

Master Thesis

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**Multiploid Non Sorted Genetic Algorithm (M-NSGA) applied
to the optimization of GHG emissions, comfort and cost of
buildings.**

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Chapter 1

Introduction

Recent studies show that building construction and operations accounts for the largest share of both global final energy use (36%) and energy-related CO_2 emissions (39%)¹ in 2018 (Figure 1.1). In addition, before the health crisis of Covid-19, greenhouse gas emissions (GHG) emissions were increasing slightly. Therefore, the buildings and construction sector appears to be a primary target for GHG emissions mitigation efforts.

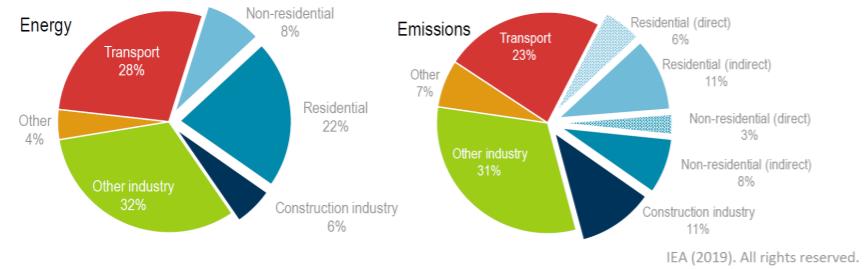


Figure 1.1: Global share of buildings and construction final energy and emissions, 2018 - Source : IEA 2019 Global Status Report for Buildings and Construction [1]

France places the building sector at the heart of its strategy to meet the challenge of climate change. Buildings account for nearly 45% of national energy consumption and more than 25% of greenhouse gas emissions.

In November 2015, 174 countries signed an agreement to plan a drastic reduction in Greenhouse Gas emissions (GHG) at the UN Conference on Climate Change in Paris. The built environment is a major GHG emission contributor and becomes a natural target in terms of mitigation potential worldwide. This agreement lead to the creation of the SNBC (Stratégie Nationale Bas-Carbone) in France. This action plan sets the objectives for the building sector: a decrease of 50% of the GHG emissions by 2030 and a decrease of 90% by 2050 (in

comparison with 2015 emissions).

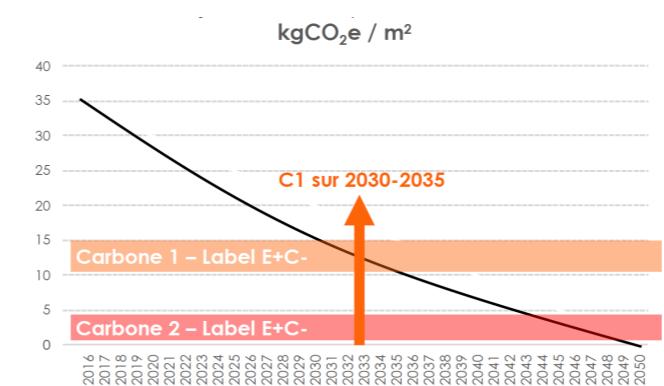


Figure 1.2: Performance trajectory of the French housing stock to 2050 according to SNBC 2018
- Source : Analyse Carbone 4, based on SNBC's carbon budgets for building on its scopes 1 and 2. [8]

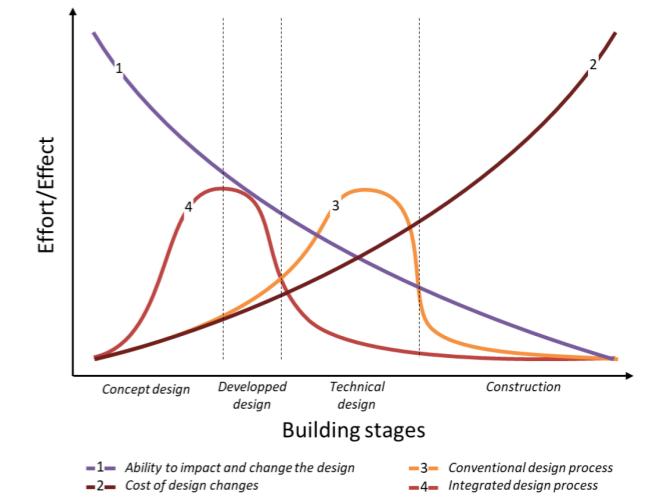


Figure 1.3: Shifting efforts earlier for an integrated design process. Source : T. Jusselme, 2020 ; Adapted from (MacLeamy, 2004; Sinclair, 2013) [14]

These objectives mean that the French housing stock must follow a CO_2 emission reduction trajectory that tends towards 0 in 2050, with a milestone value of 15 $kgCO_2\text{-eq} / m^2$ per year in 2030, which more or less corresponds to a "level 1" carbon housing stock of the E+C- Label over the period 2030-2035. In order to reach these new targets, the use of life cycle assessments in early stages of the project is critical. However, as an iterative process, this method is time-consuming and needs high resolution details. This is why in practice it is rarely used in early stages by practitioners. Yet, thinking, anticipating and designing within the constraints at early stages offers many advantages: it makes it easier reaching the targets as well as avoiding extra costs caused by unanticipated changes. The Figure 1.3 shows that the earlier the design process is integrated, the cheaper the efforts.

Two other major targets appear in the design phase of a building: comfort and cost. Albeit the GHG emissions are worrisome, these two others objectives cannot be neglected: ensuring a good comfort along the lifetime is relevant to design sustainable buildings and lowering the costs encourages the delivery of such eco-friendly constructions. AREP, whose task is to design creative solutions in resilient urban planning, low carbon architecture and ecological design for inclusive and sustainable mobility, is willing to develop an automated and simplified tool to help reach the targets defined by the French Ministry while ensuring the comfort and monitoring the investment. The central point of this internship is to investigate the feasibility of this multi-objective

¹Notes: Construction industry is the portion (estimated) of overall industry devoted to manufacturing building construction materials such as steel, cement and glass. Indirect emissions are emissions from power generation for electricity and commercial heat.

(GHG emissions, cost, comfort) optimization by using a multiploid genetic algorithm.

Chapter 2

The company

2.1 Introduction

AREP is a multidisciplinary agency specialized in the renovation and design of the train stations. Founded in 1997 by the architect-engineers Jean-Marie Duthilleul and Étienne Tricaud, it now has nearly a thousand employees and is established in four countries outside France: Switzerland, Dubai, Vietnam and China. Despite this, the company's head office and most of its skills are still located in Paris, in former Panhard automobile factories. AREP's services cover six trades, which intervene at different stages of an architectural project : architecture, engineering, urban planning, management of operations on building sites, architectural and technical programming.



Figure 2.1: AREP's open space (Panhard building).

2.2 AREP°L'hypercube

L'hypercube, founded in 2015, is the AREP research and development department which covers several of those trades. Composed by 7 people coming from various background : architecture, engineering and PhDs, this department deals with complex or coupled phenomena in building physics such as air flow, air quality, thermal comfort and the urban heat island phenomenon. For instance, figure 2.2 presents the exterior comfort levels of the Strasbourg train station forecourt. This figure was obtained thanks to the tool developed by l'Hypercube for simulating surface temperatures in an urban environment using a "weak-coupling" with the air flow simulations performed. The tool allows the calculation of comfort indicators adapted to the external environment at each point in the space. It integrates the coupling of fluid mechanics simulations, sunlight and transient heat transfer within walls.

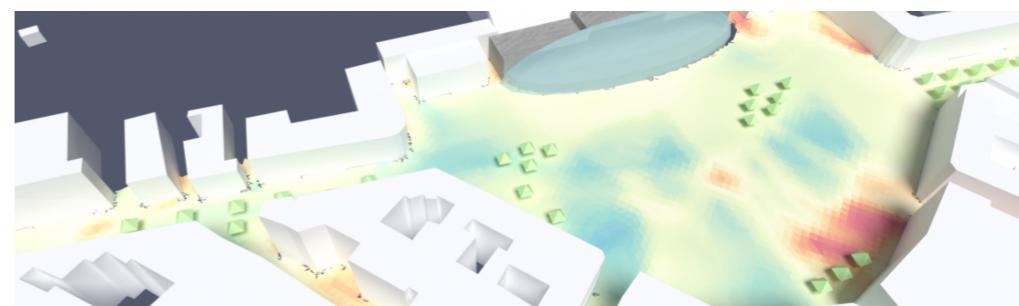


Figure 2.2: Strasbourg train station forecourt - exterior comfort.

In addition, the team has a lot of interactions with the different departments of AREP with the aim of combining the existing competences. For instance, during my internship I have worked with the Environmental and Economics departments to create the database dedicated to the products commonly used by AREP in its projects. This database served then for the carbon optimization procedures developed in the sequel. I have also worked with the Structure department to implement the function that given the height and the material of the element returns the structural width.

On a more informal level, the work atmosphere and environment are pleasant. The team is very welcoming and thoughtful which was much appreciated. Factually, this translates to a low turnover rate in the team.

Chapter 3

State of the art

In this chapter, a brief overview of the existing methods for multi-objective optimisation is proposed.

3.1 Genetic algorithms

Genetic algorithms prevail among all the studies of multi-objective optimization for buildings [16]. These algorithms are known for performing better than other optimization methods when it is mathematically impossible to provide an analytical solution, when the size and shape of the solution are unknowns or when there are many simulators capable of evaluating the solution but no good optimizers [17]. In the field of construction, these three constraints are existing : to mathematically describe the system to solve is complex owing to the hierarchical system of components (a building is composed by standardized elements, themselves composed by materials picked in a database) and their interactions with the different objectives to reach (comfort, cost, GHG emissions), the size of the solution is not fixed to avoid a lack of flexibility and finally very performant software programs exist to simulate or estimate the different objectives from a fixed configuration, but optimizers are not efficient. In addition, genetic algorithms can efficiently handle non-linear problems with discontinuities and many local minima. Moreover, they do not require to explicitly calculate the objective function's gradients but are based on improvement along iterations using the evaluation of the fitness function to assess the quality of solutions. However, one main drawback is the computational complexity, which is generally $O(MN^3)$, where M is the number of objectives and N is the population size. Fortunately, genetic algorithms such as NSGA-II

¹ and NSGA-III has tackled this issue [10, 9, 13]. Theses non-dominated sorting genetic algorithm perform

with a computational complexity of $O(MN^2)$ and they also propose a comparison method which guides the selection process towards a uniformly spread-out Pareto-optimal front.

Genetic algorithms manipulate different types and shapes of information. Most of the time, the genotypic representation is a sequence of numbers that encodes the information, as does DNA for humans. Like in nature, individual possessing several alleles for one gene could be operated. In this case, multiploidy ² have been chosen for convenience : it allows to study several wall systems for one wall while ensuring the compatibility of materials, as explained further in section 4.2. The multiploid genetic algorithms documented in the literature rely on a dominance scheme : a set of rules that dictates which allele dominates another one. This genotypic representation is known for enhancing the performance of the algorithms in some cases : when a dynamic environment is involved and when useful genetic material may otherwise be irretrievably lost ³ [20, 7].

