

ABSTRACT

ANDERSEN, BRIAN DOUGLAS. Development and Assessment of Multi-Objective Optimization Utilizing Genetic Algorithms for Nuclear Fuel Assembly Design. (Under the direction of Dr. David Kropaczek.)

MOOGLE, Multi-Objective Optimization utilizing Genetic algorithms for Lattice Enhancement, is a new genetic algorithm developed for the optimization of PWR and BWR fuel assemblies. MOOGLE advances the field of nuclear fuel management by using three-dimensional fuel rod types as the decision variables within the assembly optimization, instead of the standard two-dimensional pin cell lattice. Using fuel rod types as the genes within the genetic algorithm optimization framework allows whole assemblies to be optimized at once, rather than focusing on two-dimensional fuel lattices. Additionally, it allows core designers to easily see the economic tradeoffs between assembly performance and manufacturability through the addition of objective functions or constraints related to characteristics of the fuel rod types within the optimization, such as the number of unique rod types allowed in optimized designs.

A novel feature of the MOOGLE algorithm includes the use of a desired solution space and binning procedure to store valuable optimization solutions. MOOGLE additionally uses a tournament selection method for determining which solutions will be selected as the parents of the next generation. To preserve solution niching, solutions undergoing crossover seek to mate with solutions composed of similar rod types.

The algorithm was tested by performing a sensitivity analysis on the various parameters involved in the optimization such as mutation rate, population size, and parent selection weights. The sensitivity analysis was performed by optimizing a PWR fuel assembly with the objectives of minimizing peak pin power, minimizing peak reactivity, and maximizing end of cycle reactivity. The algorithm also demonstrated the ability to show the tradeoffs between the addition of rod types

by comparing the results of optimizations using IFBA, gadolinium, and a combination of IFBA, as well as gadolinium for a PWR fuel assembly in octant symmetry with the same objectives as the sensitivity analysis. Finally, to demonstrate the MOOGLE's ability to optimize entire fuel rod bundles, a whole BWR fuel bundle was optimized using MOOGLE.

Cases using the PWR run time averaged between 6 and 8 hours. The first BWR optimization case ran in four hours. The second BWR optimization case took between one and five days to run depending on the number of rod types used in the optimization. The reason for the long length of time to optimize the second BWR case is due to the length of time required to evaluate multiple Casmo4e problems for a single problem solution. All optimization cases were run on the RDFMG cluster at North Carolina State University. The RDFMG cluster uses six processing nodes equipped with a QUAD AMD Opteron 6320 HGST 3.5" 6TB SAS 6 GB/s, Kingston 16x 8GB 1600 MHz DDR3 and 40 GB QDR Infiniband.

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Development and Assessment of Multi-Objective Optimization Utilizing Genetic Algorithms for
Nuclear Fuel Assembly Design.

by
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DEDICATION

For my parents, Catherine and Douglas. Thank you for all of your love and support over the many years.

BIOGRAPHY

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LIST OF ACRONYMS AND ABBREVIATIONS

MWD/MTU	Mega-Watt day per metric ton uranium
U.S. NRC	United States Nuclear Regulatory Commission
PWR	Pressurized water reactor
BWR	Boiling water reactor
IFBA	Integral fuel burnable absorber
GA	Genetic algorithm
MOO	Multi objective optimization
FORMOSA-P	Fuel Optimization for Reloads – Multiple Objectives by Simulated Annealing - PWR
NCSU	North Carolina State University
PPF	Power Peaking Factor
BOL	Beginning of Life
EOC	End of Cycle
CPR	Critical Power Ratio
SA	Sensitivity Analysis
BP	Burnable Poison

Chapter 1 INTRODUCTION

1.1 Overview

Nuclear fuel management is the production, use, and disposal of fuel used by nuclear reactors. A principle focus of the field is the economical design of nuclear fuel assemblies that meet the operational and safety constraints of nuclear reactors. These designs must incorporate factors such as higher burnups, effective reactivity management, and the utilization of standardized fuel rod types in order to create a wide array of fuel bundles. Incorporation of these factors improves the cost of fuel bundles and nuclear reactors [1]. Safety constraints include limits on $F\Delta H$ and Fq , the radial and axial power peaking, as well as limits on core reactivity. Other safety constraints include maintaining safety margins for issues such as minimum departure from nucleate boiling and dryout [1]. Often, satisfying these safety constraints forces sacrifices in cost factors. Therefore, core designers must strike the right balance; designing fuel that minimizes manufacturing costs, maximizes profits, and meets all safety constraints.

The physical design of fuel assemblies does much for minimizing manufacturing costs and meeting safety constraints, however, these components are fixed. In order to maximize profits and ensure that safety constraints are met, core designers focus on the radial and axial distribution of fuel pins with varying enrichments [1]. Enrichment is the percentage of Uranium-235 contained in the fuel. Enrichments are limited to values less than 5% [2]. Although varying enrichments are used to control the power as much as possible, fresh fuel assemblies have a high reactivity. [1] Reactivity is the amount by which the nuclear multiplication factor, K , differs from a value of unity. New fuel assemblies have a high reactivity, valuable for powering a nuclear chain reaction for an extended period of time. The core reactivity however must be zero to maintain the core

multiplication factor at unity [3]. This means that methods must be implemented to control this reactivity.

The first method for controlling reactivity is the use of poisons. Reactivity poisons in a pressurized water reactor (PWR) core include control rods in the reactor core, chemical shim added to the reactor moderator, and burnable poisons within fuel rods in the assemblies. Boiling water reactors (BWR) rely solely on control rods and burnable poisons in the fuel bundle. Both BWRs and PWRs use gadolinium as a burnable poison. Gadolinium is placed in select fuel rods and uses set combinations of Gd_2O_3 - UO_2 to form the control material [1]. IFBA, a coating of zirconium diboride (ZrB_2) applied to the outside of fuel pellets, is another burnable poison specific to PWRs that was developed by Westinghouse for the VANTAGE-5 fuel [4]. Burnable poison placement is vital for fuel assembly design, as the same poison in different locations within a fuel assembly will have drastically different effects on pin powers and reactivity within the fuel assembly. Additionally, the cost of burnable poisons makes it desirable to use as little as possible to achieve the desired decrease in reactivity [1].

The second method for controlling reactivity is the use of complicated core loading patterns, such as the one shown in Figure 1-1, to utilize already “burnt” fuel with lower excess fuel reactivity in combination with new fuel to reduce the overall core average excess reactivity. Greater flexibility in the number of assemblies used in the core allows for greater management of the radial reactivity peaking and improves the burnup of all fuel used in the reactor core. Greater numbers of fuel assemblies can come at a steep price however as the numbers of specific rod types and enrichments increases.

Designing a single, economical fuel assembly for a nuclear reactor that meets the operational and safety constraints is challenging. Designing multiple economically viable fuel

assemblies increases the difficulty further. This difficulty motivates the proposal of a new genetic algorithm, MOOGLE, for the design of nuclear fuel assemblies.

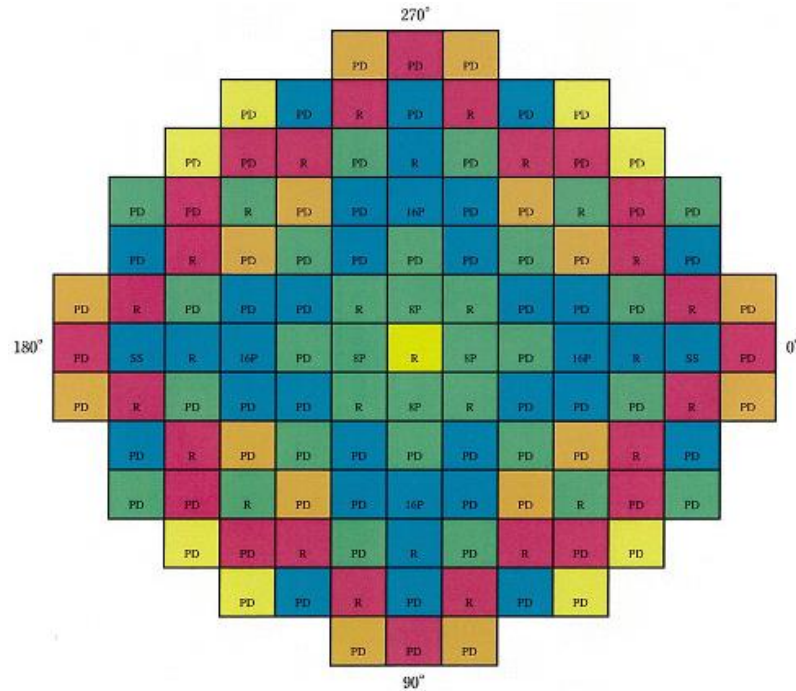


Figure 1-1: Fuel loading pattern for a nuclear reactor core [5].

MOOGLE performs multiple objective optimizations for BWR and PWR fuel assemblies to design a suite of PWR and BWR fuel assemblies that meet design and safety constraints, while maintaining manufacturing feasibility. This allows for greater flexibility in nuclear core fuel reload patterns. MOOGLE improves upon currently existing optimization methods by utilizing fuel rod types, rather than pin types, as the decision variable. The use of fuel rod types facilitates the analysis of manufacturing costs versus fuel performance improvements through the addition of rod types, something that isn't possible in codes that only optimize based upon fuel enrichment. Additionally, the use of fuel rod types as the decision variable allows for 3D models of fuel assemblies to be utilized. This improves upon many currently existing optimization codes that only improve a 2D fuel lattice.

1.2 Literature Review

The survey of previous work shows genetic algorithms are not new to nuclear fuel management. Fuel lattices for PWRs and BWRs have been optimized using a variety of methods, including genetic algorithms. Three-dimensional assemblies have also been optimized.

Martin-del-Campo et. al. developed a genetic algorithm capable of optimizing the enrichments and gadolinium concentrations in a BWR radial lattice. Their optimization sought to: (1) minimize the average lattice enrichment, (2) achieve an average gadolinium concentration $G(x)$ equal to a target G_{target} , (3) achieve an infinite multiplication factor k_{inf} equal to the target $K_{\text{inf target}}$, and (4) to attain a power peaking factor (PPF) lower than a limit value PPF_{max} , and if possible, to minimize it [6]. Information on k_{inf} and PPF were obtained using the neutronic simulator Helios developed by Studsvik Scandpower [7].

A multi-objective fitness function determined the value of different solutions in their optimization. Their fitness function is presented in Equation 1.1 [6]. The fitness function used by Martin-del-Campo et al is complex, involving finally tuned weights and sub equations to measure the fitness of each solution in the optimization. The use of fitness functions such as these is undesirable, because they essentially limit the algorithm to only being able to solve one problem. Should a new optimization objective be introduced, the entire fitness function must be re-tuned.

$$F(x) = C + w_E * E(x) + w_G * \Delta G(x) + w_p * (PPF(x) - PPF_{\text{max}}) + w_k * D_k(x) \quad 1.1$$

Castillo, et. al. performed a comparison of several artificial optimization methods [8]. They sought to optimize the gadolinium and enrichment distributions in a fuel lattice for a boiling water reactor. The methods that were compared were Ant Colony Systems, Artificial Neural Networks, Genetic Algorithms, Greedy Search, and hybrid Path Relinking. For the comparison, a common multiple objective optimization (MOO) cost function was shared between all optimization

methods. Their results depicted that Greedy Searches produced the best lattice designs, but GAs and Path Relinking were the two best methods in terms of global cost and reliability [8]. This shows that GAs remain a powerful optimization method.

Rogers et al used adaptive simulated annealing (ASA) to optimize the radial pin enrichments and burnable poisons in a PWR fuel lattice [9]. ASA is an open source code written in C [10]. Simulated annealing is another artificial optimization method like GA's. Simulated annealing is based on the natural process of materials cooling from high to low temperature, ultimately reaching the lowest achievable energy state [9].

Rogers et al minimized the PPF of a 15 x 15 lattice in octant symmetry at beginning of life. Their optimization included standard design constraints such as prohibiting placement of gadolinium bearing pins in periphery locations and holding water rod and instrument tube locations fixed. Two heuristic rules were implemented that limited the locations of where gadolinium bearing pins could be placed based on a correlation between gadolinium placement and PPF [9].

Similar to Martin-del-Campo et al, Rogers et al used a complex fitness function in their optimization. Additionally, ASA evaluated a large number of solutions to optimize the different cases evaluated, and only produced one optimal solution for each case analyzed [9].

Ortiz-Servin et al combined a greedy search with a neural network to optimize the radial and axial zones of a BWR fuel bundle. Their method, GreeNN, uses a simple greedy search to optimize the radial distribution of a fuel lattice, and then uses a neural network to determine the optimal axial layout. The two-dimensional lattices were optimized with the simple goal of finding the lowest PPF for the lattice. The three-dimensional bundle optimization sought to maximize end of cycle (EOC) kinf while satisfying thermal limits and cold shutdown margin [11]. Casmo4 and

Simulate-3 were used to analyze the two dimensional lattices and three dimensional fuel bundles respectively [12] [13].

GreeNN successfully optimizes the reactor physics and safety limits of three-dimensional fuel bundles; however, GreeNN is not applicable to real world design problems. Figure 1-2 shows the axial layout used in the optimization, where each neuron is one axial fuel level [11]. Each color in Figure 1-2 describes a different zone in which fuel lattices may be placed. Based on the GreeNN system, each of these axial zones would be composed of a different two dimensional lattice. This means each fuel rod used in the fuel bundle is unique. This means high manufacturing costs for building fuel bundles designed by GreeNN. Manufacturing multiple fuel bundles based off of GreeNN for use in one reload batch would be economically impossible.



Figure 1-2: Axial distribution of fuel bundle where each axial level represents one neuron.

1.3 Casmo4e

All lattice physics calculations were performed using Casmo4e. Casmo-4 is a multigroup two-dimensional transport theory code for burnup calculations on BWR and PWR assemblies. The code geometry utilizes cylindrical fuel rods in a square pitch array and can handle a variety of fuel materials [12].

The two-dimensional transport solution uses the method of characteristics and can be carried out using several different energy group structures. A seventy-energy group library covering the energy range 0 to 10 MeV stores the nuclear data. Casmo4e handles thermal expansion automatically and calculates resonance cross sections for each individual pin. A fundamental mode calculation incorporates leakage affects [12].

Casmo-4 handles direct microscopic depletion of burnable absorbers in the main calculation. Depletion is tracked through each individual pin cell, and a predictor-corrector

approach calculates depletion, which greatly reduces the number of steps without reducing accuracy [12].

Chapter 2 MOOGLE ALGORITHM DESCRIPTION

The MOOGLE algorithm advances the field of nuclear fuel management by using rod types as the genes and rod maps to define the problem. For purposes of MOOGLE, the number of unique fuel rod types is a proxy for manufacturing cost. Binning of the solution space is also novel. MOOGLE provides a simple optimization framework readily available to solve a wide range of lattice optimization problems. By using rod types as the decision variable, and using a simple fitness method based on ranking, the MOOGLE algorithm can solve two-dimensional lattice optimization problems just as easily three-dimensional fuel assembly optimization problems without any changes to the algorithm. Binning of the solution space allows designers to see all of the different designs, as well as their strengths and weaknesses side by side in order to select the designs that work best for them within the core loading pattern. Additionally, use of rod types as the decision variable allows designers to see the tradeoffs between cost and performance for various numbers of rod types. These advancements make the MOOGLE optimization algorithm a novel contribution to the field of nuclear fuel management.

2.1 Brief Description of Genetic Algorithms

Genetic algorithms (GA's) optimize a population of solutions based on the mechanics of genetics and natural selection. GA's utilize historical population information to randomly search a solution space in a manner more efficient than a standard randomized walk. John Holland, K.A. De Jong, and colleagues first developed GAs at the University of Michigan in 1975. Dr. Holland's students, with David Goldberg potentially being the most well-known, further developed and popularized the GA [14].

GAs apply to a range of problems such as game playing, function optimization, and search optimization of large scale combinatorial optimization problems like nuclear fuel lattice design or the well-known traveling salesman problem. GAs are adept for parallel programming, allowing a large section of the solution space to be searched quickly and provide a wide array of different solutions [14]. A disadvantage of GAs are that they provide no proof an optimum solution has been found [8]. Goldberg notes that GAs do not necessarily reach the best solution within the space and that combining GAs with another search method such as Tabu searches often yields better results than the GA search alone [14]. GAs also propagate undesirable solutions for several generations, which wastes computational resources [6].

2.2 Genes, Genomes, and Chromosomes

Genetic algorithms utilize a genome. The genome, typically a string of characters or binary numbers, represents all the information of a solution, and can be modified to create new solutions through the manipulation of genes, which represent individualized aspects of the problem [14].

The fuel assembly design problem is a placement problem where the optimal fuel rod type configuration for the fuel assembly is sought. The MOOGLE algorithm utilizes a gene pool and chromosome map to describe solution genomes. The gene pool describes the physical characteristics of the fuel rods used in the optimization. The gene pool also states which genes are allowed on which chromosomes. The chromosome map divides the geometry of the fuel assembly design problem into different radial regions that define where rod types may or may not be used in the solution of the design problem.

Table 2-1 and Figure 2-1 present examples of the gene pool and chromosome map for the rod lattice optimization problem. Figure 2-1 represents a 17x17 PWR lattice in octant symmetry. By surveying Table 2-1 and Figure 2-1, the following observations can be made. First, by

designating the guide tubes and water rods as individual chromosomes with one allowed gene on that chromosome, these items are held fixed within the problem. Second, all fuel genes may be expressed in the chromosome 1. Third, the fuel gene containing gadolinium may not be expressed in chromosome 4. These observations demonstrate the simplicity of describing a problem within the MOOGLE framework.

Table 2-1: Example of Gene Descriptor List for the Lattice Optimization Problem.

LOCATION	GENE NUMBER	FUEL TYPE	ROD TYPE	DESCRIPTION
1	1	1	1	Fuel rod using 4.4% w/o uranium
1	2	2	1	Fuel rod using 4.95% w/o uranium
1	3	3	1	Fuel rod using 4.95% w/o uranium and 3% Gd.
1	4	1	4	Fuel rod using 4.4% w/o uranium with IFBA coating.
2	1	0	2	Guide Tube
3	1	0	3	Water Rod
4	1	1	1	Fuel rod using 4.4% w/o uranium
4	2	1	2	Fuel rod using 4.95% w/o uranium
4	3	1	4	Fuel rod using 4.4% w/o uranium with IFBA coating.

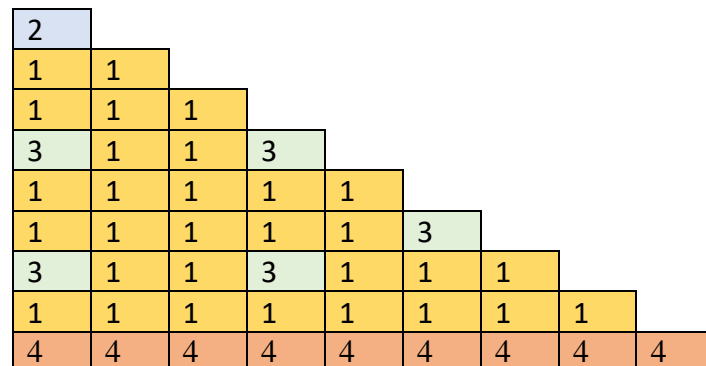


Figure 2-1: Chromosome map for the lattice optimization problem for a 17x17 PWR assembly.

The MOOGLE algorithm's simplicity makes it adept for solving a wide range of problems in nuclear fuel design. The example depicts a problem description for a 17x17 PWR fuel lattice; however, optimization of a BWR fuel bundle is just as easy using MOOGLE.

