, their learning criterion rely on a local approach. Alternatively, the *stepwise uncertainty reduction* (SUR) chooses iterative points by reducing the future expected uncertainty related to the quantity of interest ([Bect et al., 2012](#)). If this method was proven to be theoretically more consistent ([Bect et al., 2019](#)), its scaling ability is still a bottleneck.

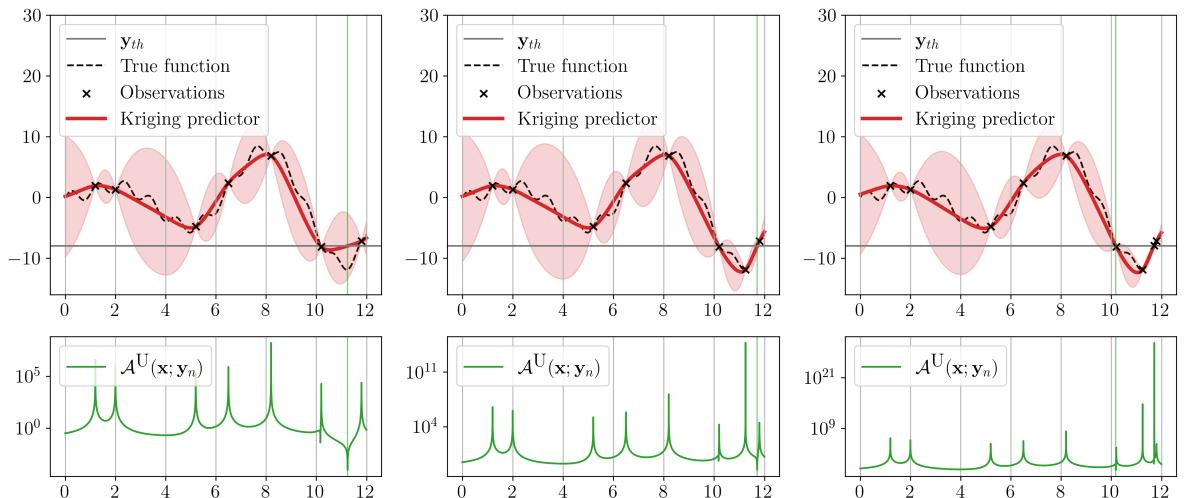


Figure 1.15 Illustration of the deviation number learning criterion

1.7.4 Summary and discussion

This section brought the attention on surrogate modeling in the context of computer experiments. Statistical learning in this framework is made specific by the capacity of the analyst to choose the repartition of the learning set and the small data constraint (mostly due to the costly numerical models manipulated). In this context, many methods are used, however Gaussian processes became popular in UQ as they consider a prior structure of uncertainty that is conditioned by observations (at the edge between a Bayesian and a frequentist approach). To enhance the learning for specific purposes (e.g., optimization or contour finding), active learning methods iteratively add learning points in the subdomain of interest. For some applications, the system studied might be modeled for different fidelities (each presenting different computational costs). Multi-fidelity surrogate modeling is an active field of research, associating observations from different fidelities to improve the learning (Fernández-Godino et al., 2016). Such methods are relevant for models with a very high computational cost (typically in computer fluid dynamics).

In UQ, surrogate models are used for uncertainty propagation (step C) and inverse analysis (step C'). Surrogate modeling is made difficult when the functions present discontinuities (or strong nonlinearities), high dimension, stochasticity, or nonscalar inputs or outputs. To deal with high dimensional problems, unimportant inputs can be screened using sensitivity analysis (see Section 1.6.1), otherwise, model order reduction methods might be used [ref ?]. When the function is stochastic, different approaches allow to fit the function and its intrinsic variability (Binois et al., 2019; Baker et al., 2020; X., 2022).

Provided a strict validation process, surrogate models are a great opportunity for uncertainty quantification. However, many regulatory authorities are still reluctant to the use of surrogates, although their error is often much smaller than the modeling error (i.e., the error between the actual physical behavior and its numerical modeling).

1.8 Conclusion

This section gives a literature overview of the main steps in uncertainty quantification. From uncertainty modeling, uncertainty propagation, sensitivity analysis to surrogate modeling. To ease the methodological presentation, all the illustrations from this section are reproducible using the Python/OpenTURNS scripts available on the GitHub repository mentioned earlier.

Finally this work, the numerical models exploited are supposed to be accurate, but they obviously carry some modeling uncertainty (Oberkampf and Roy, 2010). In fact, prior to uncertainty quantification the model should be calibrated to make it match some physical information (e.g., measurements). Numerical model calibration is also called data assimilation when a stream of measured data is available.

The aim of this work is to apply the tools presented in this chapter to offshore wind turbine models, therefore the next chapter introduces the numerical models manipulated in this thesis.

PART II:

CONTRIBUTIONS TO UNCERTAINTY QUANTIFICATION AND PROPAGATION

*Le doute est un état mental désagréable,
mais la certitude est ridicule.*

VOLTAIRE

PART III:

CONTRIBUTIONS TO RARE EVENT ESTIMATION

La résignation est un suicide quotidien.

H. BALZAC

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