Genetic algorithms have been used in the building construction sector for decades. However, to the best of our knowledge, multiploidy has not been exploited yet. Chardon & al. optimized the cost and energy of single family houses according to material databases [4]. They used a genetic algorithm for the optimization and two other software programs for cost estimation and energy simulation. The interaction between all the software programs were insured by a vectorized representation and its encoder/decoder. In practice, the genetic algorithm was working with the vectorized representation while the energy simulation system was working with the BEM ⁴ file. Brangeon & al used a similar approach for the cost and energy optimization of integrated refurbishment of collective housing [3]. These two studies used the Non-Sorted Genetic Algorithm II (NSGAII) implemented in the DEAP library of Python. Barbaresi & al used a 2 phases procedure to optimize a wine-making and storage building [2]. First, in the phase 1 they run the genetic algorithm with fictitious materials and thus continuous variable. During the phase 2, they create 3-materials constructions, picking from a material database that best fit the theoretical values identified in the Phase 1. This approach : continuous and discrete optimization allows to uniformly cover the search space and then to investigate it in deeper details than a 1 phase (discrete optimization) does. In addition, the 2 phases procedure is slightly faster and returns more energy efficient solutions. Chen et al. firstly conducted a sensitivity analysis to discard non-influential design parameters and reduce the problem space for further optimization [5]. To minimize the lighting, cooling and heating demand while maximize the PV energy production, NSGA-II is first conducted on the original design space. Then the weighted sum method is applied with HGSPSO (hybrid generalized pattern search particle swarm optimization) to conduct an equivalent mono-objective optimization of the net building energy demand. The second optimization was conducted with a reduced dimension of input variables by excluding non-significant parameters based on preliminary sensitivity analyses.

¹Non Sorting Genetic Algorithm

²Having multiple copies of each chromosome

³The authors allude to the memory function that multiploidy may offer.

⁴building energy model.

3.2 Data-driven approach

Other approaches than genetic algorithm are used. Jusselme performed a Data-driven method for low-carbon building design at early stages [14]. Firstly, thousands of solutions were generated from the parametric assessment. Then the Saltelli sampling technique is used to explore the solution space [18]. In group sampling, all the parameters are assigned to some groups. The group itself act like a parameter. From the result, the analyst could determine which groups and thus which parameter were influential. Then the analyst would redo the group analysis using a different allocation of groups to complete the study. Indeed, this technique is more intricate than described above, since it has to take into account the possible interactions between parameters. Nevertheless, the Saltelli group sampling allows to reduce the number of simulations and to still isolate influential parameters and their effects. Afterwards, visualization techniques were used to easily analyse the influence of the parameters and thus choose the best solution.

3.3 Chosen approach

In summary, Non-Sorted Genetic Algorithms have proven to be an efficient tool in order to optimize multi-objective system in the construction field. Multiploidy has not been applied yet in this area. Other techniques like sensitivity analysis are sometimes used a priori to provide insights on the database and filter the parameters used for the optimization. It can also be used a posteriori to characterize the solutions. Finally, visualization techniques such as parallel coordinates emerge as a powerful tool to investigate the Pareto front as well as communicating the results.

In the light of this state of the art, a multiploid genetic algorithm approach has been chosen to tackle the multi-objective optimization.

Chapter 4

Methods

4.1 Approach

The first step of the optimization is to define the variables and the study framework. This study focus on the minimization of the materials and implementation costs, the minimization of the materials GHG emissions over all the life cycle and the optimization of the comfort using the physiological effective temperature (PET) as indicator. The energy consumption as well as the building's end of life are not taken into account. The genetic algorithm creates variants of the building by changing the wall systems as well as the materials used. Other parameters like orientation, shape or location are fixed. Designing the HVAC¹ system is handled by the software used for the thermal simulation, i.e. EnergyPlus.



Figure 4.1: Parameters and variables.

A 3D model of a building is composed by hundreds of elements (walls, floors, roofs, windows, etc). However, many of these elements share the same insulation system and materials. Thus, rather than allocating an insulation system and materials to an element, the algorithm works with zones. Inside a zone, all the elements of one type² share the same insulation system and materials composition. For convenience, several zones can be used to allocate different insulations systems and materials for elements. For instance, in the case of a train station, there are typically two different zones : offices and halls. These zones have different comfort objectives and should not share the same wall system and material composition.

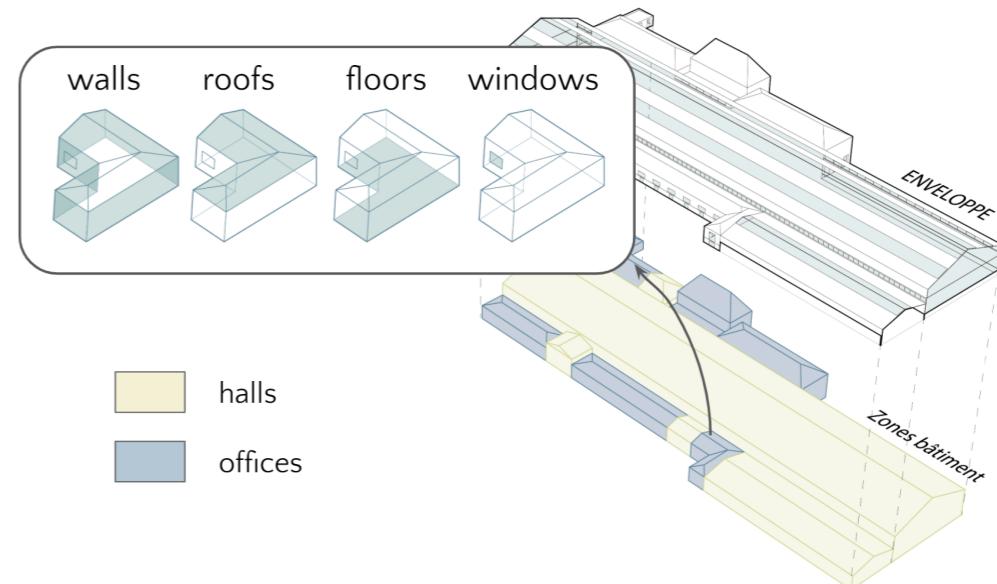


Figure 4.2: Element types of one zone.

¹heating, ventilation and air-conditioning

²one type of element can be wall, floor, roof, window, etc.

³the INIES database provides environmental and health declaration sheets (FDES)

The major drawback of this approach is to consider the same width for structural material whether the element is located at the first or the n^{th} floor. Which is not really the case in practice. To counter this drawback, a function that maps the width of the structural material according to the floor and the structural material itself (structural wood and concrete do not have the same mechanical properties at the same width) is implemented. The algorithm will select afterwards the product in the database that best matches the width given by the function. Structural design is far more complex, this approach only yields an estimation of the width for the structural material in order to include it in the dynamic thermal simulation.

For a better estimate of the comfort, the cost and the GHG emissions, materials are picked into a database that includes both INIES³ and products commonly used by AREP. Since the products of the database are highly detailed, there are only compatibles with particular wall systems. To ensure this compatibility inside the algorithm, each product of the database have received tags. A tag is composed by 3 keywords : [function]-[element]-[insulation-system]. The first keyword defines the function of the product, whether it is for the structure, the insulation or the coating. Then the second keyword determines for which element (wall, floor, roof, windows, etc) the product is available. Finally, the last keyword gives the compatibility with the wall system. One product may receive several tags.

4.2 Encoding

The next step is to develop an encoding system in order to manipulate the variables within the genetic algorithm. During the optimization, operators doing the crossover or the mutation are dedicated to the evolution of the population towards fitter individuals. Like in biology, those operators use the genotype⁴ to produce children. In our case, the genotype is a sequence of integers that contains the information about wall systems and materials used. The complexity of the encoding ensues from the dependencies between the wall systems and the materials. Indeed, not all materials can be used in every wall system. There are compatibility issues owing to real life construction systems. To avoid dealing with those dependencies inside the operators, the system of tags have been deployed and multiploid individuals are used.

⁴the particular type and arrangement of genes that each organism has

⁵the visible features of living beings

WS_i = Wall System N°X
1 color = 1 allele

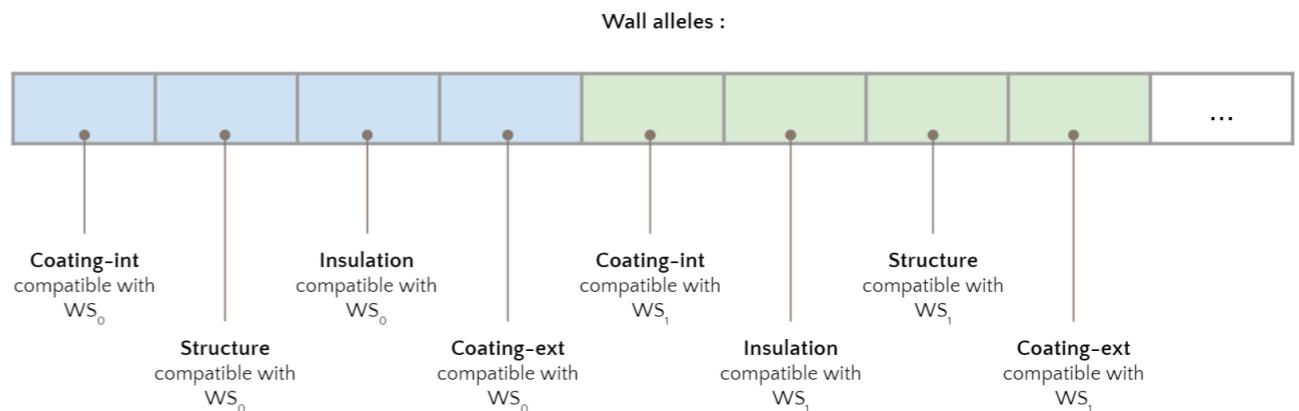


Figure 4.3: Multiploid representation for walls inside a zone.

In biology, genes may have several versions, they are called alleles. Each allele codes for a particular phenotype⁵, for instance the colour of the eyes. In this encoding system, the idea is used to code the different wall systems. Each allele describes a wall system and its materials. As depicted by figure 4.3, an allele is described by variable names that indicate the layers' configuration of the wall system (interior toward exterior) and also by the variable's value, which imposes the material picked for one layer. Indeed, each variable inside an allele is linked with a particular tag and thus with a list of compatible materials. The value of a variable is the material's index in the corresponding list. Each variable has a defined and fixed place (*a locus*) within the sequence. Since materials are only compatible with certain wall systems, this approach allows easy exchange of genotype pieces between individuals. Using this multiploid representation allows making crossovers between two individuals by just swapping the variable's values.

Given the description above, the encoding system is mathematically described as follows : let V be the sequence of integers that encodes the information about the variant. V is composed by n variables, called v_i . Each variable has its own range definition called R_i^d .

$$V = \begin{bmatrix} v_1 & \dots & v_n \end{bmatrix} \quad (4.1)$$

With $v_i \in R_i^d = [l_i, u_i]$, l_i and u_i are respectively the lower and upper bound of the range definition for the i^{th} variable. This range definition is used for initialization as well as for the mutation operations. This range is fixed by the compatible list of materials associated with the variable.

Going further into the description : the vector V is sequenced by genes : g_k , which are vectors composed by

the variables v_i . Each sequence g_k is composed by the alleles : a_j^k , which are themselves a sequence composed by the variables v_i (describing which material has to be picked for one layer of the insulation system described by this allele). The gene is described by one last variable : the one that selects the expressed allele, this variable is called s^k . In the following description, the i^{th} variable that describes the j^{th} allele of the k^{th} gene is called : $v_{j,i}^k$. Thus, the sequence g_k representing the k^{th} gene of the variant is defined as follows :

$$g_k = [s_k \ v_{1,1}^k \ v_{1,2}^k \ \dots \ v_{1,q_1^k}^k \ \dots \ v_{m_k,1}^k \ v_{m_k,q_m^k}^k] \quad (4.2)$$

With m_k the number of alleles of the k^{th} gene, and q_j^k the number of variables of the j^{th} allele.