PWR fuel assemblies contain top and bottom blanket regions, as well as burnable absorber cutback regions; however, optimizing only the radial fuel lattice extending over the dominant central axial region is sufficient to optimize the entire assembly. Optimization of BWR fuel bundles, on the other hand, involves multiple radial fuel lattices extending over several axial fuel regions. MOOGLE can easily optimize both problems through the implementation of the gene pool which utilizes rod types and chromosome map.

2.3 Population Size

Population sizes depend on a variety of factors including computational resources and problem complexity. The population of multiple solutions allows GA's to search a large breadth of the solution space, and the population of solutions also helps the optimization to escape from local optimal solutions. If a GA uses too small of a population, convergence will occur too quickly; too large of population's waste computational resources [15].

MOOGLE calculates population size based off of the formula used in FORMOSA-P [16]. Population size is determined by the total number of possible genes. The total number of possible genes are the sum of all genes that may be expressed in a given gene location over the entire genome. For the lattice optimization problem, this is the sum of all the different rod types allowed in a given location for all rod positions. Population size is calculated as:

$$N_{pop} \approx 10 * \sqrt{N_{genes}} \quad 2.1$$

These processes may be illustrated through our previous example. Returning to Table 2-1 and Figure 2-1, four rod types are allowed in region 1, one in region two and three, and three in region four. There are thirty rod locations within region 1, one location within region 2, five locations in region 3, and nine locations within region 4. This means the total number of all possible genes is:

$$N_{genes} = 30 * 4 + 1 * 1 + 5 * 1 + 9 * 3 = 153$$

The square root of one hundred fifty-three, rounded to the nearest whole number is:

$$\sqrt{153} \approx 12$$

The population size for our example is then one hundred twenty.

2.4 Initialization Population Creation

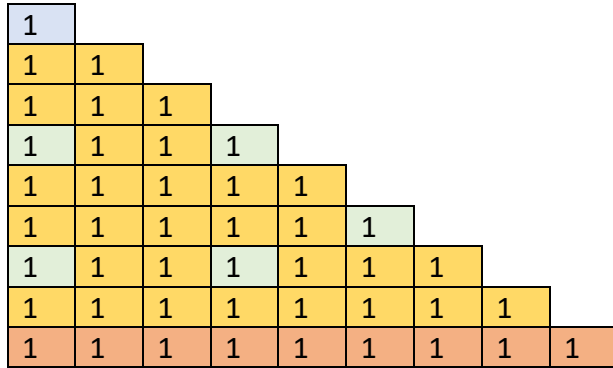
Traditionally, random solutions from the available gene pool compose the initial population [14]. The MOOGLE algorithm does not follow this approach. Instead, the MOOGLE algorithm uses every homogeneous combination of chromosomes to form the initialization population.

Figure 2-2 illustrates this for the example problem. As the figure shows, the first four solutions in the initial population would be comprised of the three possible genes allowed in chromosome 4, indicated in red, combined with the first gene allowed in chromosome 1, indicated in gold. The sequence then repeats, now with the second allowed gene in chromosome 1. Chromosomes 2 and 3 remain constant because only one gene is allowed in these locations. The total initialization population size for the example problem would be twelve solutions.

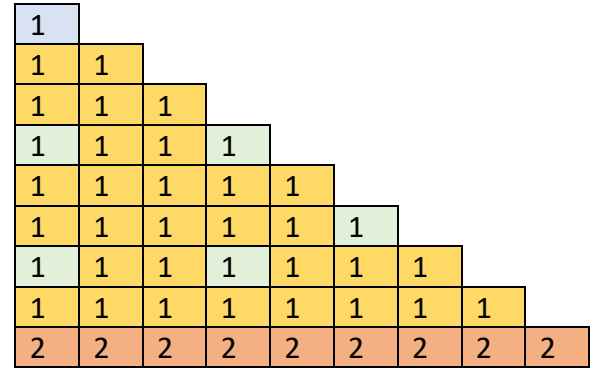
A homogenous or semi-homogeneous genome is likely to be close to the optimized solution for one of the optimization parameters, motivating this decision. Using a good, non-random initialization population to produce the starting population significantly reduces the computational time over a random, relatively bad, initial population, especially for the lattice optimization problem.

In fuel assembly design, twenty rods containing gadolinium is often given as the upper limit on the amount of burnable poison allowed in an entire fuel assembly [9]. By using a random starting population, most assemblies will have far more gadolinium rods than this upper maximum.

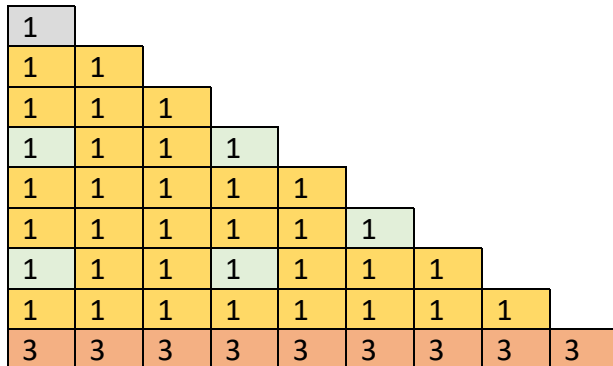
From an optimization standpoint, it makes no sense to waste computational resources by starting with an infeasible population of solutions. The use of an initialization population created through homogeneous combinations of chromosomes allows the optimization to have a better starting population without the need for overcomplicated heuristic settings or in-depth knowledge of the problem.



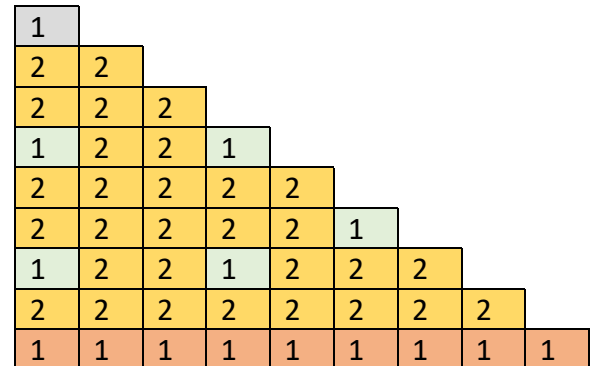
First solution generated



Second solution generated



Third solution generated



Fourth solution generated

Figure 2-2: First four solutions within initialization population for example problem.

2.5 Survival

In accord with Charles Darwin's theory of evolution, that species evolve to become more fit for their environment, one designs their GA so that the population of solutions increases over time [14]. The literature review showed that a common method is to use a fitness based off of the optimization objectives [6] [9] [11]. Another common method is to use Pareto sorting to identify non-dominated solutions of value along the Pareto front [17]. The Pareto front represents the

optimal solution tradeoffs for competing objectives, with solutions on the Pareto front being non-dominated by any other solutions to the optimization problem [18]. An example of a Pareto front is provided in Figure 2-3.

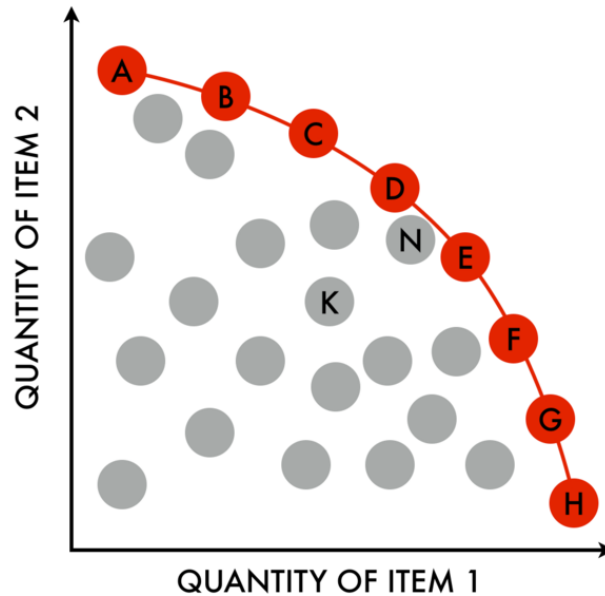


Figure 2-3: Example of a two objective Pareto front [19].

MOOGLE uses a novel binning method for determining solutions of value, rather than the two previously discussed methods. The basis for this decision stems from the optimization of a PWR fuel lattice using two objective functions. The objective was minimizing peak pin power and minimizing reactivity at beginning of life. A Pareto front for the optimization was created, and as expected, showed a tradeoff between reactivity and pin power. Unexpectedly, none of the solutions developed were of particular value to a core designer. The solution lattice composed entirely of rods utilizing IFBA as a burnable poison achieves a low pin power and extremely low reactivity. Through Pareto selection, any solutions with a higher reactivity and pin power were eliminated, although these solutions are more desirable from a design standpoint. These unexpected optimization results motivated the creation of novel method for storing desirable solutions that

didn't require complex tuning of a fitness function and preserved solutions that, although dominated by other solutions, still held value to a core designer.

Figure 2-4 shows the steps of the binning survival process. Calculate a fitness for each solution based on Equation 2.2. The number of bins is calculated using Equation 2.3. The bin in which each solution is placed is calculated using Equation 2.4.

$$F = \sum_{i=1}^{N_{objectives}} w_i R_i \quad 2.2$$

Where w_i is a user supplied importance ranking to that objective, and R_i is the rank of that solution for that optimization objective.

$$N_{bins} = \frac{obj_{maximum} - obj_{minimum}}{width_{obj}} \quad 2.3$$

Where $obj_{maximum}$ is the maximum value of the objective currently existing within the allowed solution space, $obj_{minimum}$ is the minimum value for that objective that currently exists within the solution space, and $width_{obj}$ is the desired width of each bin for that objective.

$$Bin_{\#} = \frac{obj_{score} - obj_{minimum}}{width_{obj}} \quad 2.4$$

The desired solution space focuses and improves the optimization. During the use of a standard Pareto selection for the multi-objective optimization, it was found that limiting the desired solution space improved optimization performance by having fewer, yet more desirable results. Additionally, these reduced results cause fitter parents to be selected each generation.

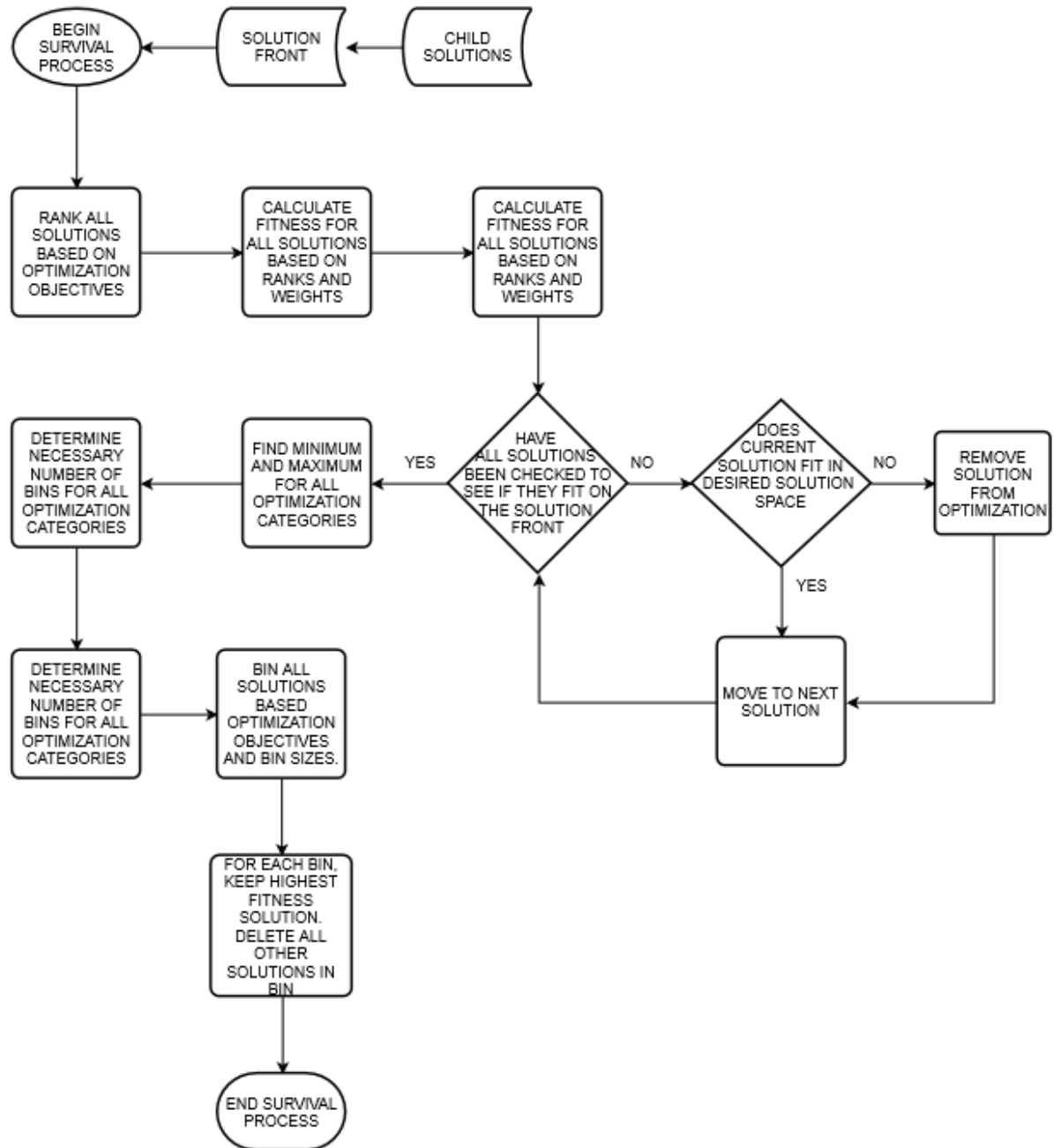


Figure 2-4: Flow chart for binning survival process

Reducing computational time by only using the minimum number of bins required motivates the use of Equation 2.3. Two possible methods were identified for the binning process. The first method used a fixed number of bins, while the second method used a fixed bin size. Fixed bin sizes are used over a fixed number of bins because fixed bin sizes provide better resolution

over the solution space by being able to add or remove needed bins. This enhanced resolution makes it easier to identify valuable solutions and provides clarity of the current solution space to the designer.

The overall motivation for binning is to reduce the number of solutions that are kept in the optimization. All solutions within the same final bin should be thought of as having equal value. Using a fitness is simply a convenient means for choosing a solution to represent the binned space.

2.6 Parent Selection

Determining which solutions pass their genes on to the next generation is one of the core parts of a genetic algorithm [14]. The MOOGLE algorithm uses a somewhat complicated method to decide which solutions in the desired solution space should act as the parents to the next generation of solutions. A flow chart for the parent selection process can be found in Figure 2-5.

MOOGLE uses two methods for determining which solutions are passed on to the next generation. If the number of solutions in the desired solution space is less than the desired number of children, then all solutions will get the opportunity to pass on their genes to the next generation. When there are more possible parents than children though, a tournament is used to decide which solutions will get to reproduce. Tournaments are a common, highly effective method for determining which solutions are selected as the parents of the next generation [20]. Tournament methods are valuable for determining parents because they ensure the population advances towards more desirable fitness metrics while maintaining solution diversity through the randomness of pairings in the tournament brackets [21].

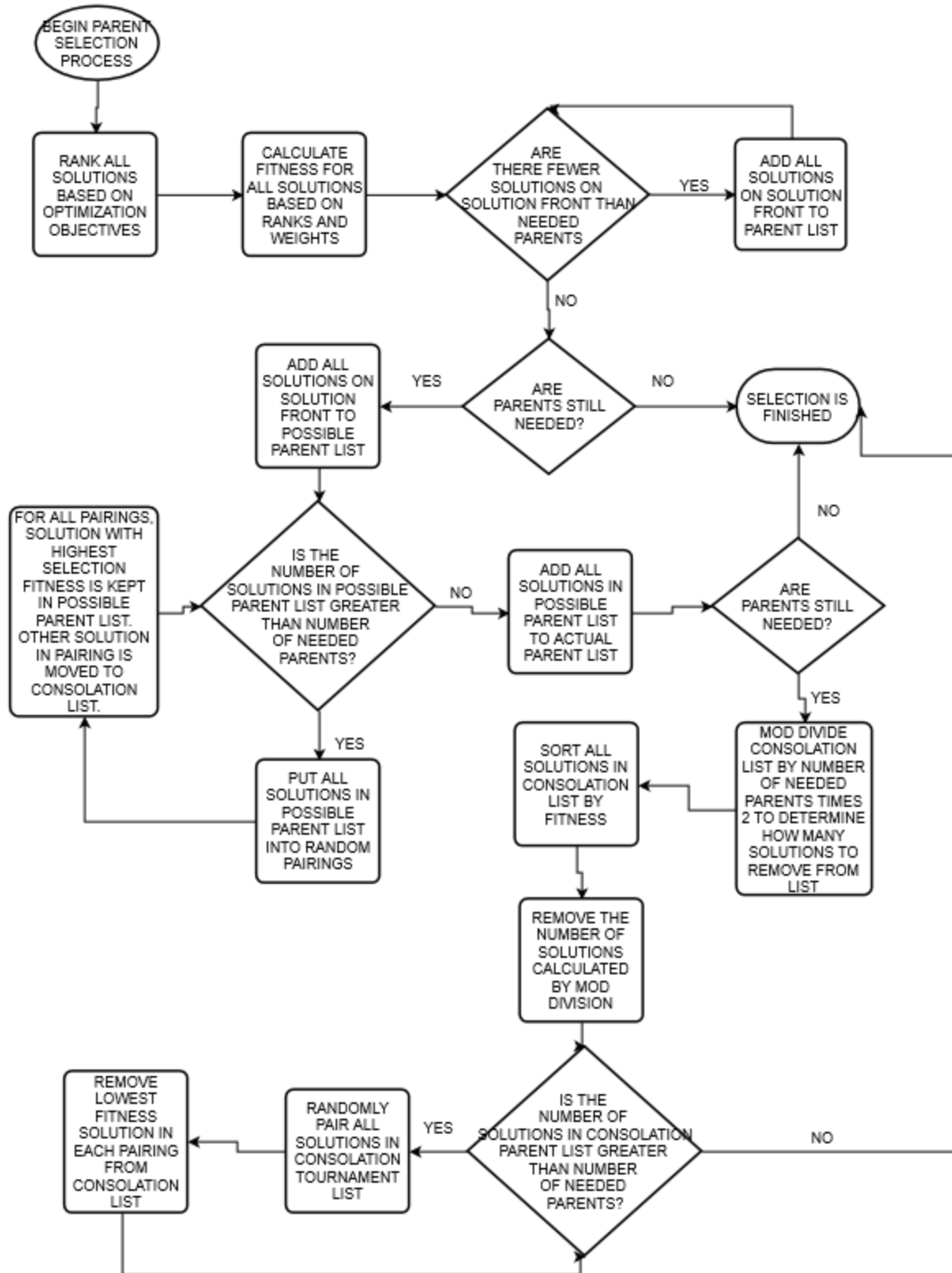


Figure 2-5: Flow chart of parent selection process.

2.7 Reproduction

The final key element of GA's so far undiscussed is generating new child solutions from the selected parent population. GA's utilize crossover and mutation to create the next generation of children [14]. The three specific reproduction methods used in the MOOGLE optimization algorithm are crossover, single mutation, and double mutation. The process used for determining how parents reproduce in the MOOGLE algorithm is illustrated in Figure 2-6.