One variant is composed by several genes describing the insulation system of the walls, the floors, the roofs and also the windows. The sequence V defines the genotype. As contrary, the phenotype is defined by the expressed alleles of the genes. The expressed allele is selected according to the value of the s_k variable. The sequence that defines the phenotype for one gene is then the following:

$$g_k^e = [s_k = l \ v_{l,1}^k \ v_{l,2}^k \ \dots \ v_{l,q_l^k}^k] \quad (4.3)$$

V^e is thus the sequence of integers that only contains the expressed genes g_k^e , $k \in \llbracket 1, m_g \rrbracket$, with m_g the number of genes. Although the encoding is complex, it allows to ease the programming by eliminating the dependencies. For instance, initializing a variant is done by picking one integer in the range definition of each variable. Likewise, the mutation operation is done by randomly assigning a new value within the range definition. The mutation is activated whether a random draw is inferior as the probability of mutation noted p_m . It is remarkable that it may mutate both non-expressed and expressed variables.

$$\forall i \in \llbracket 1, n \rrbracket, \text{ if } p < p_m, v_i = \text{random}(l_i, u_i)$$

The multiploid representation is especially convenient to perform crossovers. Supposing there are two variants represented by the vectors V_a and V_b , crossing those two variants is done by simply swapping the variables.

$$V_a = [v_1^a \ \dots \ v_n^a]$$

$$V_b = [v_1^b \ \dots \ v_n^b]$$

A crossover produces two children : V_{ab} and V_{ba} . Indeed, V_{ab} has the same base as V_a and receives the swapped variables of V_b and vice versa for V_{ba} . Moreover, according to the crossover type ⁶, one or more variables are

swapped. For instance, if the index of the swapped variables are : $[1, 2, 3]$, the children will be :

$$R_{ab} = [v_1^b \ v_2^b \ v_3^b \ v_4^a \ \dots \ v_n^a]$$

$$R_{ba} = [v_1^a \ v_2^a \ v_3^a \ v_4^b \ \dots \ v_n^b]$$

In this case, using classic haploid ⁷ individual ⁸ extremely complicates the mechanisms of the initialization, mutation and crossover because one variable may describe different layer of different wall systems and thus cannot be linked with a fixed compatible list of materials. For instance, for the easiest operation of initialization, it means that the dependencies between the wall systems and the materials should be solved by a system of rules and iterations.

Notations : The followings notations are adopted for clarity :

- The Genotypic space G is the space that contains all the combination of 1-dimensional sequence of integers V described above.
- The Phenotypic space P is the space that contains all the combination of 1-dimensional sequence of integers V^e described above.

4.3 Multiploid Genetic Algorithm

The studied problem poses two technical issues for using classical optimization, which uses derivative. Firstly, since materials are picked in a database, the input variables of a potential optimization function (i.e. the genotype in this case) are discrete and not uniformly distributed in space, which poses convergence issues for derivatives-based optimization, such as gradient methods. Secondly, the relation between the inputs and the outputs may not be explicit. For instance, the comfort is computed as a post-processing of building thermal simulation data. With regard to these difficulties, using an evolutionary algorithm such as the Non-dominated Sorting Genetic Algorithm-II (NSGA II) is relevant since it has already proven to perform well over similar problems.

As described by Deb & Al, the algorithm uses classical operators such as mutation and crossover to evolve the population but operates a clever selection based on the Pareto front density as well as the non domination

⁶One point, two points, uniform, etc.

⁷Organism with one set of chromosome, meaning that for one gene only one allele exists in the genotype.

⁸In the genetic algorithm lexicon, one individual is one possible configuration of the sequence V.

rank to guide the population towards a uniformly spread-out Pareto-optimal front [10]. As explained in the previous section, the genotypic representation is multiploid by convenience. However, instead of implementing a dominance scheme as explained by Yang [20], the dominance is ruled by one variable per gene : s_k . This variable is subjected to all the operators during the evolution, hence the allele dominance appears like a parameter tuned by the algorithm itself. This approach allows benefiting from the memory function of the multiploidy but prevents from establishing a dominance scheme and thus biasing *a priori* the combination of alleles.

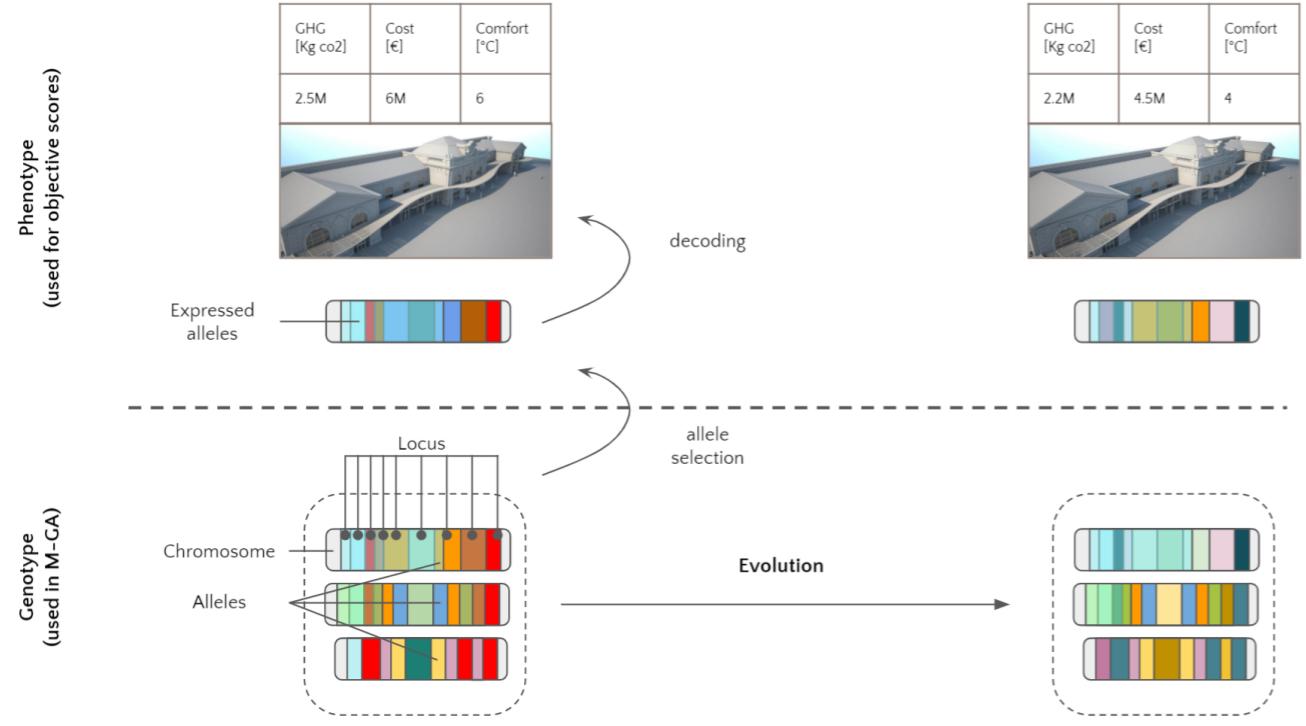


Figure 4.4: Use of genotype and phenotype.

The genetic algorithm uses the genotype, *i.e.* all the alleles, whereas the objectives are computed over the phenotype, *i.e.* only the expressed alleles. As it is depicted in figure 4.4, one multiploid individual has several chromosomes. All the chromosomes share *loci*, which are the positions in a chromosome of a particular gene or allele. Depending on the chromosome size, the *locus* may receive a different number of alleles. The genetic algorithm performs the crossover and the mutation on all the genotypic representation, *i.e.* the vector V described section 4.2. Once the expressed alleles are selected, the phenotype of an individual is fixed. Afterwhile, the phenotype is decoded to produce the 3D model on which the cost, the GHG emissions and finally the comfort (via EnergyPlus) are computed.

The genetic algorithm minimizes five objectives :

- **The GHG emissions** [kg CO₂-eq] which are computed from the INIES products. The phase A1 to C4 of

the life cycle analysis (LCA) are taken into account.

- **The minimum and maximum costs** [€] which are respectively the addition of whether the lower bound or the upper bound of the product's price range provided by the AREP's Construction Economy department. This price range includes the material's cost as well as the installation one.
- **The hot and cold comfort** [°C]. These values represent the positive and negative temperature difference between the calculated *Physiological Equivalent Temperature* (PET) and the median temperature (20.5 °C) of the comfort range : [18, 23]. The physiological equivalent temperature is the air temperature at which, in a typical indoor setting (without wind and solar radiation), the heat budget of the human body is balanced with the same core and skin temperature as under the complex outdoor conditions to be assessed [11].

The initialization of the algorithm is performed by a *Latin Hypercube sampling*. This technic is a quasi-random sampling that attempts to distribute samples evenly over the genotypic space. It is designed to maximize the minimum distance between points and places the latter in a randomized location within its sampling interval. It allows to constitute a good starting point for the genetic algorithm since it better covers the parameter space than a random initialization.

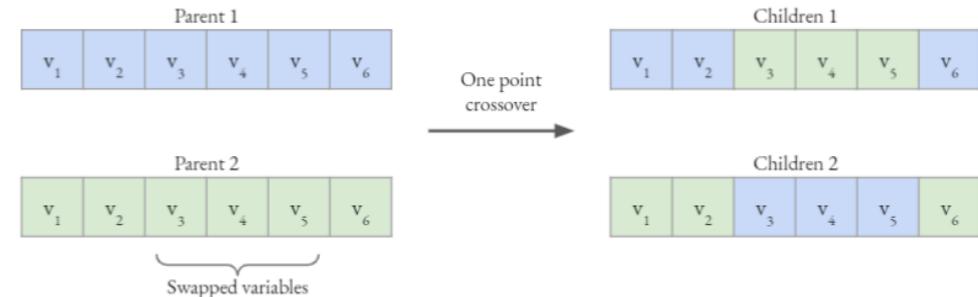


Figure 4.5: One point crossover.

Concerning the mechanisms of the evolutionary algorithm, the mutation used is the one described in section 4.2. Several crossovers were tested : one point, two points and uniform. For all the crossovers methods used, the variables exchanged keep the same *locus*. One crossover between two individuals forms two children.

- The one point crossover is done by selecting a point in the genotype and exchanging a piece of it. The variables exchanged are side by side. The mechanism is illustrated in figure 4.5.
- The two points crossover follows the same mechanism but operates the crossover with two different points of exchange.
- The uniform crossover picks random variables and swaps them with the other individual.

4.3.1 Convergence's indicators

The indicators are used to compare different evolutionary mechanisms (crossover, mutation, hyperparameters, etc.) in order to understand how the multiploidy impact the algorithm's convergence and to identify the best behaviour. The indicators are described below :

- **Hypervolume Size** : this indicator reveals how the searching space evolves. It is computed at the end of each generation in order to compare the evolution speed and the expansion of the hypervolume. This indicator is an n_o -dimensional hypervolume computed between the individuals delimiting the border of the space search and a reference point, where n_o is the number of objectives. The reference point is computed according to the method proposed by Ishibuchi & al for fair comparison [12]. This indicator is easily understandable in two dimensions as depicted figure 4.7.

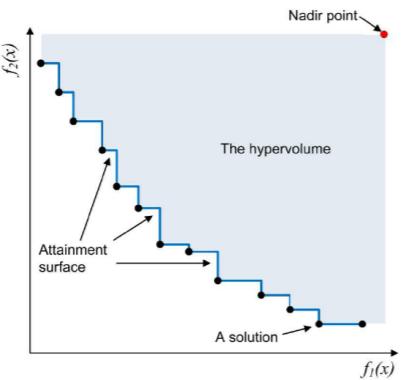


Figure 4.6: Hypervolume in two dimension [19]

To characterize the evolution of the hypervolume size along the generation, a hypervolume score is computed as the percentage of expansion per generation :

$$s_H = \frac{H_{n_g} - H_0}{H_0 \times n_g} \times 100 \quad (4.4)$$

Where H_0 and H_{n_g} are respectively the hypervolume size at the first and last generation. With n_g the total number of generation.

- **The Bray-Curtis dissimilarity** : this indicator measures the dissimilarity between two sequences V_a and V_b . It is often used in ecology and biology to quantify how different two sites are in terms of the species found in those sites. This indicator is computed at each generation and between all the possible combination of a pair of individuals. The Bray-Curtis dissimilarity D is computed as follows.

$$D = \frac{\sum |u_i - v_i|}{\sum |u_i + v_i|} \quad (4.5)$$

with u and v two 1-dimensional vectors, in our case these are two sequences V described in section 4.2. To characterize the maintenance of the diversity, the average Bray-Curtis Dissimilarity is collected as each generation and then the diversity score, noted s_D is computed as the mean over the generations :

$$s_D = \frac{\sum_{i=0}^{n_g} D_i^{avg}}{n_g} \quad (4.6)$$

With D_i^{avg} the averaged Bray-Curtis dissimilarity at the i^{th} generation.

- **The new individuals rate** : this indicator measures the percentage of never encountered before individuals produced at each generation. It is used to achieve the Bray-Curtis dissimilarity indicator. The Bray-Curtis indicator is a measure on the population at the i^{th} generation, this population may include individuals created in the past generations, hence it gives more insights on the diversity conservation. While this indicator give insights on the production diversity. It is noted NIR . To characterize this rate of new appearance, the NIR score is computed as the averaged NIR over the generations :

$$s_{NIR} = \frac{\sum_{i=0}^{n_g} NIR_i}{n_g} \quad (4.7)$$

- **Objectives's score** : while the previous indicators measure the behaviour of the evolutionary mechanisms, these indicators allows to monitor the minimization of each objective. For each generation the mean of each objective is collected. Then the j^{th} objective score is computed as the percentage of evolution per generation.

$$s_{o_j} = \frac{m_0 - m_{n_g}}{m_0 \times n_g} \times 100 \quad (4.8)$$

With m_0 and m_{n_g} respectively the averaged objective score over the first and last generation.

One metric is used to integrate all the indicators. It is described with the following equation. The higher the value, the better is the hyperparameters setting:

$$score_{ga} = s_H \times s_D \times s_{NIR} \times \prod_j^{n_o} s_{o_j} \quad (4.9)$$

with n_o the number of objectives.

This indicator favours hyperparameters settings which quickly minimimmize the objectives and guarantee diversity in order to have a fast algorithm providing a variety of good solutions.

Other performance metrics were developed by Deb & al when describing the NSGA-II and III algorithms [10, 9, 13]. However, they take into account the analytic optimal Pareto front, which is not accessible in our case study.

4.4 Surrogate Model of the comfort

The comfort is computed by running a thermal simulation with EnergyPlus, then collecting all the data to compute the PET (mean air temperature, mean radiant temperature, air relative humidity, site direct/diffuse solar radiation, etc). The thermal simulation takes approximately 10min per individual, depending on the size of the 3D model. For one optimization, the order of magnitude of individuals used is 10^3 . Therefore, the computation time is about 10^1 hours on a ten cores computer for only one optimization run.

To avoid this costly time of optimization, a surrogate model is used to estimate comfort. Since two objectives of comfort are used (hot and cold), two surrogate models are employed. The models are trained during the first generation of the optimization and then used to estimate the comfort.

The input of the surrogate model is a vector that contains thermal and optical properties of the walls and windows. The variables used as input are described below :

For each wall composition of each zone, the following inputs are given to the model :

- The diffusivity of the wall : $\alpha [m^2/s]$. It characterizes the ability of the wall to transfer heat (thermal energy) through it.
- The width of the wall : $e [m]$. With the diffusivity, it gives insight on the thermal dephasing which is proportional to $\frac{e^2}{\alpha}$.
- The normalized barycenter of mass of the wall : $m_b [1]$: it indicates whether internal or external insulation is operated.

For each window of each zone, the following inputs are given to the model :

- The thermal transmittance : $U [W/K]$. It characterizes how much heat will conduct the window.
- The Solar Heat Gain coefficient : $SHGC [1]$. It is the ratio of transmitted solar radiation to incident solar radiation of an entire window assembly.

The surrogate model is operating only on a specific 3D building model and local weather. Only materials and wall systems are changing from one to another individual. Therefore, all the parameters shared by all variants such as the geometry, the orientation, the outside conditions, etc. are implicitly taken into account. The surrogate model is based on the Kriging method. Kriging, also known as Gaussian process regression, is a method of interpolation based on Gaussian process governed by prior covariances. Under suitable assumptions on the priors, kriging gives the best linear unbiased prediction (BLUP) at unsampled locations [15].

Kriging is an interpolating model that is a linear combination of a known function $f_i(x)$ which is added to a realization of a stochastic process $Z(x)$:

$$\hat{y} = \sum_i^k \beta_i f_i(x) + Z(x) \quad (4.10)$$

$Z(x)$ is a realization of a stochastic process with mean zero and spatial covariance function given by :

$$cov [Z(x^{(i)}), Z(x^{(j)})] = \sigma^2 R (Z(x^{(i)}), Z(x^{(j)})) \quad (4.11)$$

where σ^2 is the process variance, and R is the correlation.

The hyperparameters choice, sampling technics and the performance of the surrogate models are discussed in the next chapter.

4.4.1 Input specificity

Once the *Latin Hypercube Sampling initialization* is operated on the Genotypic space, the phenotype is identified and then the inputs for the surrogate model are produced. These inputs are sampled afterward to form a training set. This process has one major drawback : the parameters distribution across the input space I can not be monitored. Indeed, the *Latin Hypercube Sampling initialization* evenly distributes the parameters across the genotypic space, but this property might not be conserved by conversion to the input's space. This owes to the relation between the two spaces, as the function linking the inputs from the genotype is not bijective. Let g be a genotype and i an input : $\forall i \in I, \nexists g \in G / (f_1 \circ f_2)(g) = i$. With f_1 the function used to go from the Genotypic space G to the Phenotypic space P , and f_2 the function used to go from P to the inputs space I .

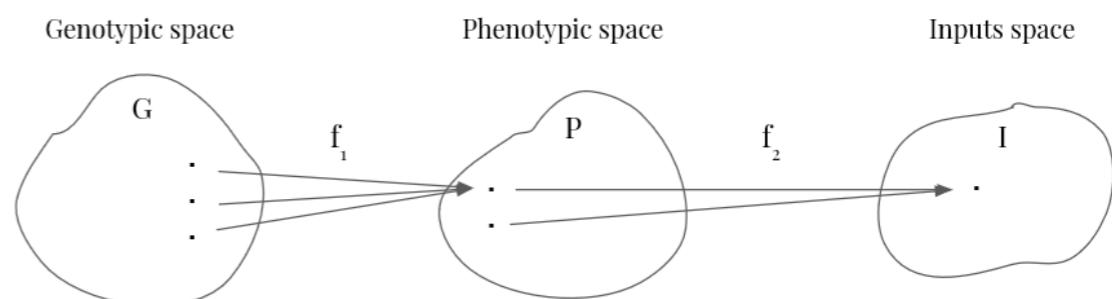


Figure 4.7: Spaces and relation

In addition, while the genotypic and phenotypic spaces contains sequences of **discrete** variables, the inputs

space I contains sequences of **continuous** variables. These two features (discrete towards continuous space plus the non bijectivity) could complexify the implementation of the surrogate model. Indeed, it could create a clustering phenomenon on the training set that prevent the Kriging method to perform well on a certain range since the estimation uses the neighbours (their influence vary according to the distance).

4.4.2 Performance's indicators

The indicators used are described below.

- **Correlation coefficient R^2** : The Bravais-Pearson linear correlation coefficient reflects a linear dependence between two variables at n_v sampled points. In the sense of this metric: the higher the value R^2 the more accurate the model is.
- **Mean Square Error MSE** : In the sense of these criteria, the lower the value, the more accurate the substitution model.
- **Average Absolute Error AAE** : In the sense of these criteria, the lower the value, the more accurate the substitution model.
- **Maximal Absolute Error MAE** : In the sense of these criteria, the lower the value, the more accurate the substitution model. This metric indicates whether a significant error is present in an area of the design space. Cases may occur where the reduced model is very good in the sense of R^2 and AAE but bad in the sense of MAE. It is preferable that the MAE error be as small as possible but the first two errors R^2 and AAE will have to be taken into account first.

For convenience, one metric resumes all the indicators. The LHS being a stochastic process, the indicators are computed over several seeds to highlight trends: the mean and the standard deviation of the indicators are collected to compute the proposed metric. The maximization of the means obtained ensures that the overall performance is good and the minimization of the standard deviations ensure that the performance do not vary too much from one seed to another. The metric is described below, the higher the metric, the better the hyperparameter setting.

$$score_{KRG} = \frac{R_{avg}^2}{R_{std}^2} \times \frac{MSE_{std}}{MSE_{avg}} \times \frac{AAE_{std}}{AAE_{avg}} \times \frac{MAE_{std}}{MAE_{avg}} \quad (4.12)$$

- **training set size** : 30 or 60. The training set size should at least be greater than two times the number of parameters.

Chapter 5

Development

5.1 Surrogate Model

- **sampling method** on I : random or uniform. All input sequences on I are numbered, the random and uniform sampling respectively randomly or uniformly pick numbers (and therefore samples) to create the training set.

Several hyperparameters were tested in order to optimize the two surrogate models used for comfort in the cold and hot season.

- θ_l ¹ **optimizer** : Constrained Optimization BY Linear Approximation (COBYLA) or Truncated Newton algorithm (TNC).

- **correlation function**² : *matern32*, *square-exp* or *abs-exp*. This function determines the evolution of the auto-correlation with the distance. If x_0 the position of the estimation, it means that it monitors the influence of the known points x_i used for the estimation according to the distance to x_0 . The choice of this function imply to have insights on the variogram shape.

$$R_{\text{matern32}} = \prod_{l=1}^{nx} \left(1 + \sqrt{3}\theta_l |x_l^{(i)} - x_l^{(j)}| \right) \exp \left(-\sqrt{3}\theta_l |x_l^{(i)} - x_l^{(j)}| \right) \quad (5.1)$$

$$R_{\text{abs-exp}} = \prod_{l=1}^{nx} \exp \left(-\theta_l |x_l^{(i)} - x_l^{(j)}| \right) \quad (5.2)$$

$$R_{\text{sqr-exp}} = \prod_{l=1}^{nx} \exp \left(-\theta_l (x_l^{(i)} - x_l^{(j)})^2 \right) \quad (5.3)$$

- **initial population size**: 150 or 300. The size of the population on which the sampling is done. Related to the genetic algorithm.

For each hyperparameter setting, 30 trainings are performed in order to use several seeds for the random and uniform sampling on I . After each training, several indicators are computed over 1000 predictions to identify the best hyperparameter setting. The 1000 prediction's input are randomly picked into a database of 5000 existing samples generated during a previous optimization. Therefore, the database contains samples from the first to the last generation of the genetic algorithm optimization with the aim of taking into account a potential deviation into the G and I spaces. Since the genetic algorithm makes the population evolve generation by generation, the population at the first and last generation might be very different. As the model is established with the first generation, the performance might decrease along the generations. The metric's score will determine if a model enrichment is necessary. In addition, this test has been realized for several seeds for the LHS initialization on G to investigate a potential effect on the results. All the results are available in appendix A and B. The next figures show the evolution of the correlation coefficient along the generation for different hyperparameter settings as well of the comparison of the comfort temperature computed with the surrogate models and EnergyPlus.