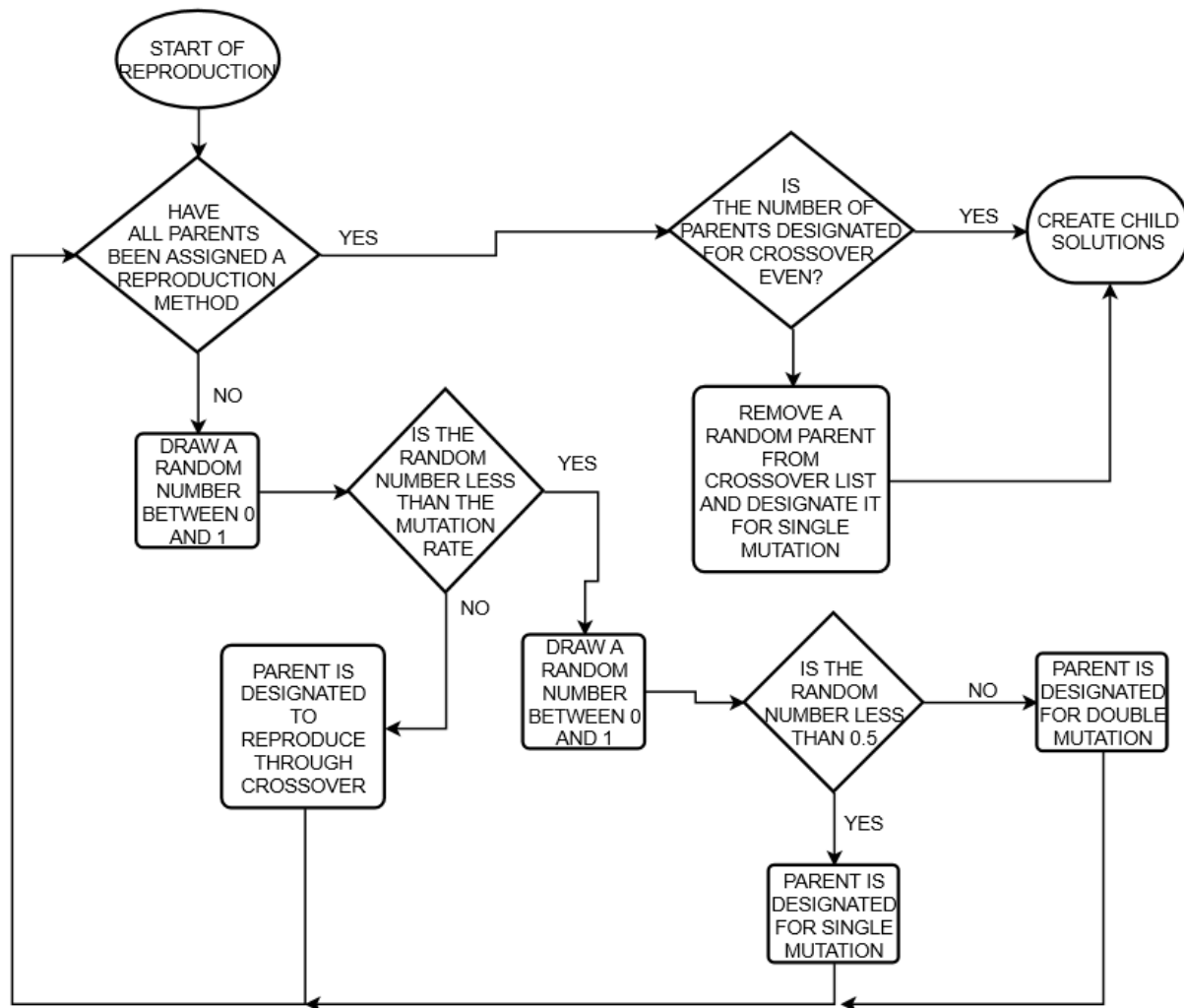


Figure 2-6: Reproduction selection method flow chart.

Crossover is the main method used to generate new solutions [14]. Crossover combines genes from two parents to create two new, unique child genomes. Crossover replicates a breeding

program by mating similar genomes that to one another. In breeding programs, it is beneficial to select animals with similar traits as mates for each other. Selecting mates with similar characteristics allows traits within the mates to be expressed faster than through random mating. This allows undesirable traits to be identified and removed faster [22].

This method has a second advantage. Crossing over two solutions that both have high fitness values but differing genomic structure rarely result in children of note [14]. Another way of saying this is that if two solutions are on differing peaks within the solution space, any children these solutions have are more likely to result in the valley between the solutions, rather on an undiscovered, higher peak than the parents.

Crossover in the MOOGLE algorithm replicates a breeding program by mating the most similar genomes together. All parents designated for crossover are stored in a list. The first parent in the list is taken as the first parent to be used in the crossover pair. The rest of the parents in the crossover list are then examined to find the most suitable mate. For each parent, the genome is analyzed to determine how many genes it has in common with the first parent. This means having the same gene in the location within the genome. The genome that has the most genes in common with the first parent is chosen as the most suitable mate and second parent used in crossover.

Once a suitable mate is chosen, genes are exchanged between the genomes to create new child genomes. Locations where genes differ in the genome of the two parents are identified as suitable locations to swap genes. Genes are swapped between the parents in half of the suitable locations, creating two new children from the genomes of the parents. This entire process is illustrated in Figure 2-7. The top row designates parents (rod lattices) that have been selected for crossover. The lattice designated as the crossover lattice is the first parent to be used in crossover. The blue squares in the lattices designated as 1st and 2nd potential mate denote locations where the

rod type differs from that of the crossover lattice. Because there are fewer differences between the 1st potential mate and the crossover lattice versus the 2nd potential mate, the 1st potential mate is selected as the most suitable partner for crossover. The second row of lattices represent the children created in crossover. The green squares represent locations in which genes (rod types) were swapped between genomes. The 1st child lattice originally was the crossover lattice. The 2nd child lattice originally was the 1st potential mate. Once a parent has successfully crossed over with another parent in the crossover list, both parents are deleted from the crossover list.

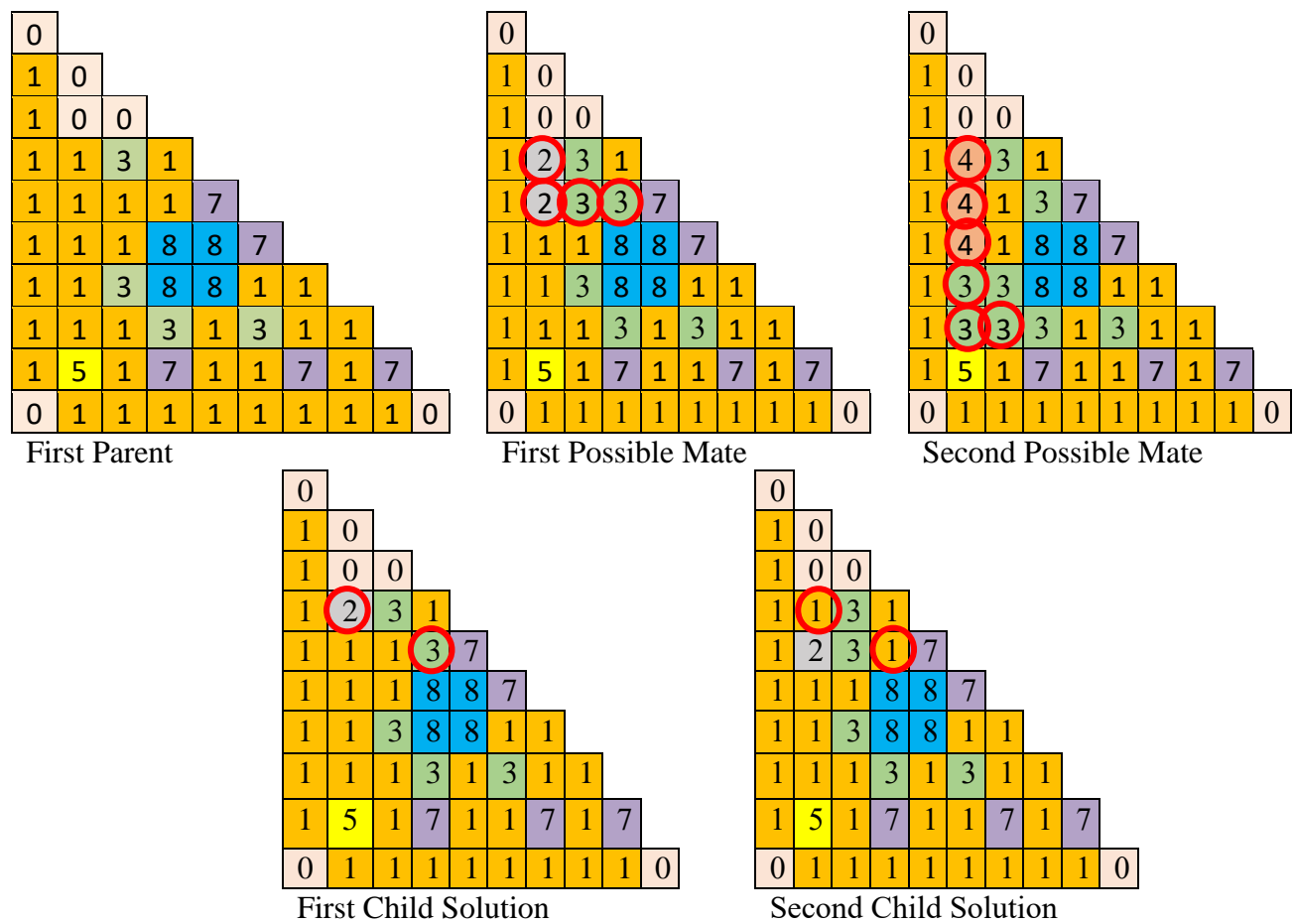


Figure 2-7: Crossover Illustration.

Mutation is the second factor to create new child populations. It is designed to replicate the random mutations that happens to genomes in nature [14]. Mutation works by selecting a gene within the genome to be altered. A new rod type is then inserted into the rod location from the list

of available rod types. For single mutation, this process occurs once, and for double mutation this process occurs twice.

Initial and final mutation rates are selected by the user. The mutation rate increases every generation based on the FORMOSA-P method [16]. Equations 2.5 and 2.6 are implemented within MOOGLE for determining the increase in the mutation rate each generation. The increase is based on the maximum number of possible generations for the optimization. This means that the target final mutation rate is often not achieved, as the solution space normally converges before the maximum number of generations is reached.

$$p_{\text{mute}}^{n+1} = 1 - \lambda_g(1 - p_{\text{mute}}^n) \quad 2.5$$

Where p_{mute}^n and p_{mute}^{n+1} are the mutation rates for the n and $n+1$ generations and λ_g is a multiplier calculated as:

$$\lambda_g = \exp\left(\frac{\ln((1-p_{\text{final}})(1-p_0))}{N_{\text{gen}}}\right) \quad 2.6$$

2.8 End of Optimization Conditions

There are two conditions that can be met for the MOOGLE algorithm to stop. The MOOGLE algorithm is considered converged when less than ten new solutions have been added to the solution space in the last five generations. If MOOGLE is considered converged, the optimization ends. The other condition is for the maximum number of generations to be reached. MOOGLE will end after that final generation. The maximum number of generations is calculated similarly to population size, using the equation:

$$N_{\text{max_gen}} \approx 5 * \sqrt{N_{\text{genes}}} \quad 2.7$$

2.9 MOOGLE Flowchart

Figure 2-8 provides a flowchart of how all individual components of the MOOGLE algorithm flow together.

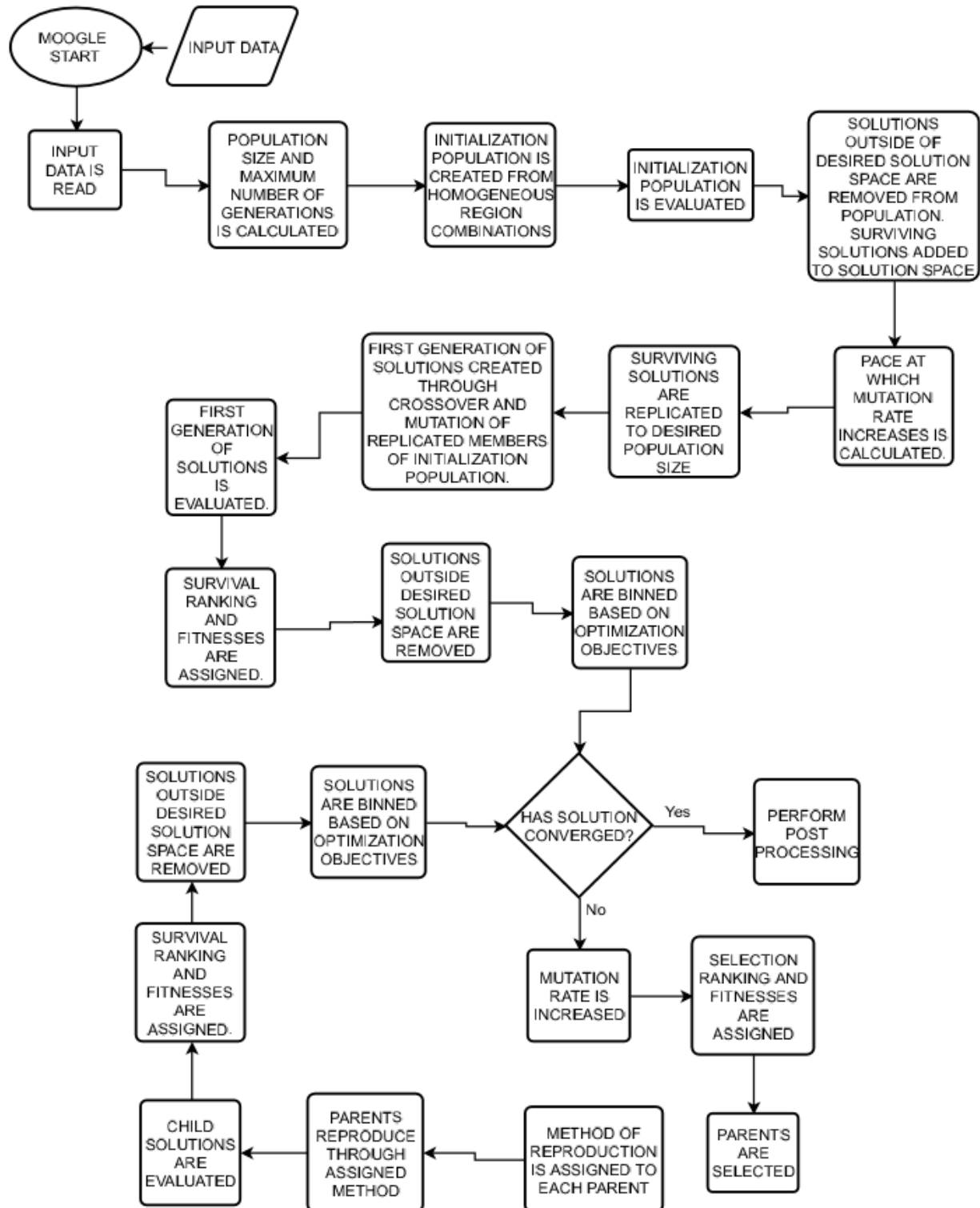


Figure 2-8: Overall flow chart for the MOOGLE algorithm.

Chapter 3 MOOGLE ALGORITHM TESTING

The MOOGLE algorithm was tested using two different assembly geometries, PWR and BWR. The PWR geometry was used to demonstrate the effectiveness of the binning method over Pareto sorting, to test the sensitivity of the algorithm to different parameters, and to analyze how the use of different BP combinations alter the results of the optimization. BWR geometry was used to compare the MOOGLE algorithm to a previously developed optimization algorithm, and to demonstrate the full fuel rod optimization capability and demonstrate the tradeoff between manufacturing complexity and increased performance through the addition of rod types.

3.1 PWR Optimization Description

The PWR geometry utilized a 17x17 fuel lattice in octant symmetry. The zone region map for the PWR optimization problem is provided in Figure 3-1. Two manufacturing design constraints were used to develop the rod zone regions: (1) The locations of guide tubes and water rods were held in fixed positions. (2) Gadolinium rods were restricted from edge pin cell locations. The rod types used in the optimization are provided in Table 3-1. Lattice designs were depleted for a burnup of 20 MWD/MTU. Reactor conditions at which the lattice designs were run is provided in Table 3-2.

2									
1	1								
1	1	1							
3	1	1	3						
1	1	1	1	1					
1	1	1	1	1	3				
3	1	1	3	1	1	1			
1	1	1	1	1	1	1	1		
4	4	4	4	4	4	4	4	4	

Figure 3-1: Rod zone region map for the PWR geometry problem.

Table 3-1: Rod List for the PWR Lattice Optimization Problem.

Location	Gene	Description
1, 4	1	Fuel rod with 4.40 % w/o uranium
1, 4	2	Fuel rod using 4.95% w/o uranium
1	3	Fuel rod using 4.40% w/o uranium and 1% gadolinium
1	4	Fuel rod using 4.95% w/o uranium and 1% gadolinium
1	5	Fuel rod using 4.40% w/o uranium and 2% gadolinium
1	6	Fuel rod using 4.95% w/o uranium and 2% gadolinium
1	7	Fuel rod using 4.4% w/o uranium and 3% gadolinium
1	8	Fuel rod using 4.95% w/o uranium and 3% gadolinium
1, 4	9	Fuel rod using 4.40% w/o uranium with IFBA coating.
1, 4	10	Fuel rod using 4.95% w/o uranium with IFBA coating.
2	1	Guide Tube
3	1	Water Rod

Table 3-2: Operating conditions used in Casm04e for PWR lattice physics calculations.

Power	110
Moderator	600
Fuel	820.5
Boron	900

Three experiments were conducted through the optimization of the PWR fuel assembly. The first experiment demonstrated how binning the solution space alters the results of an optimization over using a simple Pareto surface. The second experiment determined the sensitivity of the MOOGLE algorithm to different settings such as bin size or mutation rate. The third experiment determined how the inclusion of different burnable poison types affects the results of the optimization. To compare a solution binning method to a Pareto front method for carrying solutions forward in the optimization, a PWR fuel assembly was optimized at BOC, with the objectives of minimizing peak pin power and minimizing K_{inf} using a Pareto sorting method based on the method proposed by K.K. Mishra and Sandeep Harit [23].

The sensitivity of the MOOGLE algorithm was tested through the optimization of several different cases, each with different settings. Six cases tested the effect different selection weights had on the optimization results. Two cases tested how different population sizes affected the

optimization results. Two cases tested the effects of alternate mutation rates on the optimization results. The final three cases tested how bin size for various parameters affected the optimization results. All sensitivity test cases were compared to a standard base case. For each case, five runs were used to create the analysis dataset.

The selection weights used for each case are presented in Table 3-3. The mutation rates for all cases are presented in Table 3-4. The bin sizes for all cases are presented in Table 3-5. Each case used equal survival rates set at a value of one. All cases except the population size test case used Equation 2.7 to calculate the population size and maximum number of generations. The small population test size cases used Equation 3.1 to calculate population size. The first small population size test case also used equation to calculate the maximum number of generations.

$$N_{pop} = 5 * \sqrt{N_{genes}} \quad 3.1$$

$$N_{gen} = 2.5 * \sqrt{N_{genes}} \quad 3.2$$

Population sizes and maximum number of generations for the cases are presented in Table 3-6. The allowed solution space for the selection weight analysis cases and BP analysis cases are presented in Table 3-8. Note that in Table 3-3 through Table 3-8, if a case is not listed, its parameters are identical to the base case. Since the solution space size was altered for the bin size test cases, convergence would happen before the population was fully optimized. For this reason, these cases were set to run for the average number of generations used by the base optimization case.

To compare the effects of different burnable poisons on the optimization results, the PWR fuel lattice was optimized using BP rods that only contained IFBA, BP rods that only contained gadolinium, and then the full rod set which utilized both IFBA and gadolinium. The full rod set

case was the base case used in the sensitivity analysis. Population sizes and the maximum number of generations for the BP test cases are presented in Table 3-7.

Table 3-3: Selection Weights Used in Sensitivity Analysis.