¹ $\theta_l, l \in [1, 14]$ are the weights for the 14 parameters of the model.

²A correlation function is a function that gives the statistical correlation between random variables, contingent on the spatial or temporal distance between those variables.

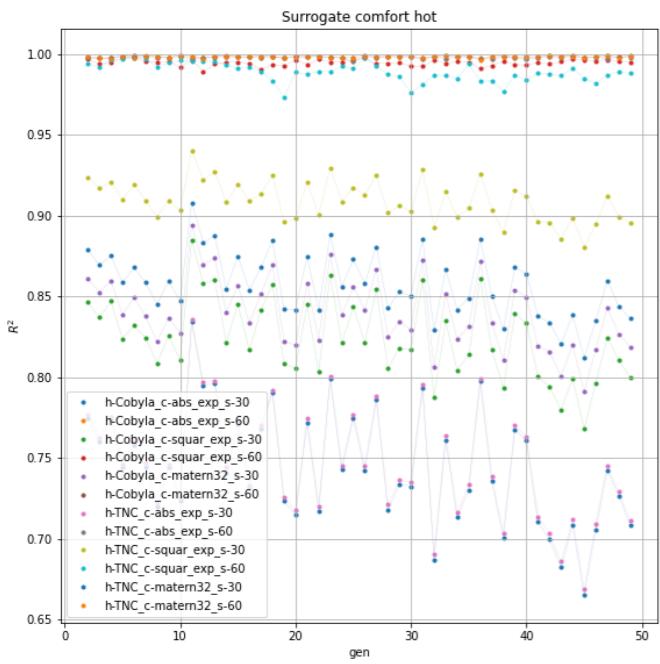


Figure 5.1: Evolution of R^2 over the generations for several hyperparameter settings

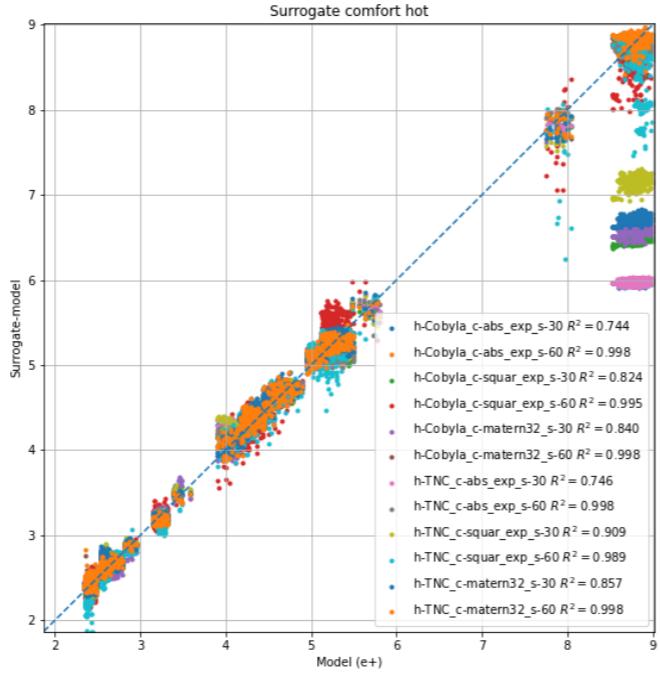


Figure 5.2: Kriging against EnergyPlus for hot seasonal comfort computation

Figure 5.1 demonstrates that for some parameter settings, the expected effect of a performance loss along the generation is present. For this parameter settings, the Kriging process captures the special features of the first generation instead of capturing the generalities. Nevertheless, for particular parameter settings, such as the following configuration : [Optimiser : Cobyla, correlation function : abs-exp, training size : 60] (orange), the surrogate model does not suffer from performance loss along the generations. Therefore, model enrichment is not necessary. Figure 5.2 illustrates the comparison between the results computed with *EnergyPlus* (X axis) and the different surrogate models (Y axis). The first bisector is also displayed in blue dashed line. On this second figure, the dispersion³ and the bias⁴ of the different models can be observed. As the building variants are compared during the optimization, it is crucial to minimize the dispersion. Likewise, it is necessary to control the bias in order to give a fair estimation of the comfort.

Finally, the models are ranked with the $score_{KRG}$ described section 4.4.2. The selected models for the hot and cold seasonal comfort are described in the following table :

model	size	sampling	optimiser	corr func	AAE_{avg}	MAE_{avg}	R^2_{avg}
hot	60	random	Cobyla	sqr-exp	0.97	0.13	0.99
cold	60	random	Cobyla	abs-exp	0.42	0.09	0.92

Table 5.1: Hyperparameter settings selected for the cold and hot comfort surrogate-model (average over 60 trainings and two different LHS initializations).

Regarding the results, using 60 samples (in comparison with 30 samples) allows to have better average for the indicators and also to significantly minimize the variation between the different trainings. Likewise, random sampling give better overall results for the $score_{KRG}$, however the uniform sampling allows the smallest variation between the trainings. Both selected models exhibit satisfying results with, on average, an excellent AAE of ~ 0.1 °C and a MAE below 1 °C. Given that the neutral zone is 5°C wide, these performances are more than satisfactory to use these surrogate models instead of *EnergyPlus* for the computation of the comfort objectives.

5.2 Genetic Algorithm

Several parameters are tested in order to identify the most efficient algorithm :

- **population size** : 300 or 150.
- **The number of generation** : 25 or 50.
- **crossover** : one point, two point, uniform.
- **The mutation probability rate MUTPB** : 0,1 or 0,2.

For each hyperparameter setting, 30 optimizations are operated to use several seeds for the LHS initialization on G , with the aim to work on average behaviours. The results showed that each crossover has pros and cons. Therefore, instead of using just one crossover, a combination of the three crossovers is used. OnePoint, TwoPoint and Uniform crossovers are used, the probability of using one of the crossovers is $\frac{1}{3}$. This combination allows better performances. On average, s_H (hypervolume size), s_D (maintained diversity) and all the s_{o_j} (minimization of the objectives) are better. Only, s_{NIR} (produced diversity) is slightly worse, going from 21.13%

³The dispersion is a random error (i.e. related to the randomness of the draw for example) called sampling fluctuation.

⁴Bias is a systematic error.

(one point) to 20.99% (mix).

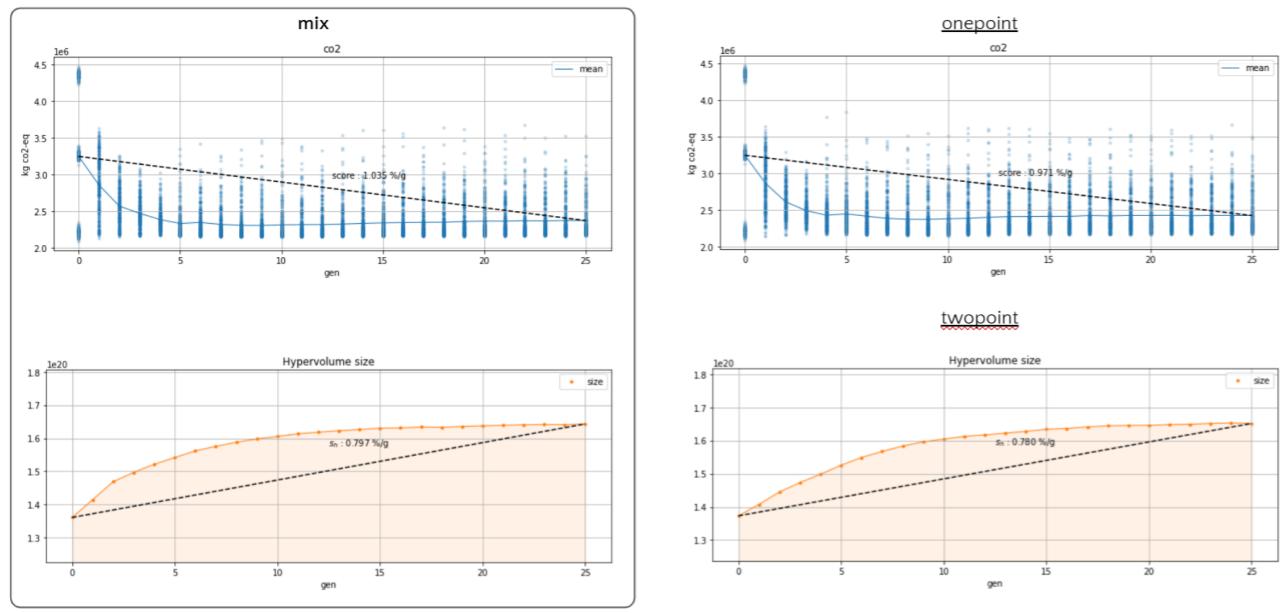


Figure 5.3: Comparison of the crossovers : Mix against OnePoint for CO₂ minimization, Mix against TwoPoint

for Hypervolume size.

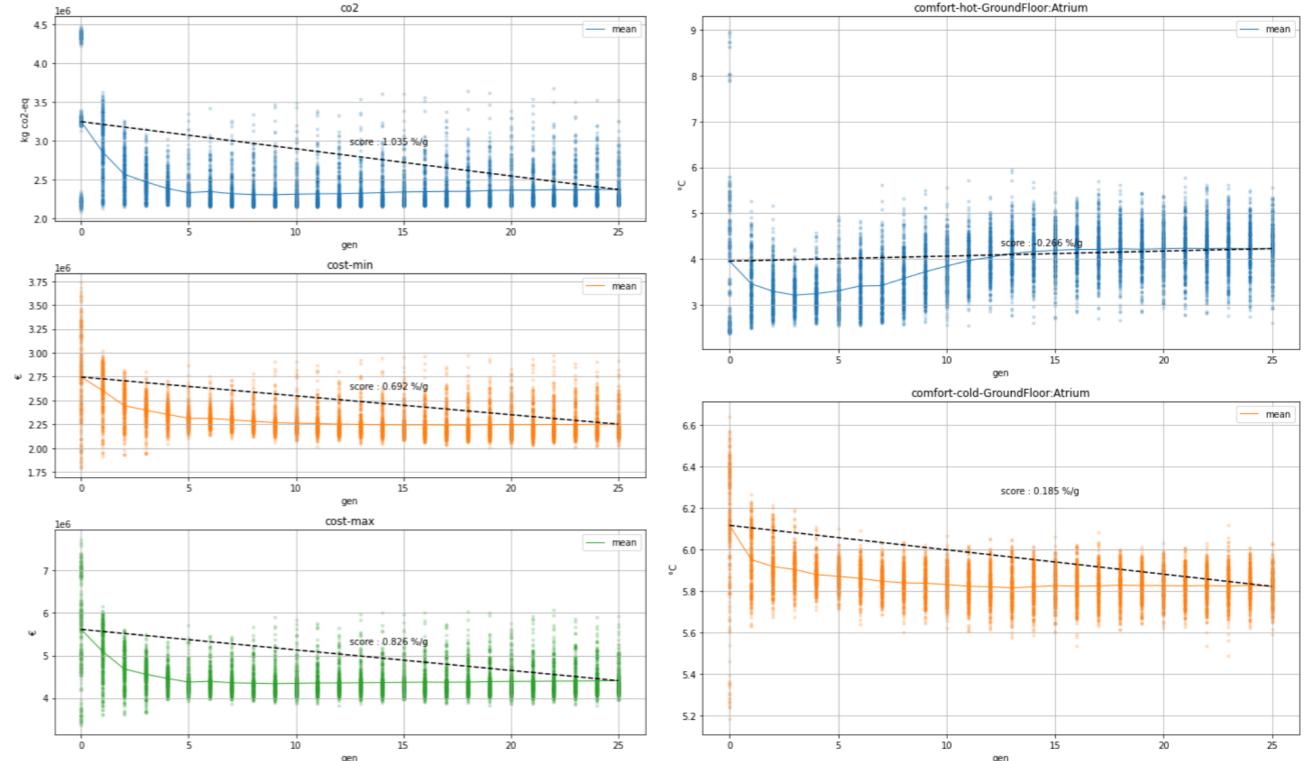


Figure 5.4: Objectives monitoring : GHG emissions, minimal and maximal costs, hot and cold comforts

On figure 5.3 above, every blue point on the Bray-Curtis dissimilarity plots is a comparison between two sequences, the blue line is the average per generation and the black dashed line is the minimization score (s_{co_2}) of this objective. For the hypervolume size plots, the hypervolume size is measured at each generation. The black dashed line is the s_H indicator. This figure shows that the combination of the three crossovers called 'mix' is better for CO₂ minimization and evolution of the hypervolume size. Other parameters, such as the population size, have to be well tuned. For instance, a genetic algorithm working with 150 individuals per generation will converge in more generations than one working with 300 individuals.