Test Case Number	Peak Pin Power Weight	Peak Kinf Weight	EOC Kinf Weight
Base	1	1	1
Selection Weight One	1	0	0
Selection Weight Two	0	1	0
Selection Weight Three	0	0	1
Selection Weight Four	1	1	0
Selection Weight Five	1	0	1
Selection Weight Six	0	1	1

Table 3-4: Initial and Final Mutation Rates Used in Sensitivity Analysis Optimizations

Case Number	Initial Mutation Rate	Final Mutation Rate
Base Case	25%	50%
Alternate Mutation Rate One	50%	75%
Alternate Mutation Rate Two	25%	75%

Table 3-5: Bin Sizes Used in Sensitivity Analysis Optimizations

Case Number	Peak Pin Power Bin Size	Peak Kinf Bin Size	EOC Kinf Bin Size
Base	0.01	0.01	0.01
Large Power Bin Size	1	0.01	0.01
Large Peak Kinf Bin Size	0.01	1	0.01
Large End Kinf Bin Size	0.01	0.01	1

Table 3-6: Population Sizes and Maximum Generations Used in Sensitivity Analysis Optimizations

Case Number	Population Size	Maximum Number Generations
Base Case	180	90
Small Population One	90	45
Small Population Two	90	90

Table 3-7: Population Sizes and Maximum Generations Used in BP Analysis Optimizations

Case Number	Population Size	Maximum Number Generations
Base Case	180	90
IFBA Only	120	60
Gadolinium Only	160	80

Table 3-8: Allowed Solution Space for SA and BP Optimizations

Parameter	Minimum Allowed Value	Maximum Allowed Value
Peak Pin Power	0	1.15
Peak Kinf	1.00	1.35
End Kinf	1.00	1.10

For the SA and BP analysis, the three objectives chosen were to minimize PPF, minimize peak kinf in the cycle, and to maximize the end of cycle (EOC) kinf at a 20 MWD/MTU burnup. Minimizing PPF improves the safety margin of the nuclear reactor. As previously mentioned, there are safety limits imposed on radial and axial peaking, FAH and Fq. Minimizing the PPF provides greater margin between the operating conditions and the limiting values. Minimizing peak kinf and maximizing EOC kinf help to minimize the reactivity swing in the reactor core that occurs as the BP burns out of the fuel assembly. Additionally, minimizing the peak kinf value minimizes the excess reactivity of fuel assemblies, reducing the use of chemical shim and control rods. Finally, high EOC kinf values allow the fuel to remain in the core longer, maximizing burnup of the fuel assembly.

Epsilon indicator distance testing was used to compare the base and test cases in the sensitivity analysis and BP analysis. [24]. The epsilon indicator distance is the total amount of distance one solution front must move in order to replace the points on another solution front. The concept is illustrated in Figure 3-2.

Epsilon indicator distance testing was performed by performing a test and base optimization with MOOGLE. The final solution spaces for the test and base cases were then

combined to create a combined solution front made up of the best solutions from both the test and base case results. An example of a combined solution front is presented in Figure 3-3. Solution fronts along the peak pin power front, peak kinf front, and EOC kinf front were created for the combined solution space, test solution space, and base case solution space. The distances between the points on the solution fronts for the test and base cases, and the combined solution fronts were then calculated.

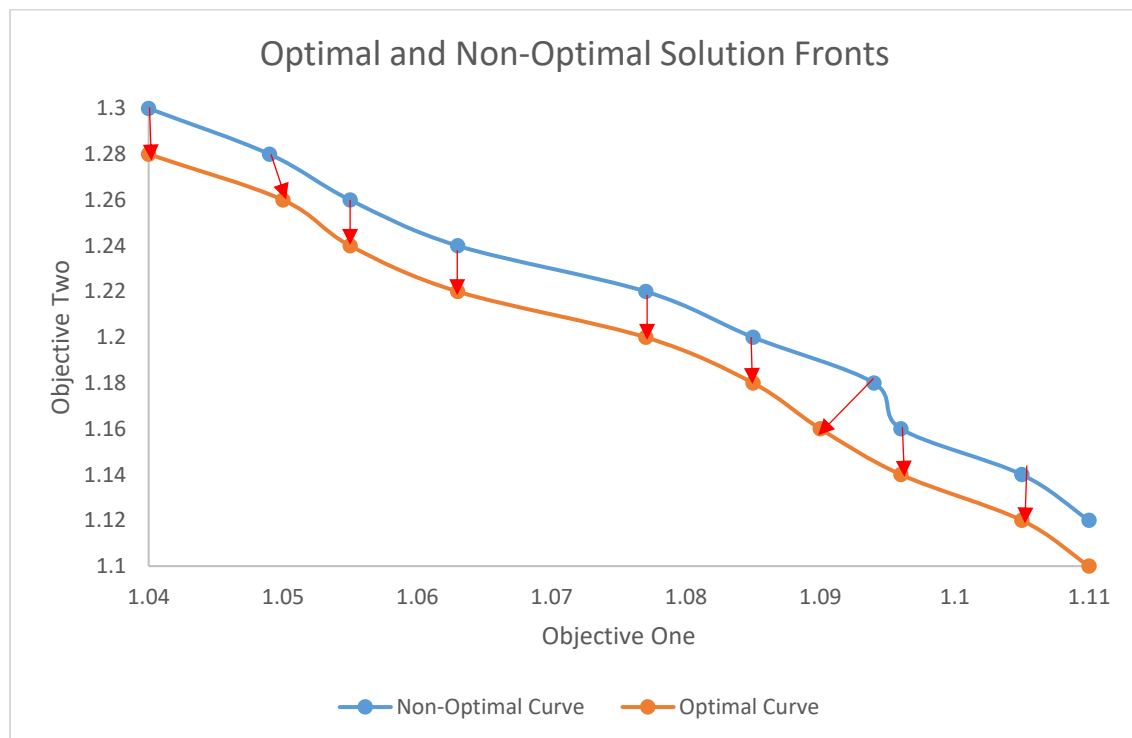


Figure 3-2: Depiction of epsilon indicator distance test. For the test, the epsilon indicator distance is the total sum of the distances each point on the non-optimal curve must move to replace the points on the optimal curve.

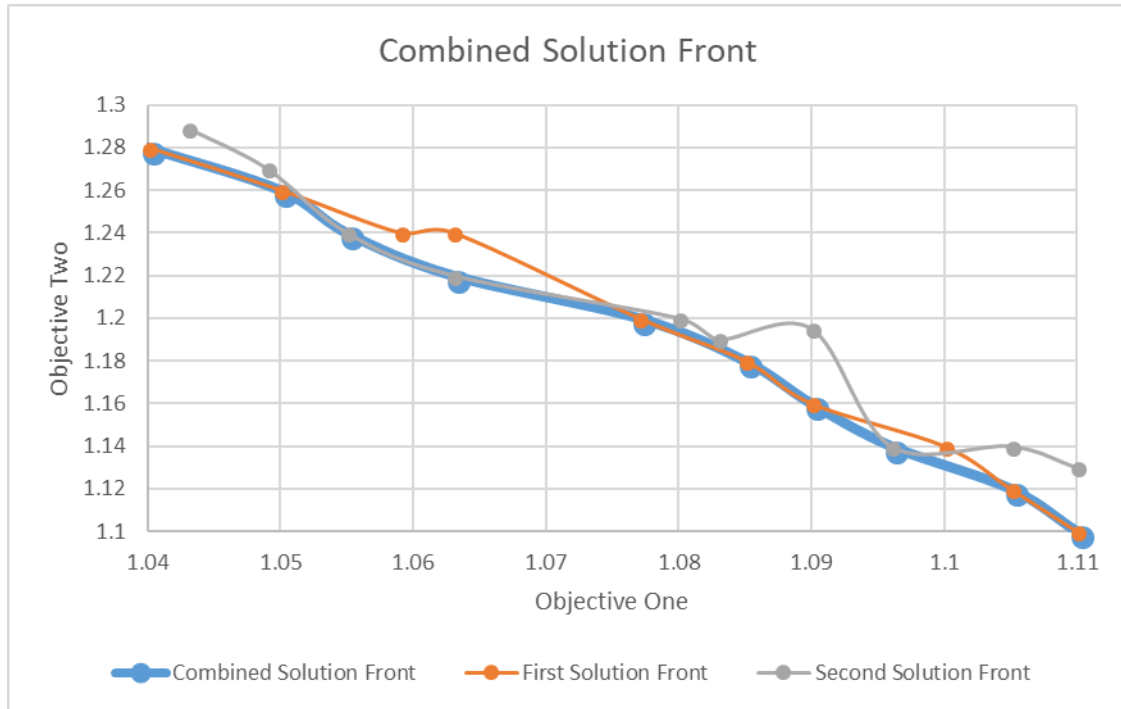


Figure 3-3: Example of a combined solution front obtained from two different solution fronts.

Solution fronts for the objectives of the optimization were calculated as follows. The bin size for the selected optimization front was kept the same. The bin sizes along the other objective fronts are collapsed so that the solution space only exists along one objective. Then, through the binning selection process, the only remaining solutions represent the most desirable solutions, forming a solution front for the objective.

The total distance from the combined solution front to an optimization run solution front is calculated by taking the distance from every point on the combined solution front to the nearest point on the optimization run solution front. To determine the minimum distance from a point on the combined solution front to the optimization run solution front, the distance from the point on the combined solution front to every point on the optimization run solution front is calculated. Distances between points are calculated using the equation:

$$distance = \sqrt{\frac{(C_{power}-O_{power})^2}{B_{power}} + \frac{(C_{peak}-O_{peak})^2}{B_{peak}} + \frac{(C_{EOC}-O_{EOC})^2}{B_{EOC}}} \quad 3.3$$

Where C represents the point on the combined solution front, O represents the value for the point on the solution front being analyzed, and B represents the size of the bin for each of the three optimization categories.

3.2 BWR Optimization Description

The optimization of a BWR fuel bundle was the second geometry analyzed by the MOOGLE algorithm. To expedite run times, two-dimensional lattice slices of a BWR assembly were analyzed using Casmo4e. Linear interpolation along a generic power curve filled in data between the lattice slices, creating a three-dimensional fuel bundle. BWR's have a bottom peaked power curve due to the increased moderation in the bottom of the reactor. The equation for modeling reactor power as a function of height is [25]:

$$Power(z) = P_{linear} \left(\frac{\pi(H+\lambda-z)}{H_e} \right) \sin \left(\frac{\pi(H+\lambda-z)}{H_e} \right) \quad 3.4$$

Where P_{linear} is the linear heat flux, H is the physical height of the reactor, λ is an extrapolated distance, and H_e is the extrapolated height of the reactor calculated as [25]:

$$H_e = H + 2\lambda \quad 3.5$$

For the optimization analysis, the linear power rate was 25.9588 w/gU. The reactor was set at a height of 12.25 feet, with an extrapolation distance of 3.097 feet. An already established void curve modeled void in the reactor core as a function of height. Moderator and fuel temperatures were determined using similar information. The power curve and void curve are provided in Figure 3-4. Figure 3-4 also shows the axial positions for the first and second BWR optimization problems.

Two problems were optimized using the BWR geometry. The first problem compared the MOOGLE algorithm and another genetic algorithm for optimizing BWR fuel bundles, Mustang.

Mustang minimized the boiling transition factor a fuel assembly at BOC with and without a target K_{inf} value [26]. Crossover and mutation worked identically to MOOGLE in the Mustang algorithm. Mustang used a composite fitness function, rather than a binned desired solution space. Additionally Mustang used a standard tournament to decide which solutions carried forward to the next generation and which solutions died out. The first problem used a single axial rod zone and many fixed rod positions. The rod zone map for the first BWR problem is shown in Figure 3-5, representing a 10x10 BWR fuel bundle in half symmetry [27]. The rod types used in the optimization are presented in Table 3-9. Similar to the PWR fuel lattice optimization problem, design constraints were used to determine which rods were allowed in each rod zone region. The design constraints here are similar to the ones for the PWR problem: (1) Water rods are held in fixed locations, (2) rods containing gadolinium are prohibited from being placed on edge locations, (3) locations of vanishing rods are held fixed.

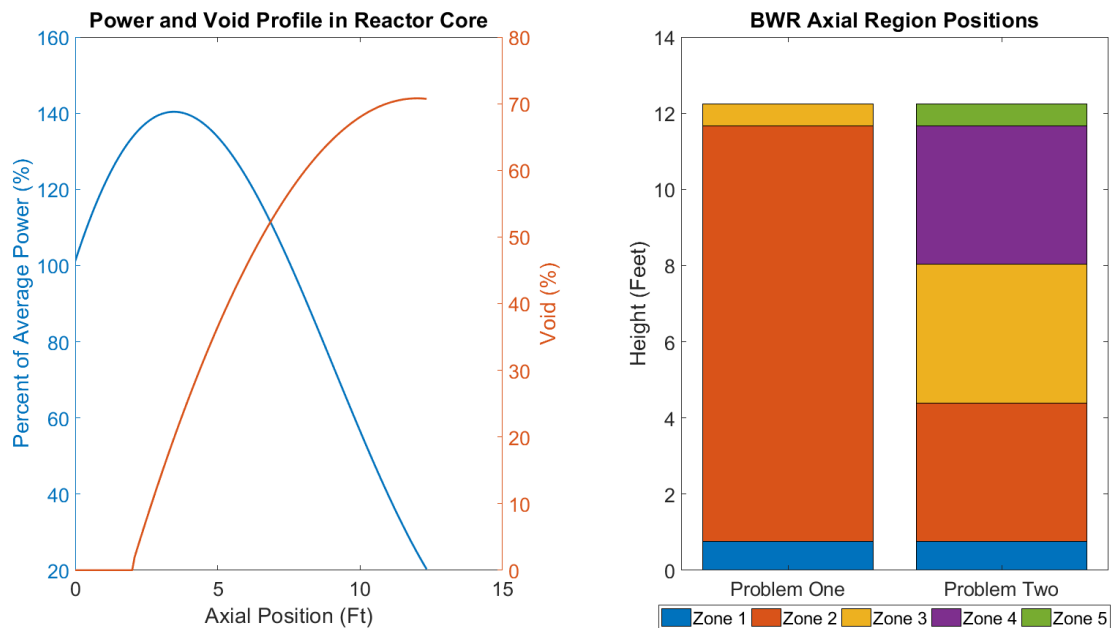


Figure 3-4: A: Axial power and void as functions of height. B: Positions of BWR axial regions for first and second BWR optimization problems.

2										
2	1									
2	1	1								
2	1	1	1							
2	1	1	1	1						
2	1	1	3	3	1					
2	1	1	3	3	1	1				
2	1	1	1	1	1	1	1			
2	1	1	1	1	1	1	1	1		
2	2	2	2	2	2	2	2	2	2	2

Figure 3-6: Rod zone region map for the second BWR optimization problem.

The three objectives for the optimization were the minimization of the bundle boiling transition factor (BTF), minimization of peak K_{inf} for the fuel bundle, and maximizing EOC reactivity for the fuel bundle.

The BTF, also known as the R-factor, is a measure of a fuel bundle's sensitivity to dryout based on changes in rod power and is a function of the relative rod powers within fuel bundles. It is used in critical power ratio (CPR) calculations. A general form for the BTF is provided by Haulin [28] and is based on the XL boiling length correlation [29]. For this study it is, calculated using the equation:

$$R = \frac{\sqrt{P} + w_s \sqrt{\sum P_s} + w_c \sqrt{\sum P_c}}{1 + w_c N_c + w_s N_s} + A \quad 3.6$$

Where P is the local integrated rod power, P_s is the integrated rod power of rods on the sides of the rod being examined, P_c is the integrated rod power for rods on the corner of the current rod. W_s and W_c are weights for the corner and side rods. N_s and N_c are the number of corner and side rods. A is an additive constant for the current rod location [28]. Figure 3-7 shows all rod powers that affect the calculated BTF of a rod in a single location.

The additive constant is used to relate relative rod power to the rods sensitivity to dryout and the values are measured by the assembly manufacturer. Additive constants are determined through laboratory testing of rod heat fluxes and fitting the experimental data to CPR correlations.

Values for the additive constants vary for each assembly design [28]. The additive constants and BTF equation used in this analysis are based on the XL boiling length correlation [29].

Table 3-10: Rod List for the second BWR Optimization Problem.

Rod Zone	Rod Number	First Axial Zone	Second Axial Zone	Third Axial Zone	Case One	Case Two	Case Three
1	1	2.00 w/o	2.00 w/o	2.00 w/o	X	X	X
1	2	3.20 w/o	3.20 w/o	3.20 w/o	X	X	X
1, 2	3	4.40 w/o	4.40 w/o	4.40 w/o	X	X	X
1	4	3.95 w/o	3.95 w/o	3.95 w/o	X	X	X
1	5	3.60 w/o	3.60 w/o	3.60 w/o	X	X	X
2	6	4.90 w/o	4.90 w/o	4.90 w/o	X	X	X
2	7	4.60 w/o	4.60 w/o	4.60 w/o	X	X	X
2	8	4.40 w/o 6.0 % Gad	4.40 w/o 6.0 % Gad	4.40 w/o 6.0 % Gad	X	X	X
2	9	4.60 w/o 5.0 % Gad	4.60 w/o 5.0 % Gad	4.60 w/o 5.0 % Gad	X	X	X
2	10	4.40 w/o 6.0 % Gad	4.90 w/o	4.90 w/o	X	X	X
2	11	4.90 w/o	4.40 w/o 6.0 % Gad	4.90 w/o	X	X	X
2	12	4.90 w/o	4.90 w/o	4.40 w/o 6.0 % Gad	X	X	X
2	13	4.40 w/o 6.0 % Gad	4.60 w/o	4.60 w/o	X	X	
2	14	4.60 w/o	4.40 w/o 6.0 % Gad	4.60 w/o	X	X	
2	15	4.60 w/o	4.60 w/o	4.40 w/o 6.0 % Gad	X	X	
2	16	4.40 w/o 6.0 % Gad	4.40 w/o	4.40 w/o	X		
2	17	4.40 w/o	4.40 w/o 6.0 % Gad	4.40 w/o	X		
2	18	4.40 w/o	4.40 w/o	4.40 w/o 6.0 % Gad	X		
3	19	Water Rod	Water Rod	Water Rod	X	X	X

Integrated rod powers are calculated using the equation:

$$P_{rod} = \frac{\sum_{i=1}^N v_i P_i}{\sum_{i=1}^N v_i} \quad 3.7$$

Where V_i is axial volume in axial location i and P_i is power in axial location i .

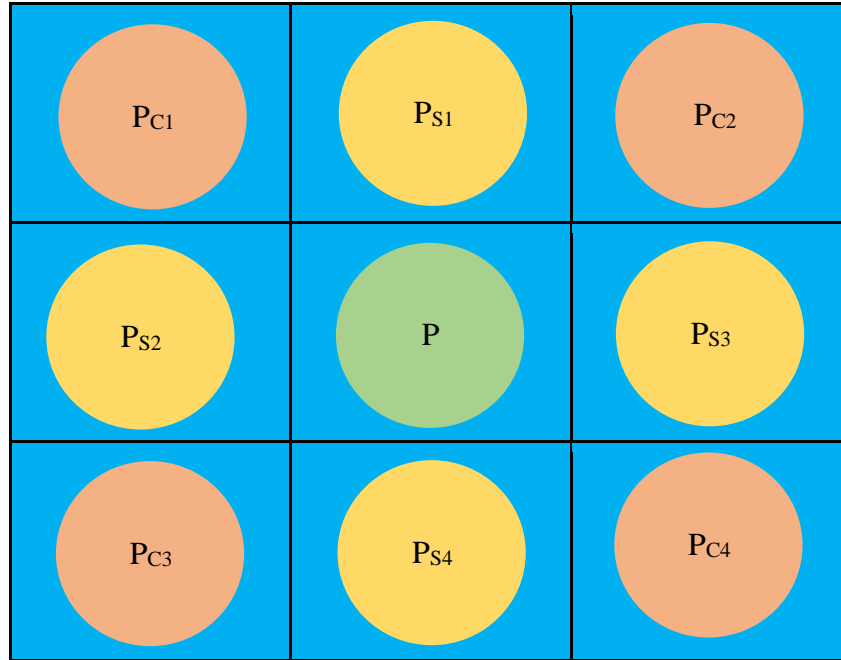


Figure 3-7: The R-factor is function of the surrounding rod power.