The retained setting is described in the table below :

pop size	init	crossover	nbr gen	MUTPB	avg s_o	s_H	s_D	s_{NIR}
300	LHS	mix	25	0.2	0.495	0.797	0.120	20.992

Table 5.2: Hyperparameter settings for multiploid genetic algorithm

Finally, all the indicators of the best configuration are displayed in the next figures.

Figure 5.4 shows the evolution of each objective along the generations. On a plot : one point is the value for one building variant, the continuous line is the average over the population, and the black dashed line depicts the minimization score for each objective. One interesting phenomenon on this figure is that the average population temperature for the hot comfort is increasing, whereas this temperature should be minimized. In fact, the algorithm minimizes the combination of 5 objectives, therefore it is totally understandable to make compromises in order to search the global minimum of this combination. In addition, the average temperature might increase, but it is only one indicator about the evolution of the population. One blue point located under the average temperature (blue line) could be part of one of the best solutions found.

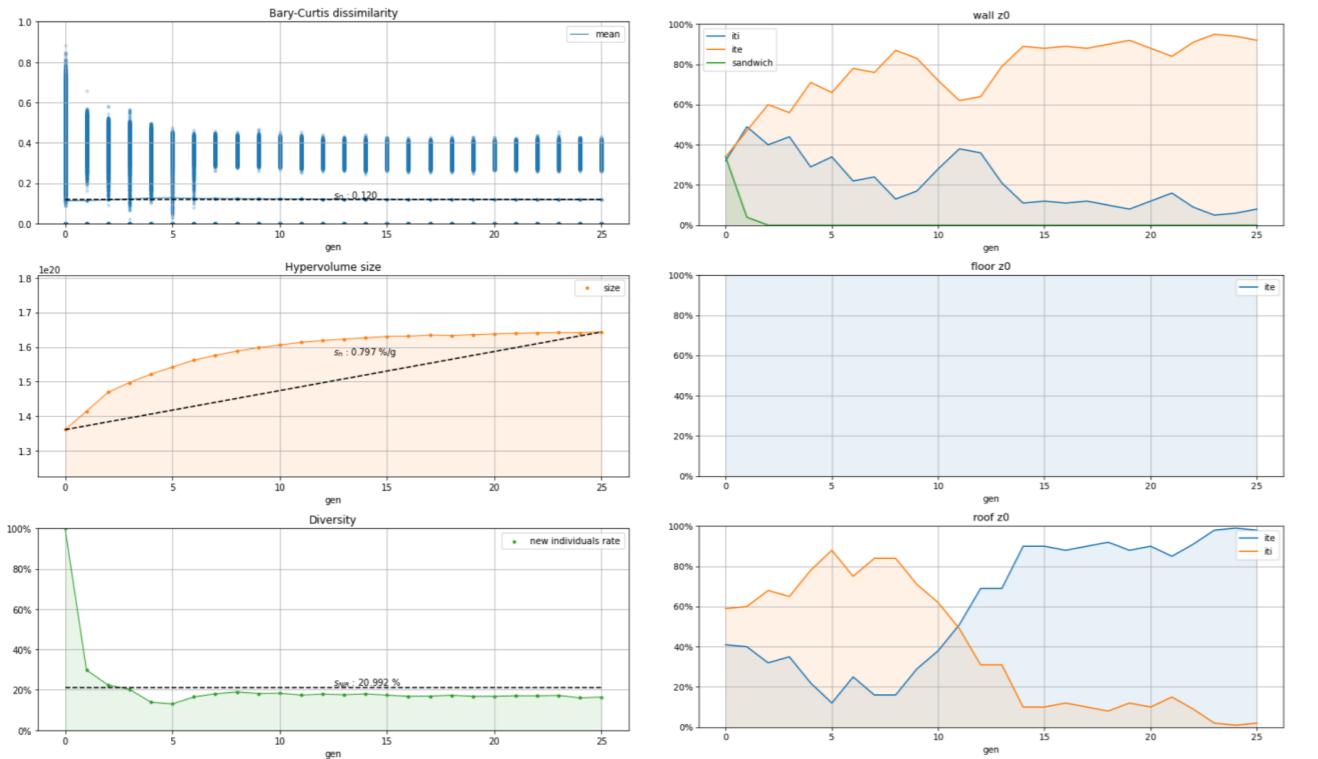


Figure 5.5: Indicators and alleles' dominance

Figure 5.5 shows the indicators on the left and the dominance of the alleles on the right. The indicators show that firstly, the diversity is maintained : The Bray Curtis dissimilarity points on the figure stay around 0.4, and there is no decrease. Secondly, it shows that the searching space is increasing faster during the first generation. In addition, the shape of the curve (flat) since the 20th generation indicates that the convergence is achieved. Finally, the rate of new individuals shows that during all the optimization, new building variants are produced thanks to certain evolutionary mechanisms (mutation, crossover). On the right side of the figure, three plots shows which allele and thus which wall system establish oneself. For instance, the first plot on the right indicates that exterior insulation (the orange curve labelled as ite) dominates the other wall system. At the 25th generation, exterior insulation represent almost 100% of the alleles for the wall system used for the walls as well as the roofs. This dominance scheme is another sign that the convergence is achieved.

Chapter 6

Results

6.1 Study case : The Atrium

The developed algorithm is tested on a simple case : The Atrium. This medium-sized building, almost only composed with windows, has 3 floors. The algorithm is tested with one zone of allocation for the variables. Parallel coordinates are used to visualize the Pareto Front¹. Wall systems, materials and objectives are displayed. One path corresponds to one building variant. Only the materials and wall systems composing the best building variants are shown.

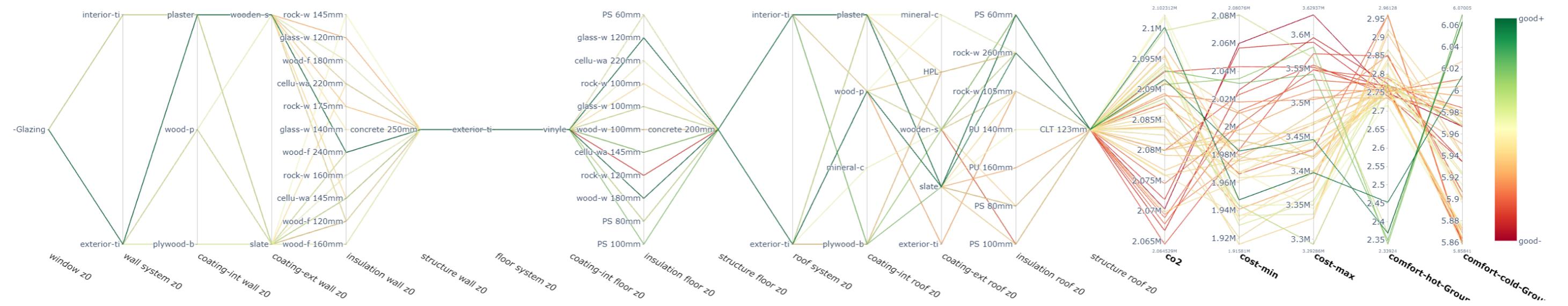


Figure 6.1: Visualization of the 50 bests building variants

¹Non dominated best building variants

From the figure, information can be easily collected to reassemble the different wall systems used for each type of element. For instance, the greener path on the figure details the following configuration for the building :

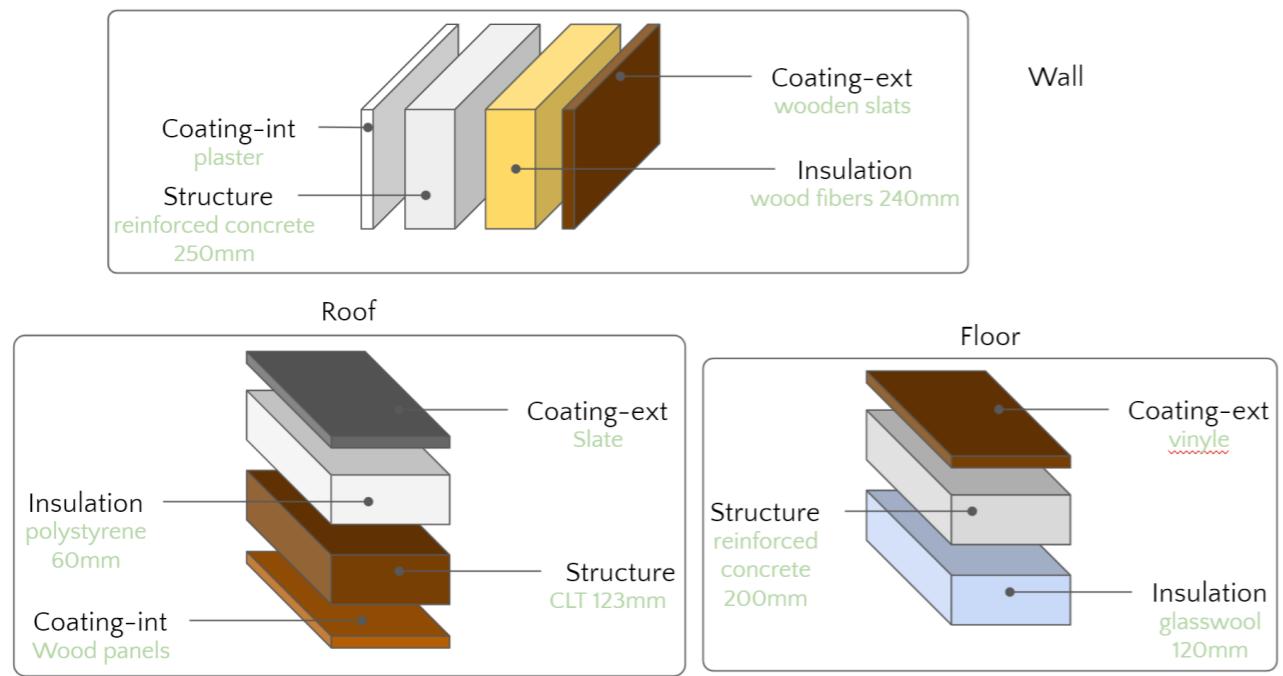


Figure 6.2: Best building variant configuration.