Chapter 4 EXPERIMENTAL RESULTS

Presented below are the comparison of binning versus Pareto sorting, the BP analysis cases, and the second BWR optimization problem. The results of the SA may be found in Appendix One: Sensitivity Analysis Results and Discussion. The results of these cases are omitted from the main body of the report for brevity.

4.1 PWR Geometry Solution Front Test Case

The first category and case tested with the MOOGLE algorithm was a comparison of Pareto front sorting versus the bin sort method used. Solution fronts for the two selection methods are presented in Figure 4-1.

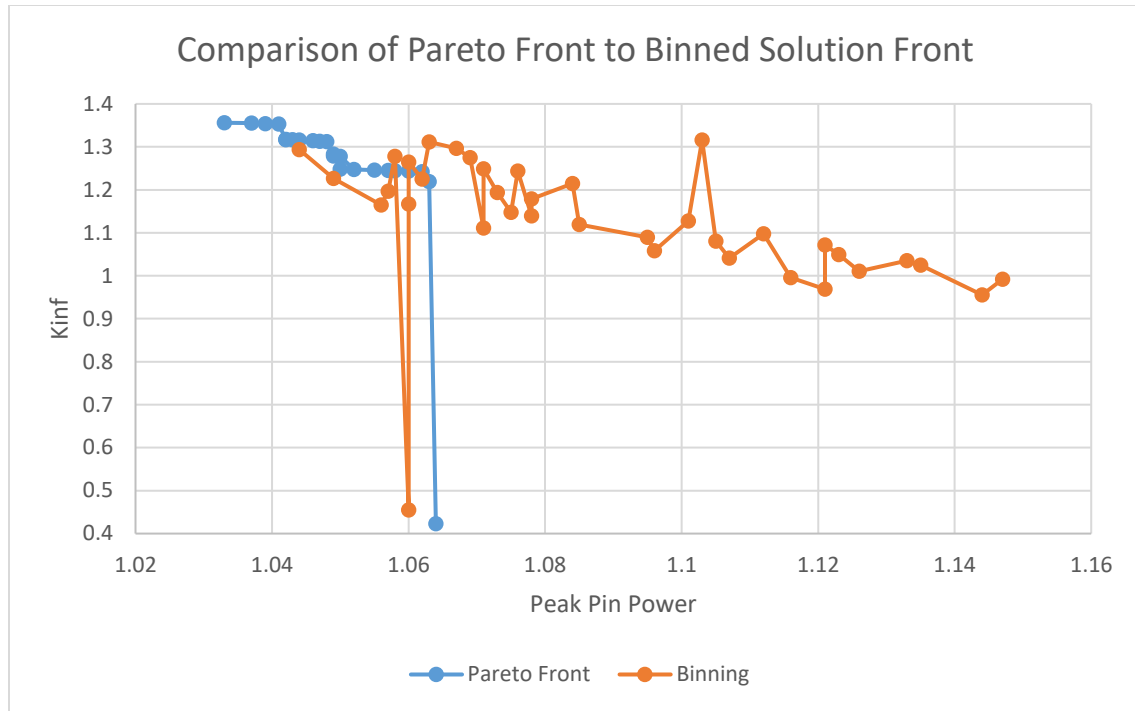


Figure 4-1: Comparison of a binned solution front to the Optimal Pareto Front for the optimization of a small number of rods at beginning of cycle.

Figure 4-1 shows that the Pareto Front method for selecting solutions produced a better minimum peak pin power than the solution front binning method. However, the binning method produced comparable results to the Pareto Front sorting method in the overlapping regions. Additionally, binning of the solution front produced a far wider range of usable solutions than the Pareto Front method.

4.2 Burnable Poison Analysis Results

The number of generations for the runs of the IFBA only and gadolinium only cases are presented in Table 4-1. The average number of solutions per bin and associated error for the average value for the optimization using only IFBA and gadolinium as BP is presented in Figure 4-2. The average number of solutions per bin and associated error in the average number of solutions for the optimization using only IFBA for BP is presented in Figure 4-3. The average and error in counts per bin for the gadolinium only case are presented in Figure 4-4. Figure 4-5 shows the burnable

poison distribution for the base, IFBA only, and gadolinium only optimization cases, and the average number of burnable poison rods used in each optimization. Figure 4-6 shows the percentage of solutions that use each rod type.

Table 4-1: Number of Generations for Burnable Poison Analysis

Analysis Name	Case Number					
	1	2	3	4	5	Average
Base	66	71	58	52	62	62
IFBA Only	62	54	62	59	61	60
Gadolinium Only	37	63	33	61	78	55

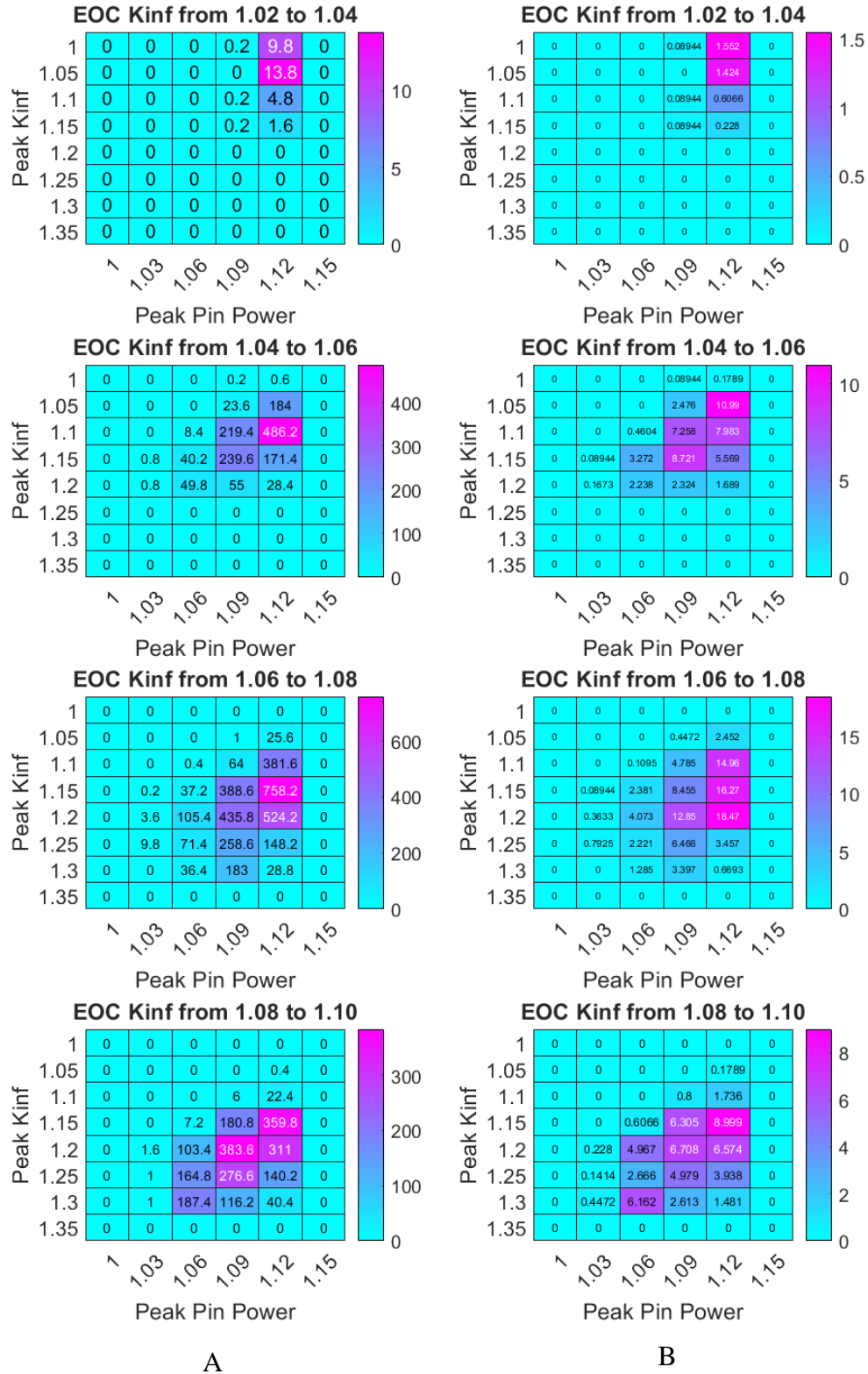


Figure 4-2: Base Case Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

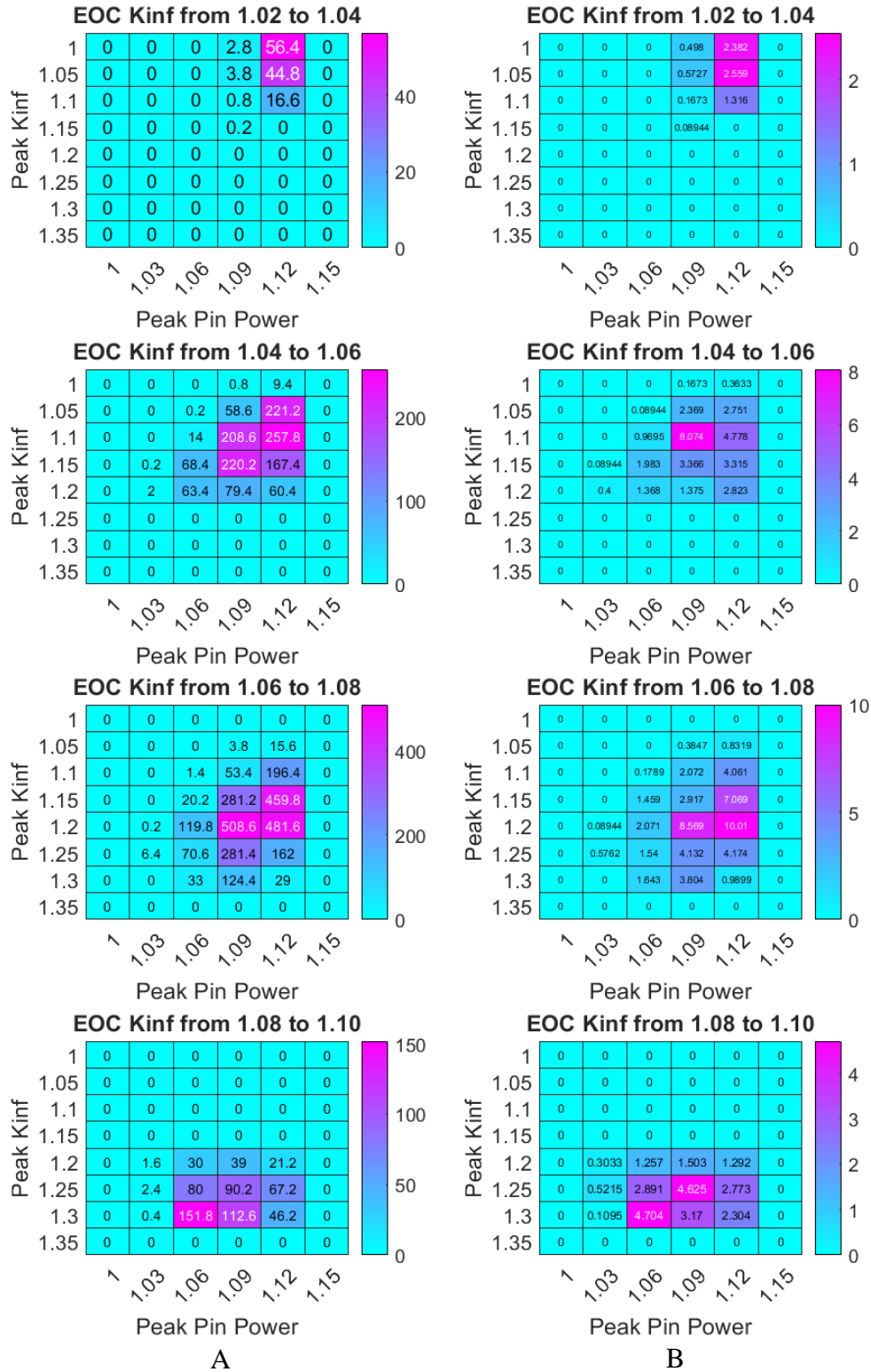


Figure 4-3: IFBA Only Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

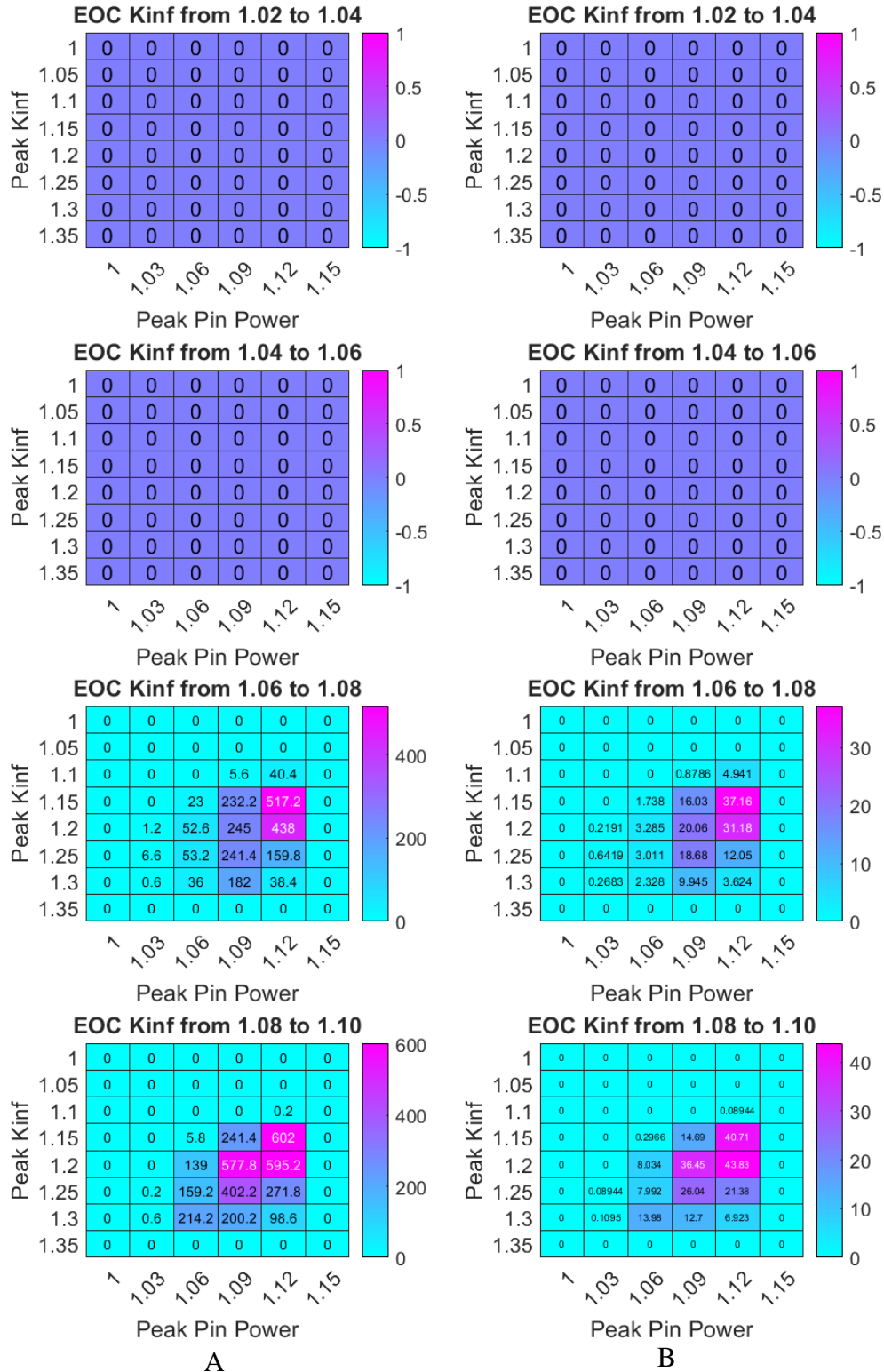


Figure 4-4: Gadolinium Only Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

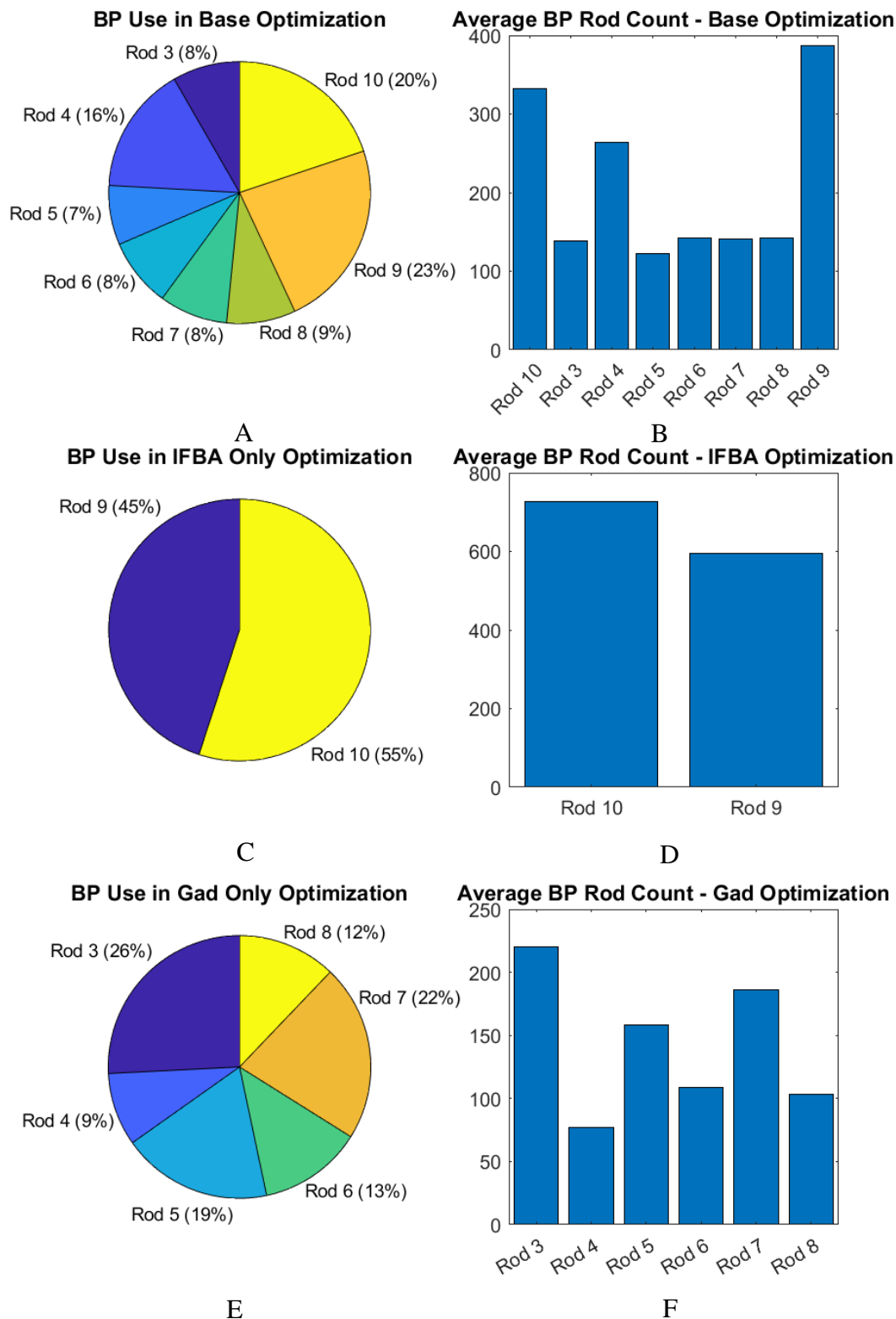


Figure 4-5: BP use in Optimizations using three different rod sets. A: BP distribution using IFBA and Gad. B: BP rod counts using IFBA and Gad. C: BP distribution using IFBA only. D: BP rod counts using IFBA only. E: BP distribution using Gad only. F: BP rod counts using Gad only.