The structure of the building is made of concrete and the roof is made of Cross-laminated timber (CLT). Wood fibers are used for wall insulation, glass wool is used for the floor insulation and polystyrene is used for the roof insulation. The exterior appears to be in wood, with a roof in slate. The interior is whether in plaster or wood panels. Triple glazing is operated. This configuration is similar from building constructed today. In terms of performance, the material and implementation cost is within the interval [1.95, 3.4] M€, the temperature difference between the PET and the median value of the neutral zone is 2.45°C for the hot comfort and 6.01°C for the cold comfort. Therefore, the neutral zone is achieved for the hot comfort but not for the cold comfort (the neutral zone is 5°C wide). As depicted in figure 6.3, the building is essentially composed by windows which feature important thermal bridges and also a worse insulation in comparison with walls. The cold comfort is then hardly achieved. Concerning the GHG emissions, it corresponds to 2868 kg co2-eq/m² FA² which is enormous in comparison with the carbon level 1 of E+C- regulation which is 1650 kg co2-eq/m² FA. However, the Atrium is a particular building with a small floor area surface and secondly, the algorithm optimizes the combination of the five objectives. Therefore, to achieve one carbon level within the optimization, penalties have to be set for the building not complying with the carbon level.

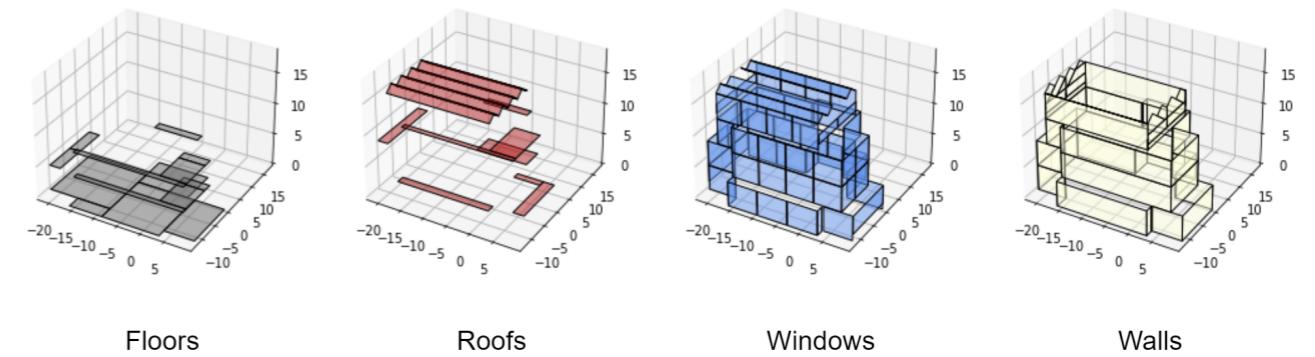


Figure 6.3: Atrium breakdown.

²Floor Area.

the beginning of the project in order to design sustainable, comfortable and affordable buildings.

Chapter 7

Conclusion

To conclude, I will summarize my work, give the limits of the algorithm and talk about research & application.

Firstly, given the optimization framework and the database created by the different AREP's department, I decided to use wall systems and materials as variables for the optimization. Since the variables are discrete, a non-derivative based algorithm is used. According to the scientific literature on building optimization, genetic algorithm was chosen to perform the minimization of the objectives : GHG emissions, comfort gap and cost.

The algorithm employed is based on the Non-dominated Sorting Genetic Algorithm II (NSGA-II) described by Deb and has the specificity to use a multiploid representation for individual (building variant). This particular representation has the advantage to ease the manipulation of the variables within the genetic algorithm. In addition, it operates different alleles that allows to establish competition between multiple wall systems for one type of element inside the building. The convergence of this algorithm is monitored by several indicators. Finally, a surrogate model based on a Gaussian process has been elaborated to compute the comfort objectives. This surrogate model allows to speed up the optimization by 10 times.

The convergence, the performances and the results of the optimization algorithm developed are satisfactory. However, the algorithm remains in the research phase and the proposed results constitute a proof of concept. Indeed, the algorithm lacks from different features to be fully operational or to meet the demand. For example, the energy consumption of the building is not an objective yet of the optimization. Likewise, the algorithm have a limited operational framework. For instance, the GHG emissions from the utilization of the building are not taken into account while they constitute a major part of the GHG emissions of the building sector.

Finally, the implementation of the multiploidy shows that this kind of representation is convenient in very particular cases. The complex encoding system allows using various genetic algorithms without any major changes. In addition, Kriging, well implemented, can safely replace software that operates dynamic thermal simulation. Concerning the application of such algorithms : it can help to guide the architect and engineer at

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Appendix A

Hot Surrogate Model - hyperparameters tuning

LHS size on G	sampling on I	sampling size	func corr	optimiser	R ²	MSE	AAE	MAE	R ² _std	MSE_std	AAE_std	MAE_std	score
150	0	30	0	0	0.903455	0.413867	0.261753	1.783252	0.114300	0.491151	0.146885	1.072766	0.000014
150	1	30	0	0	0.920417	0.341917	0.238698	1.747658	0.096813	0.416558	0.142781	1.027127	0.000029
150	0	60	0	0	0.986809	0.056773	0.106367	0.678754	0.037570	0.161483	0.063619	0.576372	0.028314
150	1	60	0	0	0.975999	0.103223	0.130566	0.937526	0.051671	0.221658	0.089834	0.775792	0.002532
150	0	30	1	0	0.963184	0.159088	0.187367	1.209716	0.055158	0.238696	0.098701	0.751861	0.000715
150	1	30	1	0	0.951415	0.209124	0.201262	1.314022	0.082326	0.354392	0.126343	0.880495	0.000139
150	0	60	1	0	0.989660	0.044719	0.133852	0.977597	0.007586	0.032920	0.032960	0.537539	1.000000
150	1	60	1	0	0.989395	0.045399	0.128102	0.918282	0.014995	0.063657	0.038069	0.421490	0.316472
150	0	30	2	0	0.945331	0.234094	0.209120	1.323164	0.069738	0.299215	0.123372	0.846979	0.000175
150	1	30	2	0	0.911388	0.378713	0.264363	1.711162	0.089374	0.382824	0.138137	0.934717	0.000032
150	0	60	2	0	0.984966	0.064799	0.128628	0.845024	0.032760	0.140803	0.061962	0.562365	0.022763
150	1	60	2	0	0.977567	0.096379	0.148913	0.958379	0.042115	0.180721	0.079862	0.641219	0.004783
150	0	30	0	1	0.932088	0.290712	0.220151	1.549880	0.082359	0.352713	0.132386	0.971949	0.000066
150	1	30	0	1	0.872874	0.546291	0.295149	2.099811	0.120509	0.518316	0.166311	1.171684	0.000006
150	0	60	0	1	0.978160	0.094389	0.124131	0.822481	0.051564	0.222642	0.086727	0.702461	0.003797
150	1	60	0	1	0.973689	0.113016	0.139087	0.959527	0.051884	0.222471	0.088114	0.812817	0.001968
150	0	30	1	1	0.958319	0.178242	0.199315	1.232558	0.063089	0.270496	0.101358	0.807918	0.000410
150	1	30	1	1	0.945839	0.234383	0.227718	1.415822	0.076776	0.332641	0.120732	0.899549	0.000118
150	0	60	1	1	0.984722	0.065095	0.137733	0.978792	0.024904	0.105515	0.053339	0.486508	0.043053
150	1	60	1	1	0.983164	0.071952	0.149524	1.004373	0.027314	0.115835	0.057049	0.515423	0.025588
150	0	30	2	1	0.948262	0.221954	0.205737	1.294723	0.066887	0.286548	0.115835	0.831998	0.000227
150	1	30	2	1	0.913466	0.369758	0.263611	1.675612	0.098502	0.421815	0.147198	0.973592	0.000025
150	0	60	2	1	0.987909	0.052074	0.123492	0.772217	0.026895	0.116074	0.052609	0.444903	0.071231
150	1	60	2	1	0.984160	0.068046	0.130165	0.854867	0.036903	0.158943	0.065925	0.542374	0.016214
300	0	30	0	0	0.887861	0.483304	0.269893	2.082349	0.122838	0.528903	0.166464	1.129578	0.000007
300	1	30	0	0	0.882500	0.505261	0.275717	2.192292	0.118701	0.511545	0.163557	1.048064	0.000007
300	0	60	0	0	0.951124	0.211000	0.155567	1.214821	0.087144	0.375508	0.129330	1.064611	0.000139
300	1	60	0	0	0.960830	0.169859	0.145875	1.129711	0.073666	0.318982	0.111604	0.953326	0.000359
300	0	30	1	0	0.936742	0.228146	0.228146	1.438601	0.081035	0.351575	0.117980	0.936889	0.000086
300	1	30	1	0	0.891451	0.466532	0.280970	1.875725	0.145288	0.623725	0.168661	1.233811	0.000005
300	0	60	1	0	0.964858	0.151497	0.169877	1.274651	0.066018	0.283920	0.103187	0.899298	0.000442
300	1	60	1	0	0.966561	0.144752	0.162608	1.276032	0.070088	0.303183	0.100501	0.821603	0.000480
300	0	30	2	0	0.890584	0.472201	0.286249	1.901441	0.104721	0.450234	0.153239	1.052229	0.000012
300	1	30	2	0	0.927457	0.313754	0.237191	1.585815	0.085090	0.366964	0.134539	0.928519	0.000054
300	0	60	2	0	0.976323	0.102265	0.138873	0.924229	0.056121	0.243086	0.090666	0.685476	0.002295
300	1	60	2	0	0.970983	0.124484	0.153545	1.031738	0.049624	0.213061	0.093386	0.716936	0.001820
300	0	30	0	1	0.864439	0.584053	0.303988	2.303634	0.120872	0.520705	0.163066	1.024489	0.000005
300	1	30	0	1	0.876949	0.528925	0.291247	2.185673	0.123957	0.532909	0.168378	1.042665	0.000006
300	0	60	0	1	0.968455	0.135579	0.134006	1.005422	0.066719	0.286677	0.102606	0.925888	0.000763
300	1	60	0	1	0.940858	0.254988	0.178169	1.406011	0.089655	0.385759	0.135981	1.085852	0.000075
300	0	30	1	1	0.927396	0.312329	0.246907	1.662499	0.091552	0.394281	0.143092	0.990103	0.000037
300	1	30	1	1	0.899156	0.436458	0.266358	1.851304	0.148714	0.643609	0.168090	1.214827	0.000006
300	0	60	1	1	0.980804	0.082485	0.152367	1.339999	0.028428	0.121854	0.062896	0.882663	0.007923
300	1	60	1	1	0.961773	0.165167	0.188225	1.424008	0.059508	0.256692	0.102217	0.867431	0.000420
300	0	30	2	1	0.894207	0.455818	0.278744	1.933316	0.114285	0.491377	0.151226	1.047200	0.000011
300	1	30	2	1	0.918752	0.348193	0.255171	1.714537	0.083077	0.356858	0.138898	0.929964	0.000041
300	0	60	2	1	0.980398	0.084627	0.139070	0.882087	0.036895	0.158728	0.071123	0.560428	0.010585
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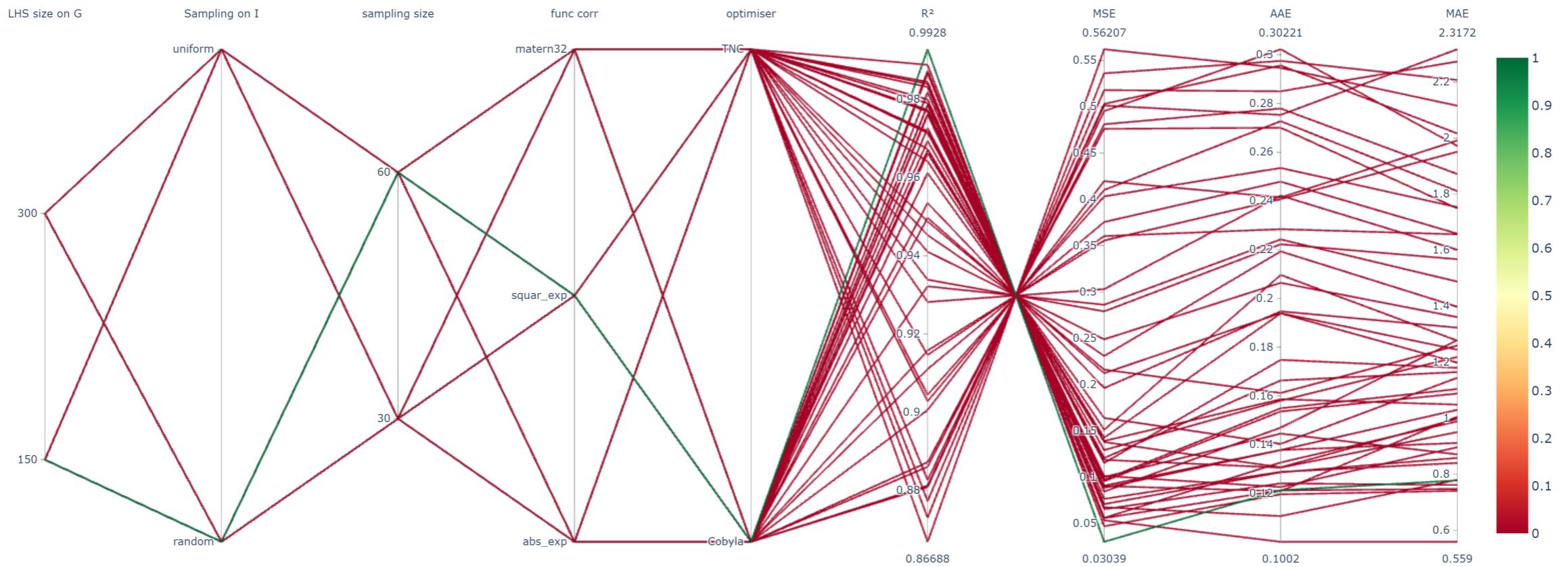