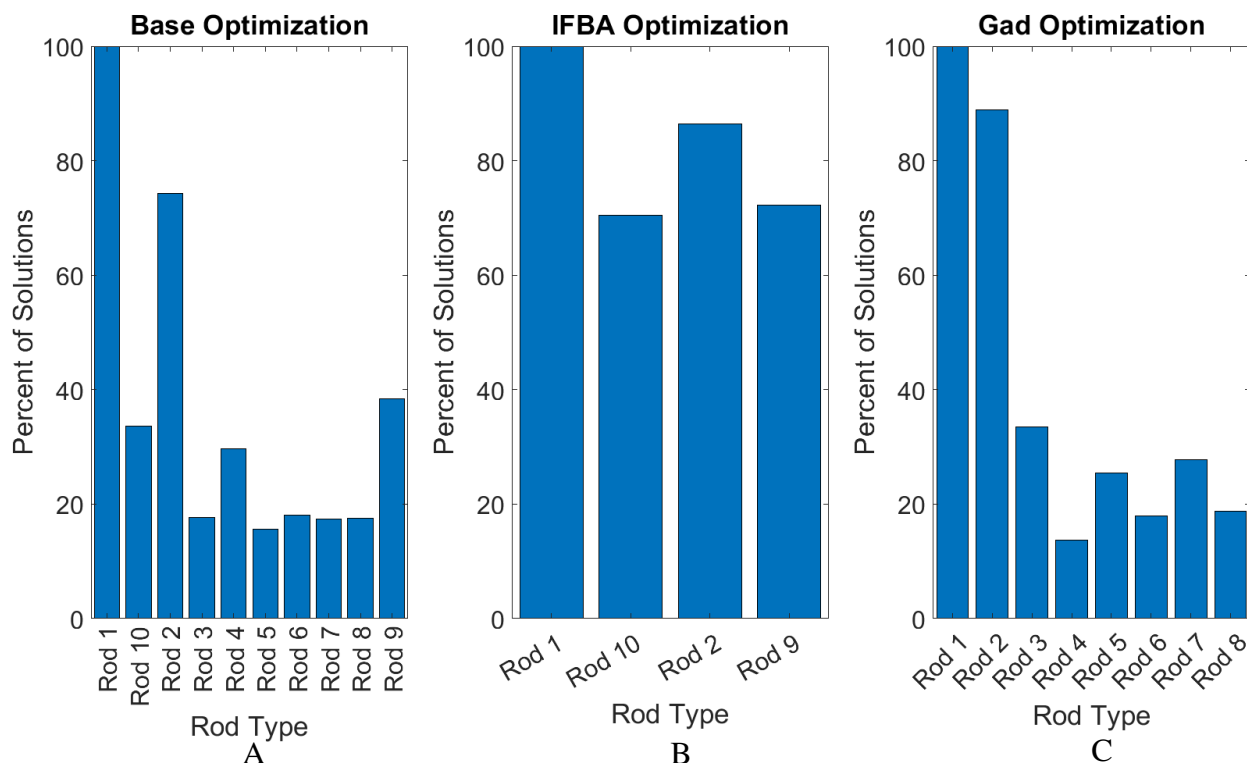


Figure 4-6: Average percentage of lattice solutions in final population using each rod type for the three rod set optimizations. A: IFBA and Gad rod set, B: IFBA Only rod set, C: Gadolinium only rod set

It is interesting to note that when both IFBA and gadolinium are used as burnable poisons, the gadolinium rods are used in relatively even amounts. Rod 4 is used more than any other gadolinium rod though. When only gadolinium is allowed as the burnable poison however, there is a clear preference. Gadolinium rods with an accompanying uranium enrichment of 4.40% are used more often than rods with an enrichment of 4.95%. Additionally, rod 4 is the least used gadolinium rod.

A solution containing both IFBA and gadolinium as the BP is presented in Figure 4-7. A solution containing only IFBA as the BP is presented in Figure 4-9. A solution containing only gadolinium as the BP is provided in Figure 4-10.

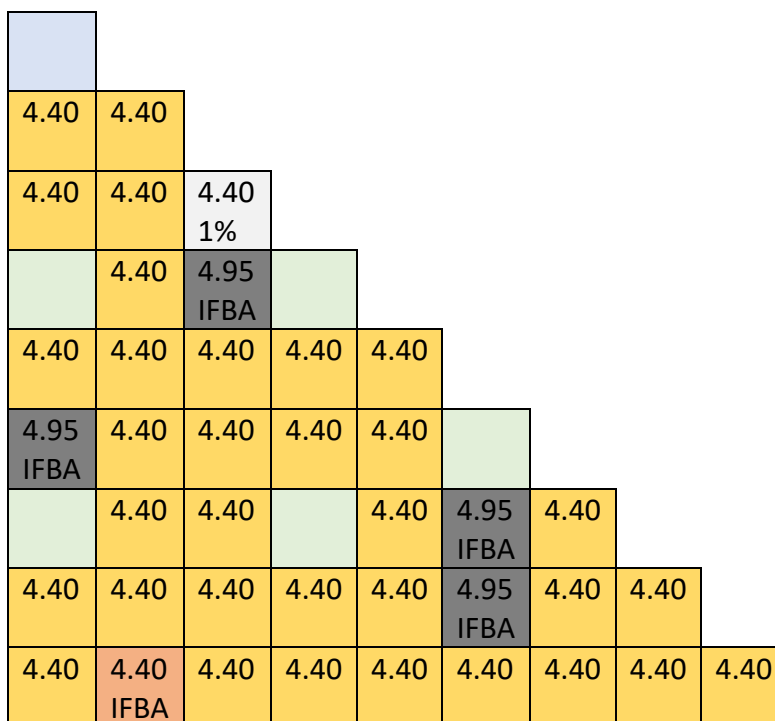


Figure 4-7: Lattice Solution combining IFBA and gadolinium as burnable poisons. The solution had a peak pin power of 1.132, peak kinf of 1.04483, and end kinf of 1.03618.

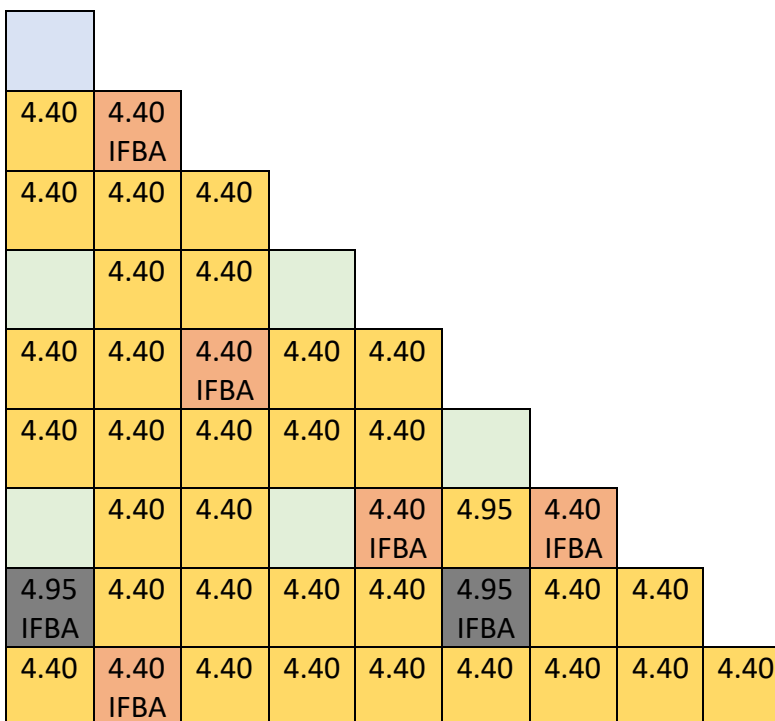


Figure 4-8: Lattice Solution using only IFBA as burnable poison. The solution had a peak pin power of 1.108, peak kinf of 1.04773, and end kinf of 1.03935.

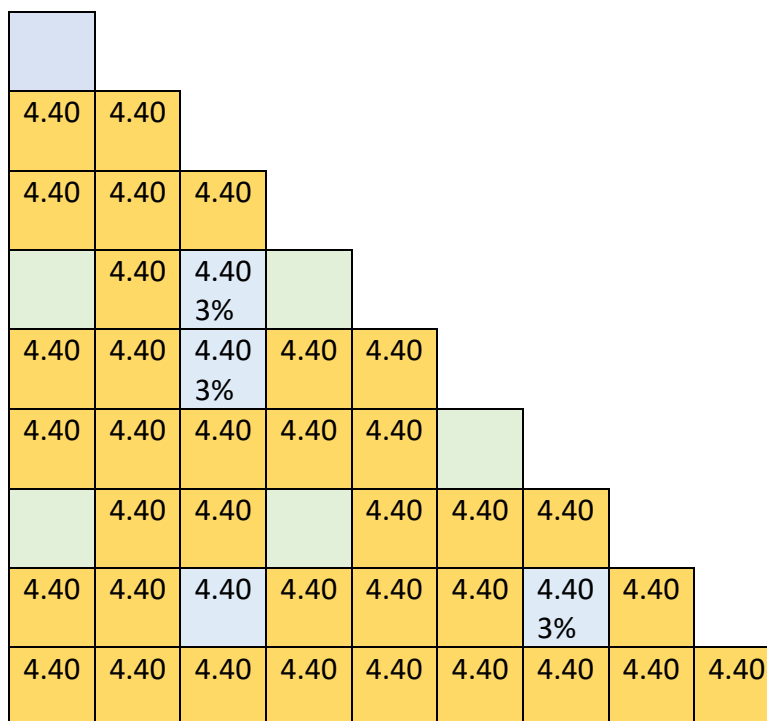


Figure 4-9: Lattice Solution using only gadolinium as burnable poison. The solution had a peak pin power of 1.141, peak kinf of 1.15309, and end kinf of 1.15309.

4.3 BOC BWR Problem

The BOC optimization of a BWR fuel bundle's BTF occurred over 26 generations. The solution space of the optimization is presented in Figure 4-10. The final population metrics for the optimization are presented in Table 4-2. The Mustang algorithm optimized two different cases. In the first case, no constraint was placed on kinf values for the optimization, so the objective was to simply achieve the lowest BTF value possible. The second case minimized BTF at a target BOC kinf value of 1.2. The most comparable results produced by MOOGLE are presented here. The minimum BTF solution is presented in Figure 4-11. The solution with the best BTF value at a BOC kinf of 1.2 is shown in Figure 4-12.

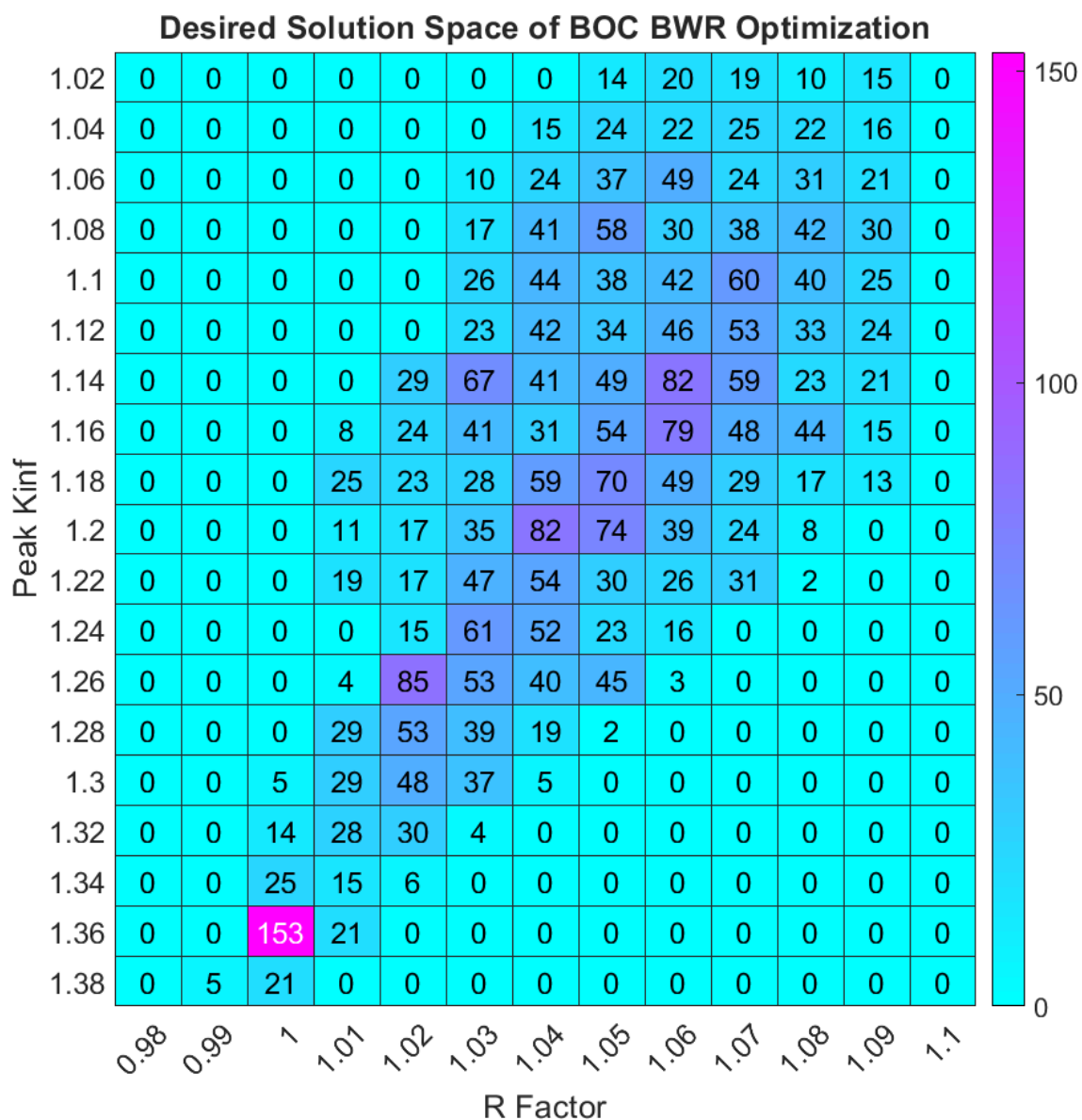


Figure 4-10: Solution space of the BOC BWR lattice optimization problem.

2.00										
3.20	3.60									
3.95	4.40	4.60								
4.40	4.90	4.60	4.60							
4.40	4.60	4.60	4.60	4.90						
4.40	4.60	4.90	0	0	4.90					
3.95	4.90	4.60	0	0	4.60	4.60				
3.60	4.60	4.60	4.60	4.60	4.60	4.60	4.60			
3.20	4.40	4.60	4.90	4.40	4.60	4.90	4.60	4.90		
2.00	3.20	4.40	4.90	4.90	4.90	4.90	4.90	4.40	3.20	

Figure 4-11: Lattice Solution with lowest R factor produced by MOOGLE Algorithm using 9 rod types for the BOC BWR optimization problem.

2.00										
3.20	3.60									
3.95	4.90	4.40 7.0%								
4.40	4.90	4.60	4.60							
4.40	4.60	4.60	4.60	4.90						
4.40	4.60	4.6 0	0	0	4.90					
3.95	4.90	4.60	0	0	4.60	4.60				
3.60	4.40 7.0%	4.90	4.60	4.60	4.90	4.60	4.40 6.0%			
3.20	4.40	4.60	4.90	4.60	4.60	4.90	4.60	4.90		
2.00	3.20	4.40	4.90	4.90	4.90	4.90	4.90	4.40	3.20	

Figure 4-12: Lattice Solution with lowest R factor produced by MOOGLE Algorithm using 9 rod types at a BOC Kinf value near 1.20 for the BOC BWR optimization problem. Note: The first row indicates rod enrichment, the second row indicates rod gadolinium concentration.

Table 4-2: Minimum, Maximum, and Average Parameter Values for BOC BWR Optimization

Parameter	Average Value	Minimum Value	Maximum Value
R factor	1.0485	0.9987	1.0917
Peak Kinf	1.163	1.024	1.361

4.4 Depletion and Multiple Zone BWR Problem

The number of generations for the three different rod numbers used for the second BWR problem can be found in Table 4-3. The number of counts per bin for the eighteen-rod case are shown in Figure 4-13. The number of counts per bin for the fifteen-rod case are shown in Figure 4-14. The number of counts per bin for the twelve-rod case are shown in Figure 4-15. Average values for the optimization objectives are presented in

Table 4-4. Minimum values for the optimization objectives are presented in Table 4-5. Maximum values for the optimization objectives are given in Table 4-6.

Table 4-3: Number of Generations for the Second BWR Optimization Problem

Number of Rods	Number of Generations
18	81
15	40
12	93

Table 4-4: Average Objective Values for the Second BWR Optimization Problem

Number of Rods	BTF	Peak Kinf	EOC Kinf
18	1.063	1.239	1.091
15	1.065	1.226	1.077
12	1.061	1.231	1.085

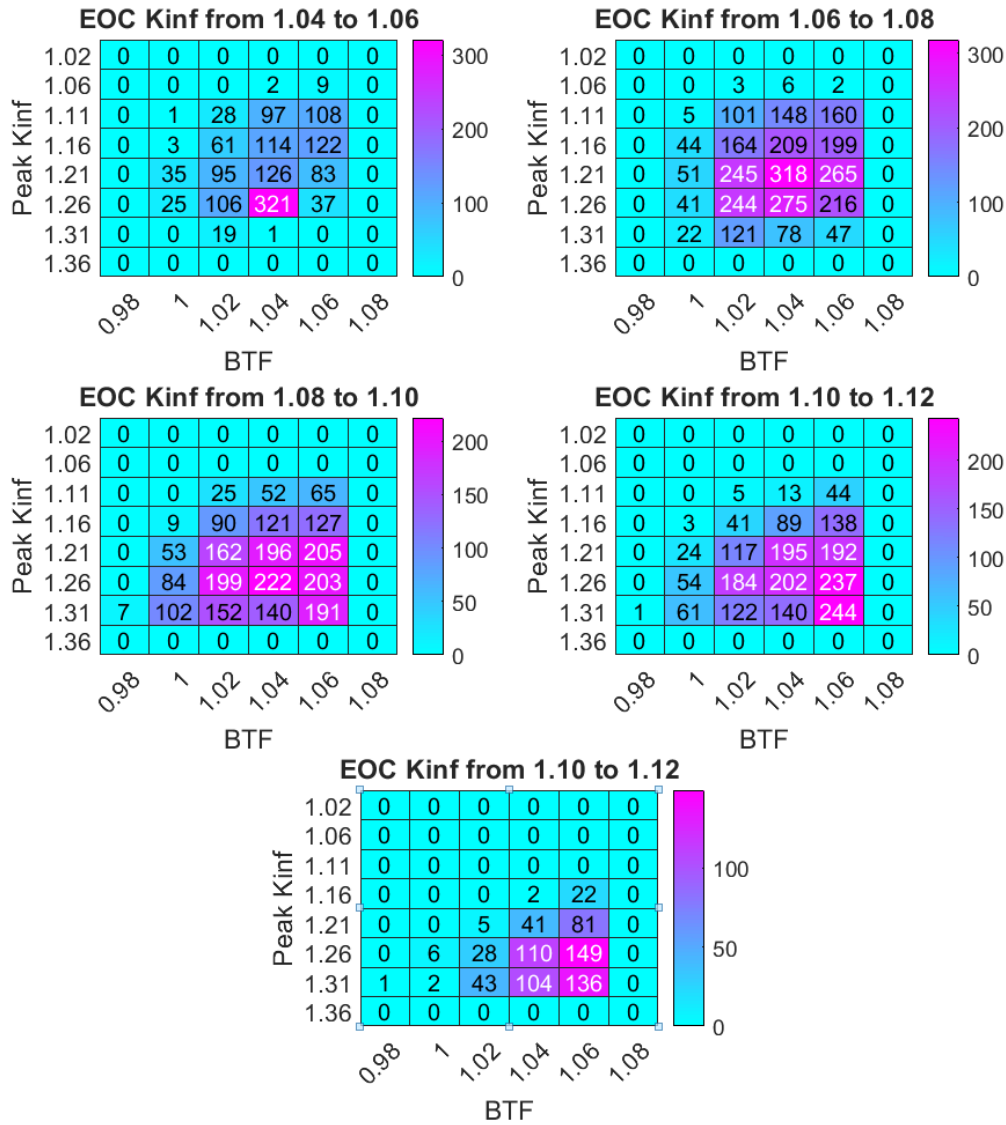


Figure 4-13: Number of Counts per bin for the second BWR problem eighteen rod case.