Figure A.1: Hyperparameter tuning - hot comfort, seed 2 for LHS.

Appendix B

Cold Surrogate Model - hyperparameters tuning

LHS size on G	sampling on I	sampling size	func corr	optimiser	R ²	MSE	AAE	MAE	R ² _std	MSE_std	AAE_std	MAE_std	score
150	0	30	0	0	0.837063	0.028776	0.117116	0.528457	0.166330	0.029377	0.037479	0.175660	0.001265
150	1	30	0	0	0.830424	0.029948	0.118804	0.530514	0.189685	0.033499	0.041950	0.193678	0.000738
150	0	60	0	0	0.919046	0.014297	0.090780	0.423977	0.028367	0.005010	0.013004	0.078214	1.000000
150	1	60	0	0	0.915622	0.014902	0.093163	0.417147	0.034165	0.006033	0.015184	0.088476	0.494194
150	0	30	1	0	0.752827	0.043655	0.143562	0.680672	0.179812	0.031755	0.042890	0.189571	0.000329
150	1	30	1	0	0.791236	0.036871	0.132589	0.648023	0.156773	0.027686	0.037018	0.191562	0.000702
150	0	60	1	0	0.809290	0.033569	0.131028	0.696187	0.093401	0.016493	0.026895	0.180240	0.003065
150	1	60	1	0	0.833117	0.029472	0.122709	0.608317	0.115897	0.020468	0.031413	0.183608	0.002396
150	0	30	2	0	0.822255	0.031388	0.21671	0.569436	0.165354	0.029193	0.041452	0.172953	0.000946
150	1	30	2	0	0.772652	0.040150	0.134166	0.630991	0.211660	0.037376	0.047779	0.208782	0.000249
150	0	60	2	0	0.872495	0.022519	0.110940	0.556779	0.055440	0.009790	0.017710	0.137655	0.041029
150	1	60	2	0	0.855306	0.025556	0.114376	0.563790	0.093910	0.016587	0.027781	0.169606	0.006120
150	0	30	0	1	0.834823	0.029170	0.114648	0.522405	0.198457	0.035048	0.044761	0.195895	0.000678
150	1	30	0	1	0.746976	0.044687	0.134015	0.64814	0.279336	0.049332	0.059493	0.253709	0.000084
150	0	60	0	1	0.911649	0.015603	0.093383	0.424937	0.060241	0.010636	0.019161	0.103507	0.100278
150	1	60	0	1	0.908317	0.016192	0.095851	0.445035	0.036765	0.006493	0.016244	0.092714	0.316591
150	0	30	1	1	0.704794	0.052139	0.157135	0.731203	0.178331	0.031494	0.041859	0.195576	0.000221
150	1	30	1	1	0.675575	0.057296	0.162851	0.750547	0.218870	0.038655	0.050582	0.217350	0.000090
150	0	60	1	1	0.813548	0.032928	0.130037	0.646575	0.124849	0.022050	0.031871	0.185309	0.001564
150	1	60	1	1	0.767469	0.041067	0.142795	0.719243	0.133521	0.023580	0.034923	0.190377	0.000752
150	0	30	2	1	0.776483	0.039475	0.135036	0.643692	0.195374	0.034502	0.045674	0.202020	0.000315
150	1	30	2	1	0.765424	0.041424	0.138360	0.613638	0.203257	0.035894	0.047249	0.196966	0.000277
150	0	60	2	1	0.855961	0.025441	0.114382	0.583138	0.081235	0.014348	0.024384	0.165391	0.009287
150	1	60	2	1	0.864428	0.023943	0.112762	0.564598	0.078986	0.013948	0.023366	0.171187	0.011138
300	0	30	0	0	0.820204	0.031754	0.116579	0.504104	0.227633	0.040202	0.051413	0.217416	0.000372
300	1	30	0	0	0.844623	0.027442	0.110912	0.504568	0.165968	0.029315	0.038922	0.203454	0.001236
300	0	60	0	0	0.900257	0.017617	0.092012	0.417202	0.117041	0.020673	0.029108	0.160037	0.010223
300	1	60	0	0	0.902796	0.017169	0.093172	0.422590	0.081851	0.014460	0.023115	0.129872	0.032533
300	0	30	1	0	0.782512	0.038408	0.134020	0.620066	0.184906	0.032655	0.044044	0.188394	0.000424
300	1	30	1	0	0.700496	0.052895	0.154610	0.694693	0.238521	0.042122	0.052938	0.226953	0.000088
300	0	60	1	0	0.824332	0.031025	0.123369	0.638644	0.128492	0.022696	0.032492	0.179529	0.001716
300	1	60	1	0	0.810556	0.033455	0.129542	0.634643	0.136480	0.024100	0.035869	0.202395	0.001068
300	0	30	2	0	0.808874	0.033755	0.126905	0.599014	0.150163	0.026517	0.037090	0.196144	0.000955
300	1	30	2	0	0.811311	0.033326	0.127475	0.577308	0.134032	0.023672	0.036071	0.178248	0.001403
300	0	60	2	0	0.876790	0.021759	0.106055	0.533416	0.096037	0.016957	0.024881	0.152354	0.009987
300	1	60	2	0	0.871632	0.022669	0.109951	0.520512	0.076476	0.013506	0.020914	0.142844	0.018844
300	0	30	0	1	0.802058	0.034959	0.121797	0.569915	0.198271	0.035018	0.044770	0.235987	0.000390
300	1	30	0	1	0.851956	0.026146	0.109718	0.501770	0.157490	0.027813	0.036982	0.180538	0.001751
300	0	60	0	1	0.913864	0.015212	0.090156	0.404926	0.068973	0.012178	0.021886	0.114975	0.067384
300	1	60	0	1	0.872097	0.022590	0.101538	0.473061	0.131801	0.023280	0.033460	0.183524	0.003692
300	0	30	1	1	0.697525	0.053419	0.153455	0.783194	0.217155	0.038349	0.046852	0.253318	0.000095
300	1	30	1	1	0.692315	0.054344	0.157185	0.762871	0.191419	0.033807	0.043426	0.215547	0.000152
300	0	60	1	1	0.807942	0.033921	0.130398	0.662712	0.116368	0.020554	0.030942	0.187572	0.001718
300	1	60	1	1	0.783588	0.038215	0.133423	0.6560348	0.169904	0.030000	0.040094	0.220263	0.000454
300	0	30	2	1	0.745475	0.044948	0.141210	0.669540	0.209788	0.037048	0.047924	0.211312	0.000193
300	1	30	2	1	0.779860	0.038876	0.132511	0.604760	0.186307	0.032903	0.043555	0.215265	0.000377
300	0	60	2	1	0.879904	0.021210	0.107570	0.506169	0.057311	0.010122	0.019456	0.114779	0.050905
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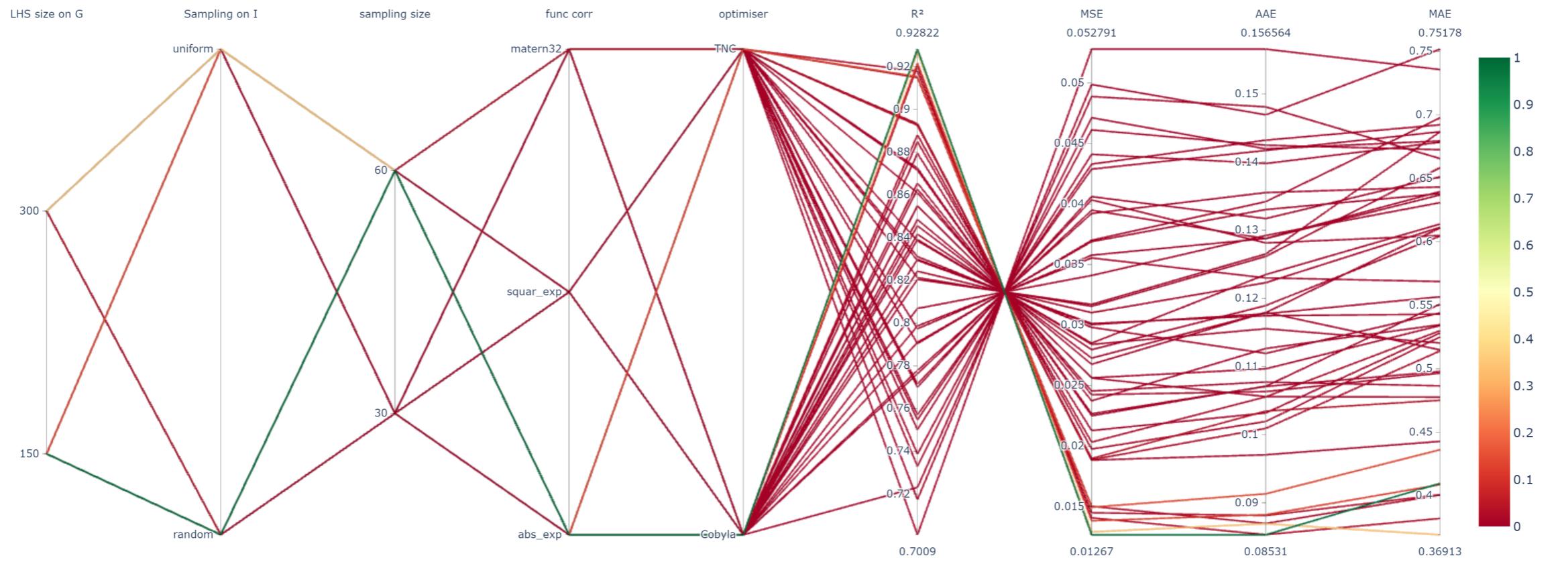


Figure B.1: Hyperparameter tuning - cold comfort, seed 2 for LHS.