Table 4-5: Minimum Objective Values for the Second BWR Optimization Problem

Number of Rods	BTF	Peak Kinf	EOC Kinf
18	1.012	1.086	1.051
15	1.021	1.093	1.053
12	1.013	1.087	1.050

Table 4-6: Maximum Objective Values for the Second BWR Optimization Problem

Number of Rods	BTF	Peak Kinf	EOC Kinf
18	1.100	1.374	1.141
15	1.098	1.344	1.100
12	1.099	1.354	1.118

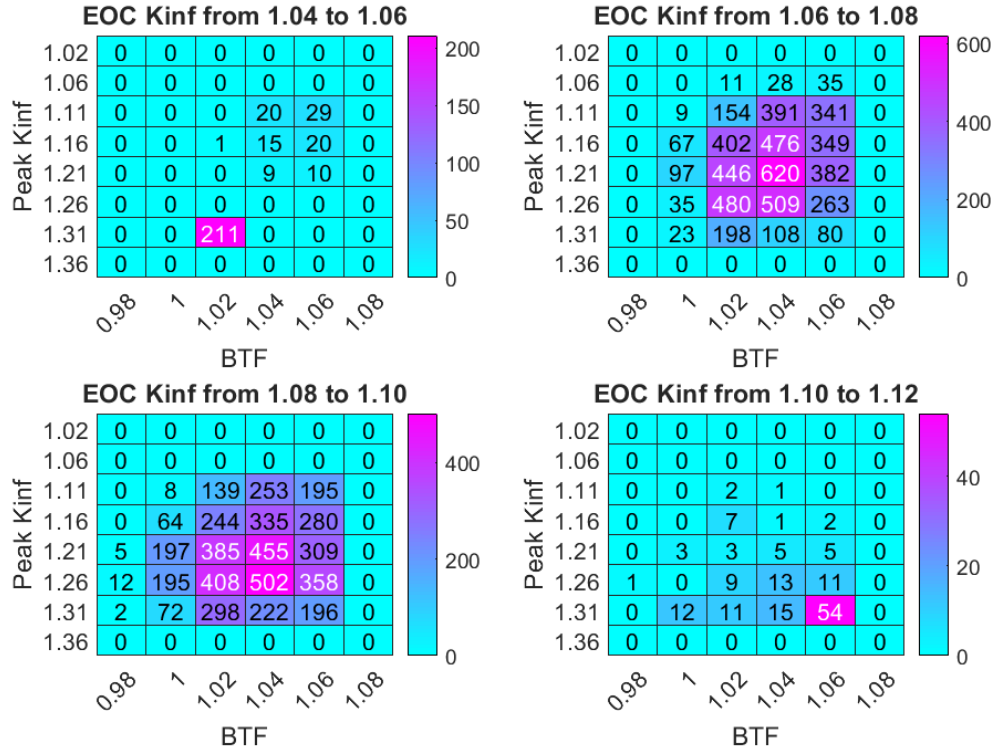


Figure 4-14: Number of counts per bin for the second BWR problem for the fifteen-rod case.

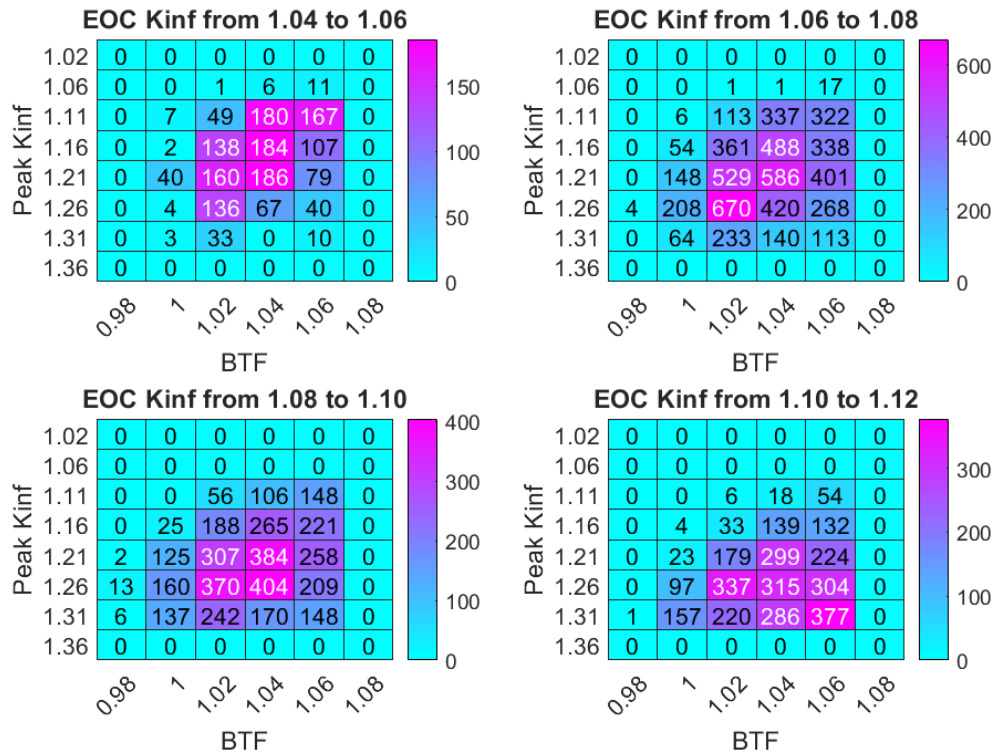


Figure 4-15: Number of counts per bin for the second BWR problem for the twelve-rod case.

The breakdown of rod use is shown in Figures 4-16 and 4-17, and Table 4-7. Figure 4-16 and Table 4-7 shows how the percentage each rod type makes up in the optimization for the three different cases. Figure 4-17 shows the percentage of lattices containing each rod type. It is interesting to note that rods using gadolinium in the bottom axial zone are used in preference over rod types containing gadolinium in upper zones. The figures show that rods containing gadolinium in the lowest zone of the rod are used more than other rod types containing gadolinium.

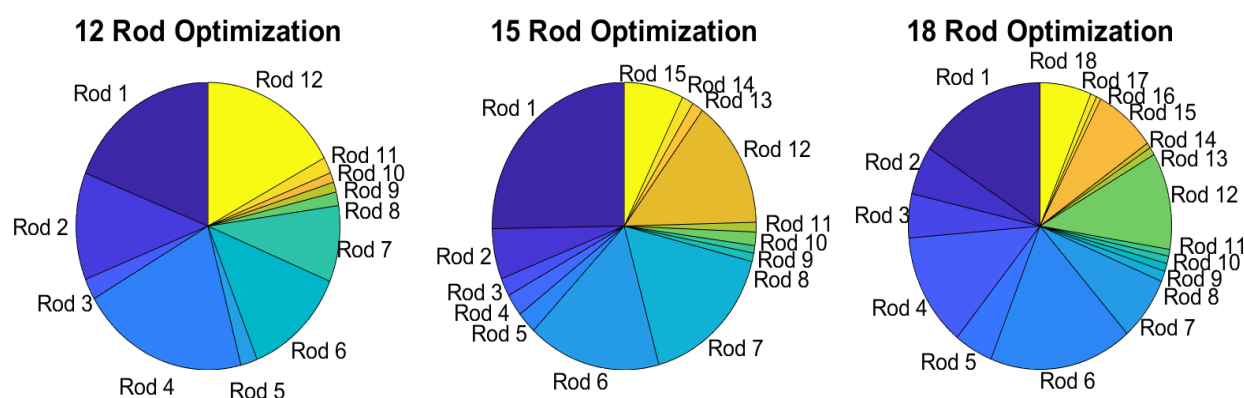


Figure 4-16: Comparison of rod types used by the three different optimization cases for the second BWR optimization problem.

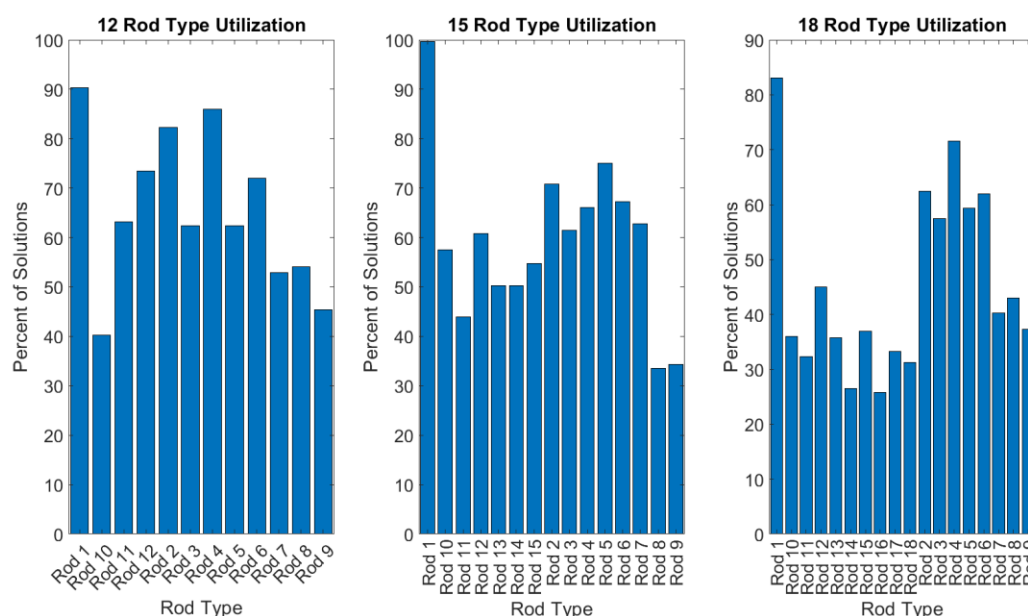


Figure 4-17: Percent of lattices containing each rod type for the second BWR optimization problem.

Table 4-7: Percentage of Rod Types Used in Second BWR Optimization

Rod Number	Percent of total rods used in Optimization		
	18 Rod Case	15 Rod Case	12 Rod Case
1	16	25	19
2	5	6	12
3	5	2	2
4	13	2	21
5	5	2	2
6	18	16	13
7	7	17	9
8	1	1	2
9	1	1	1
10	1	2	1
11	1	1	2
12	11	14	17
13	1	1	
14	1	1	
15	8	7	
16	1		
17	1		
18	6		

Chapter 5 Analysis of Results

Two methods are employed to compare different optimization cases to each other. The first method is epsilon indicator distance testing, in which an optimal solution front composed of the five base and test runs is compared to the ten individual optimizations. The second method compares the solution spaces explored by the test and base optimization cases.

5.1 Burnable Poison Analysis Discussion

Table 5-1 gives the average distances between the individual optimization runs of the base and test case and the optimal solution front composed of these cases. Figure 5-1 compares the solution front and solution spaces of the IFBA only test and base cases. Figure 5-2 compares the solution front and solution spaces of the gadolinium test and base cases. Figure 5-3 directly compares the solution fronts and solution spaces of the IFBA only, gadolinium only, and base case which used both gadolinium and IFBA as BP.

Table 5-1: Average Distance Comparison of IFBA and Gad Only

Case Name	Case Part	Average Distance for EOC Kinf Range				
		1.02 – 1.04	1.04 – 1.06	1.06 – 1.08	1.08 – 1.10	Total
IFBA	Test	2.69	8.88	14.31	67.80	93.67
	Base	7.08	13.35	14.44	14.79	49.66
	Difference	-4.39	-4.48	-0.13	53.00	44.01
Gadolinium	Test	NA	NA	43.67	31.07	74.74
	Base	3.78	9.73	14.62	14.61	42.74
	Difference	3.78	9.73	29.05	16.45	32.00

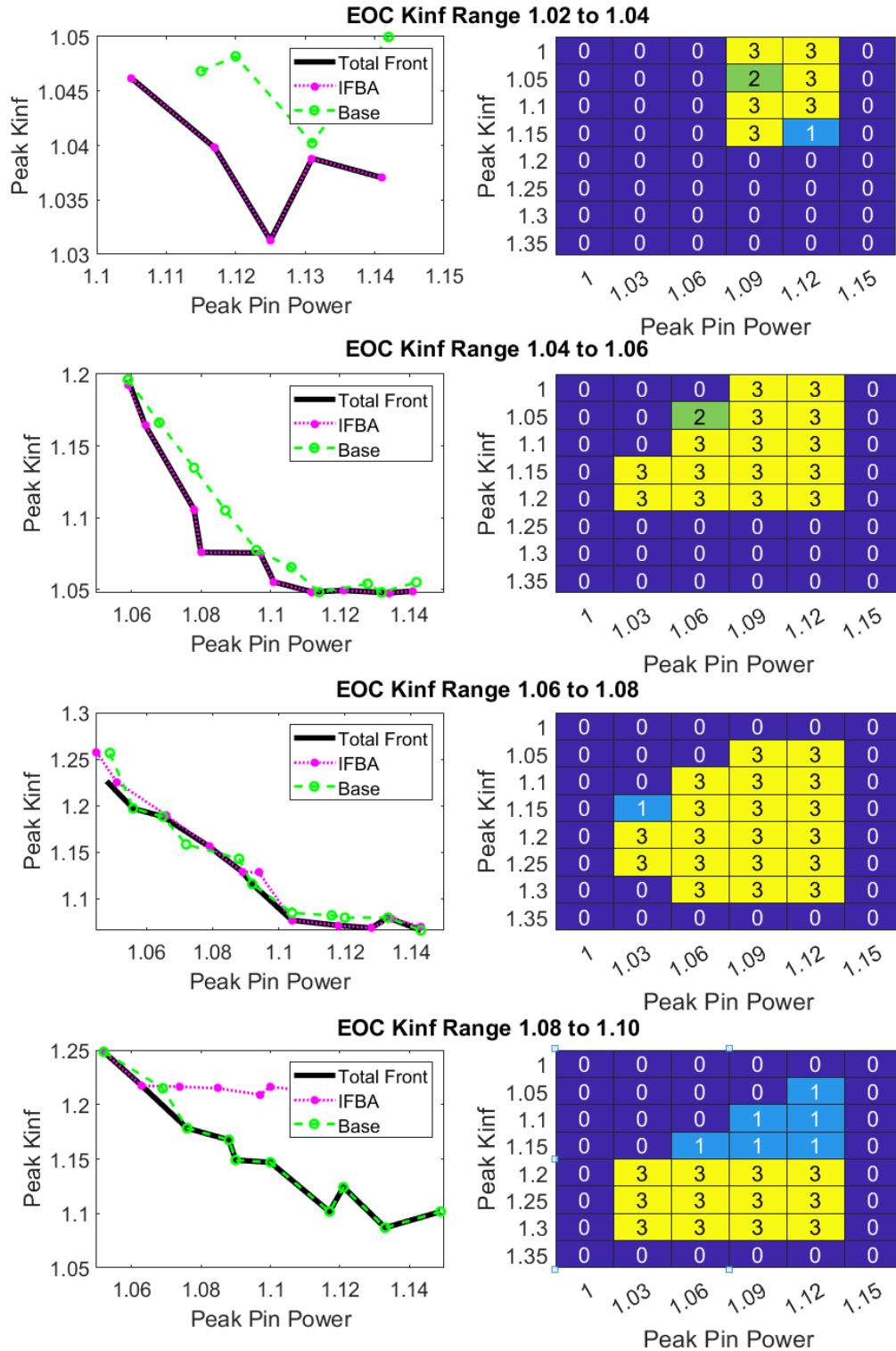


Figure 5-1: Solution Front and Solution space comparison between base and the IFBA only test cases. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.

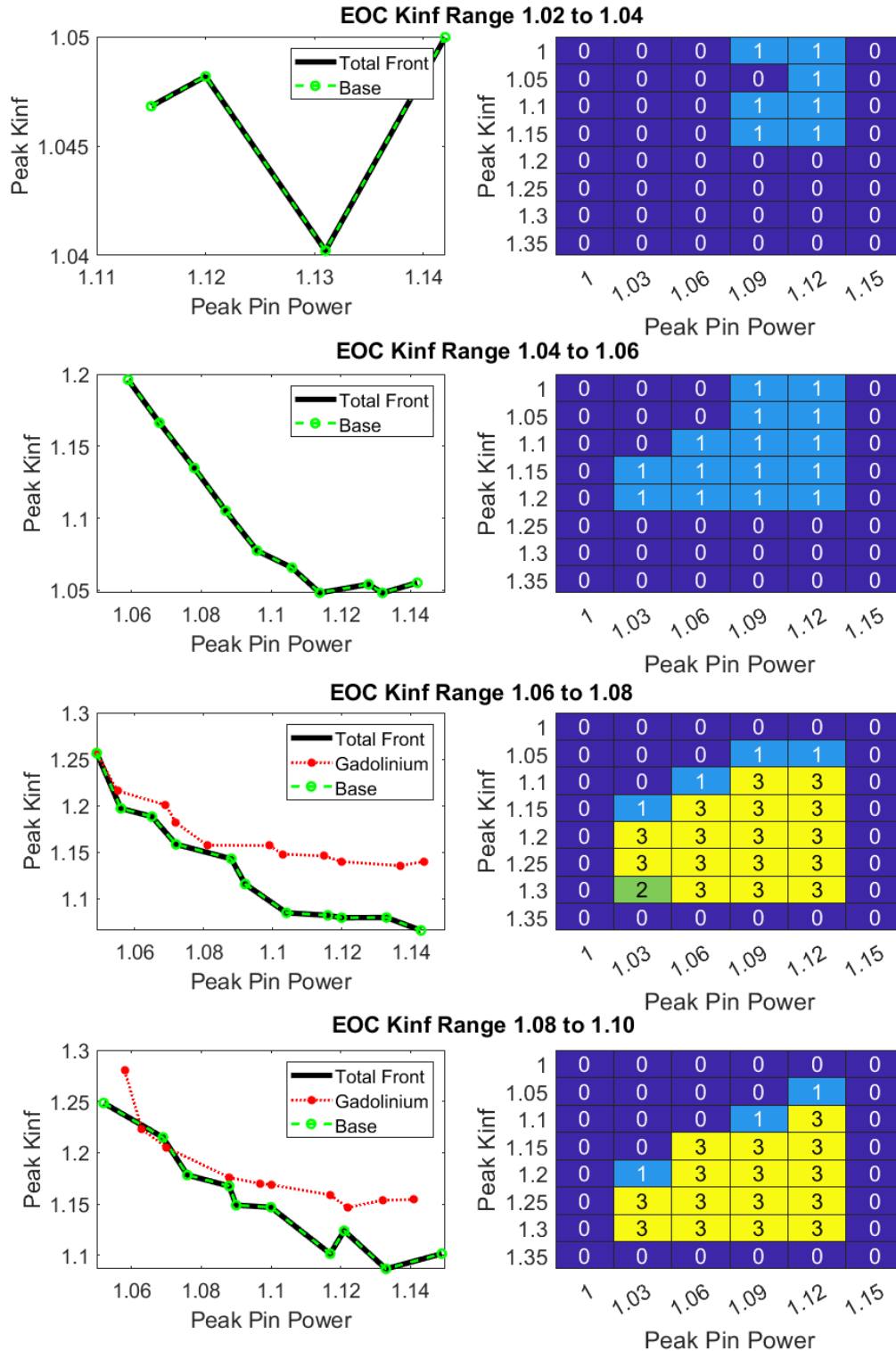


Figure 5-2: Solution Front and Solution space comparison between base and the gadolinium only test cases. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.

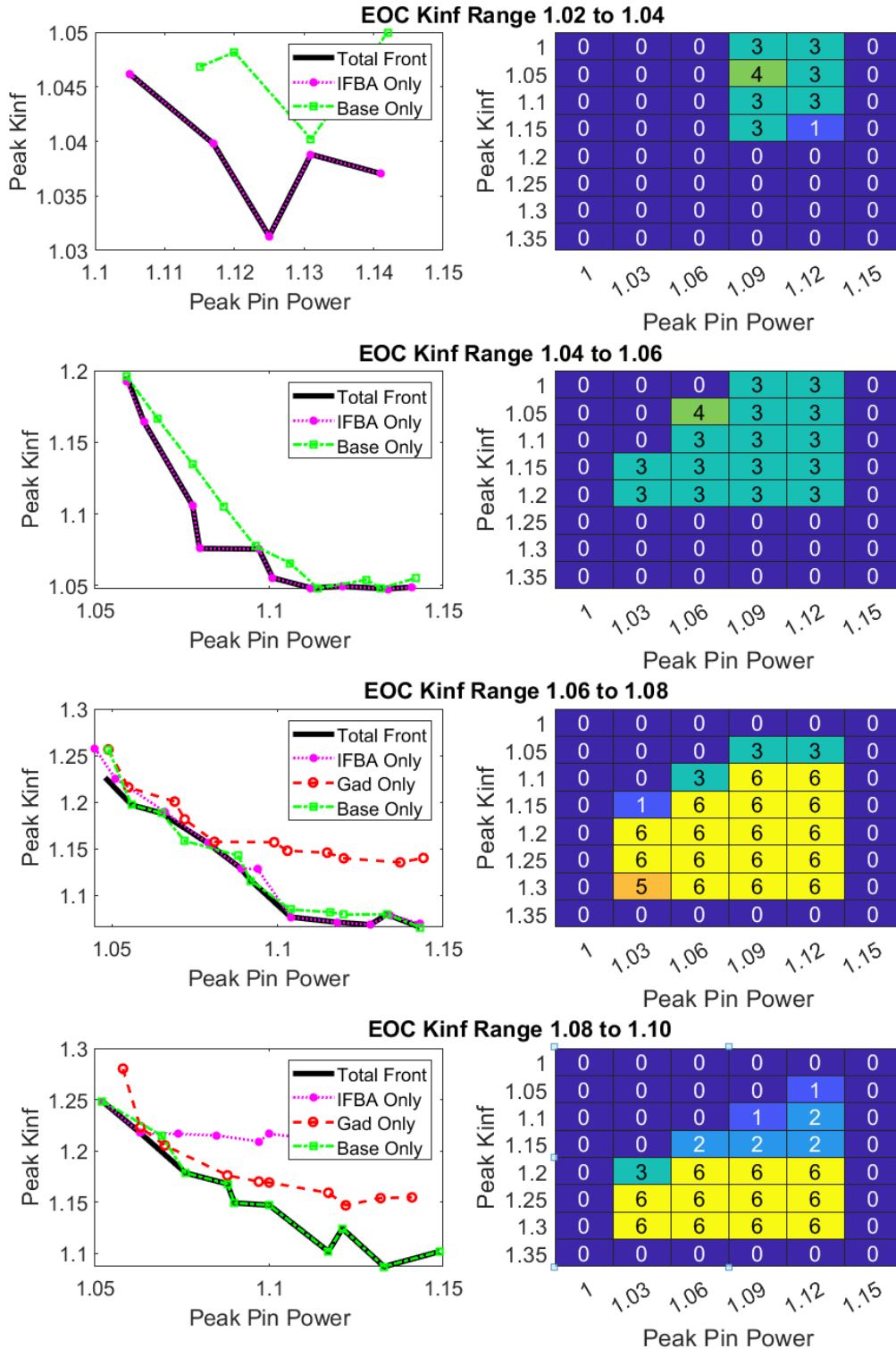


Figure 5-3: Solution Front and Solution space comparison between base, ifba only, and gadolinium only test cases. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by ifba and base. 3 is filled by gadolinium and base. 4 is ifba only, 5 is gad only, and 6 is all three cases.

It is important again to note that the results presents in Figure 5-1 through Figure 5-3 represent the desired solution space. This means that it would be incorrect to assume that because no solutions are presented for the gadolinium case that have an EOC kinf value less than 1.04, that the use of gadolinium makes such an EOC kinf value impossible. What this indicates, is that no solutions exist that meet the requirements on PPF or peak kinf.

Peak kinf and EOC kinf values are generally correlated, with a high peak kinf indicating a high EOC kinf, and a low peak kinf indicating a low EOC kinf. Gadolinium is a strong burnable poison; a single fuel rod containing gadolinium has a noticeable impact on PPF and kinf. Several gadolinium rods are required to achieve low EOC Kinf results. These rods will have a strong effect on PPF. The reason why no solutions using only gadolinium are presented for lower EOC kinf regions is that designs at these EOC kinf violate the limits on PPF placed on the optimization. This same reasoning likely explains why higher EOC IFBA solutions are not found.

Figure 5-3 illustrates the topics of the previous paragraph well. Figure 5-3 also shows that by combining IFBA and gadolinium as a burnable poison, one gets significantly improved control over reactivity without having to sacrifice on PPF. The large impact gadolinium has can be used for course reactivity control, with IFBA added to provide a fine tuning.

5.2 BOC BWR Optimization Discussion

Figure 5-4 provides a tradeoff between BTF and Kinf at BOC. The tradeoff curves displays the behavior expected, that minimized BTF and minimized Kinf come at the cost of one another. The solution properties of the two solutions presented in Figure 4-11 and Figure 4-12, as well as the results of the Mustang algorithm are presented in Table 5-2.

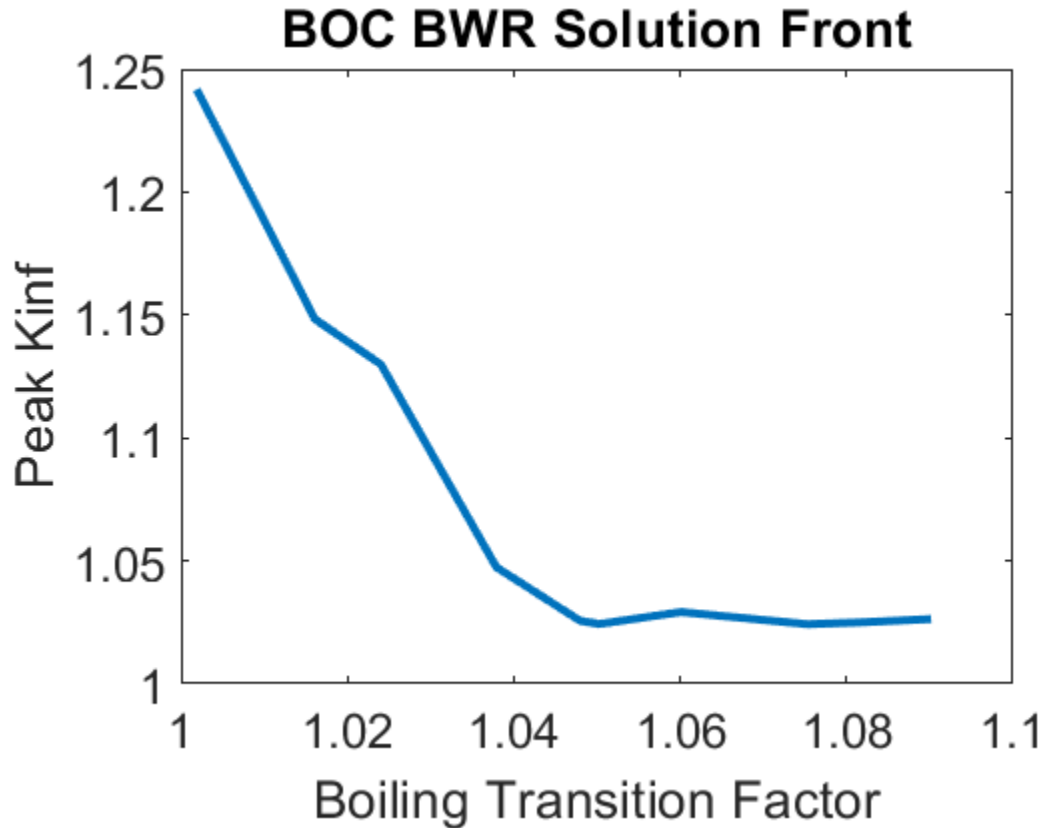


Figure 5-4: Solution front curve for BOC BWR optimization problem.

Table 5-2: Comparison of MOOGLE algorithm results to the Mustang Algorithm

Optimization Code	R factor	Peak Kinf
MOOGLE	0.9987	1.3615
MOOGLE	1.016	1.1997
Mustang	1.001	1.1074
Mustang	1.029	1.1994

Mustang was tested using two different cases. In the first case, no constraint was placed on kinf, and the goal was simply to achieve the lowest possible BTF value possible. This is shown in line three of Table 5-2. The second case was to minimize BTF with a target Kinf of 1.2. These results are shown in row four of Table 5-2. MOOGLE, in a single run, produced results that bested both of the Mustang cases. MOOGLE found an overall lower BTF value than the unconstrained Mustang case, as shown in row one of Table 5-2. Additionally, at a BOC kinf value of 1.2, MOOGLE produced a lower BTF value, as seen by comparing rows two and four of

Table 5-2. This clearly demonstrates that MOOGLE improves on its predecessor the Mustang algorithm.

5.3 Depletion and Multiple Zone BWR Problem

A comparison of the solution front of the three different rod counts provided in Figure 5-5. Distances between the solution fronts and an optimal front created from the three different cases is provided in Table 5-3. A comparison of the solution spaces covered by the three cases is provided in Figure 5-6.

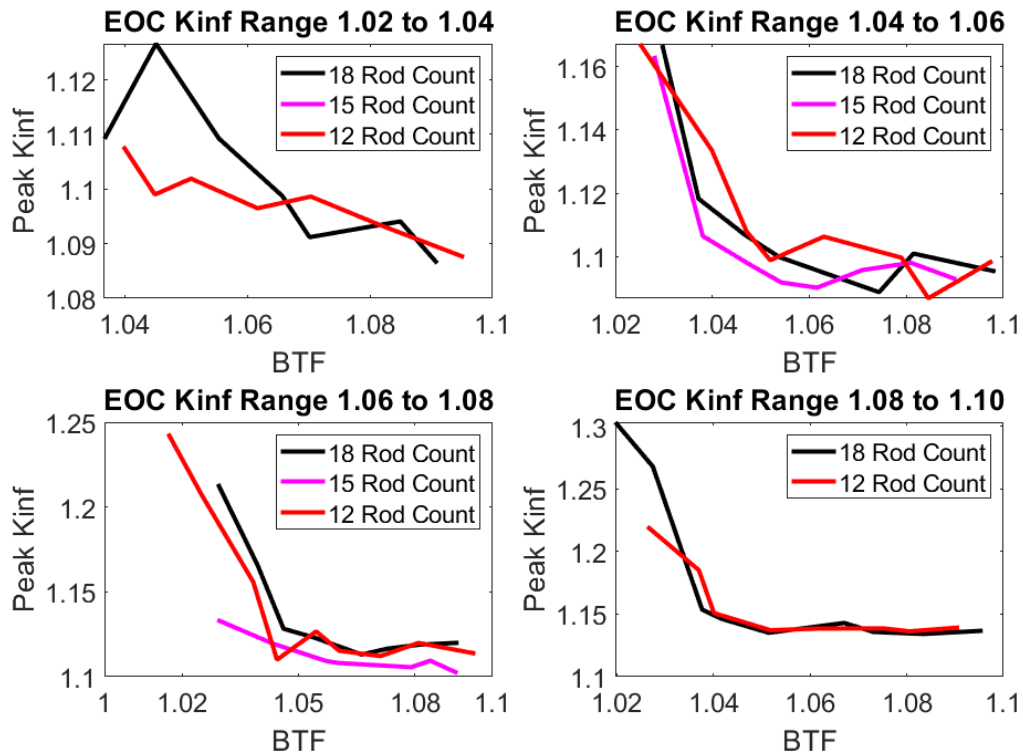


Figure 5-5: Solution front for the 12, 15, and 18 rod cases of the second BWR optimization problem.

Table 5-3: Distance between the three cases of the second BWR optimization problem

Rod Number	Average Distance for EOC Kinf Range				
	1.02 – 1.04	1.04 – 1.06	1.06 – 1.08	1.08-1.10	Total
18	3.020	8.533	14.199	5.474	31.226
15	20.236	0.371	12.272	NA	32.879
12	2.923	7.154	9.445	12.526	32.048

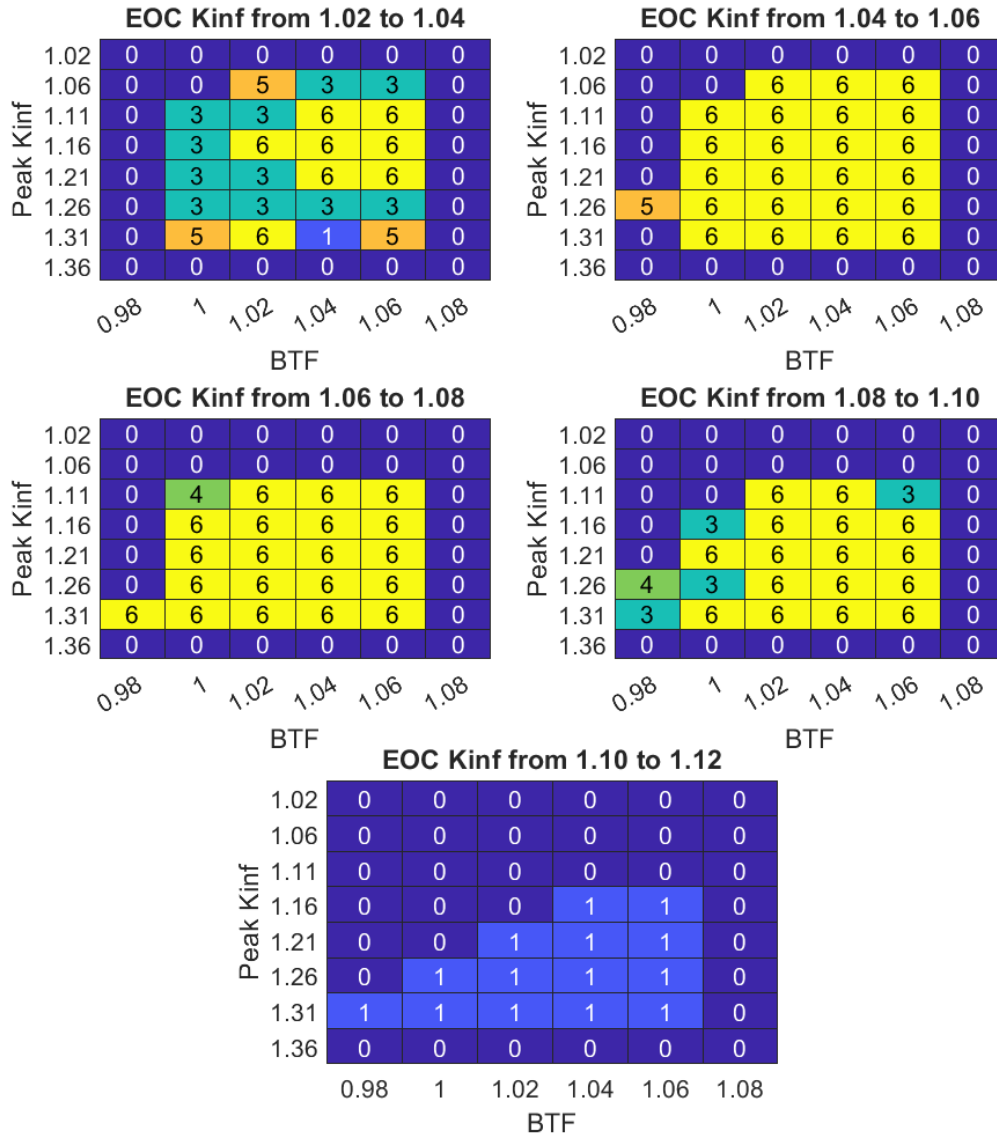


Figure 5-6: Comparison of the Solution spaces covered by the three different rod cases. 1 indicates bin is only filled by 18 rod case. 2 indicates bin is fill by 15 and 18 rod case. 3 indicates bin filled by 12 and 18 rod case. 4 indicates only filled by 15 rod case. 5 indicates bin filled only by 12 rod case. 6 indicates bin is filled by all three cases.

As Figure 5-5, Figure 5-6, and Table 5-3 show, the results are not very consistent between the three different cases. Such behavior should not be expected because the twelve and fifteen rod cases are subsets of the eighteen rod case, meaning that the fifteen rod case should show the same or improved behavior on the twelve rod case, and the eighteen rod case should do the same. Unfortunately, this is the result of an inconsistent analysis caused by problems with the torque job

submission script on the cluster used. A proper analysis of the three results would likely show much more consistent results between the three different rod analyses.

This does not mean that the three analyses are of no value whatsoever though. What they do show is that the rod types fifteen and eighteen rod cases do not significantly improve the results of the optimization. This demonstrates the MOOGLE algorithms ability to allow core designers to see the improvements, and subsequent increase in manufacturing costs, that the use of additional rod types causes. In this case, the six additional rod types added do not significantly improve the optimization. In this case, the core designer would feel confident knowing that they can use the simplest optimization results and still get excellent performance from the designed fuel.

Chapter 6 Conclusions

Solution Front Comparison

The results show that binning the solution front produces a much wider array of solutions than a Pareto front sorting method. This allows designers to get a wider range of practical solutions to their design problem than if they used the Pareto front method.

Sensitivity Analysis

The results of the SA depict that the MOOGLE algorithm is sensitive to various settings. The SA shows that uniform selection weights allow the optimization to search the widest solution space possible. This wider solution space search allows for better solutions to be developed. Altering these weights can reduce the effectiveness of the MOOGLE optimization. Additionally, MOOGLE requires a large population and high number of generations to effectively search the solution space for complicated problems. The mutation rate test cases show that crossover is the most effective method for generating new solutions, and that higher mutation rates do not benefit the optimization. Finally, the results of the large bin size test cases show that not binning some

parameters does not affect or improves the results of the optimization. As shown by the optimization though, binning all parameters still provides valuable optimization results.

Burnable Poison Analysis

The burnable poison analysis shows that combining IFBA and gadolinium as burnable poisons in fuel assemblies produces more optimal assemblies than using solely IFBA or gadolinium. This goes with the general design principle that greater flexibility in the number of rod types allows for better designs to be developed.

This analysis also demonstrates the MOOGLE algorithm's ability to provide designers with the cost-benefit analysis of using additional rod types. For this case, it demonstrates that using additional rod types provides better solutions than using only one type of burnable poison.

First BWR Optimization Problem

The first BWR optimization indicates that the MOOGLE algorithm improves upon its predecessor, the Mustang algorithm. In a single optimization, MOOGLE was able to produce better results than those found by the Mustang algorithm. The results found by the Mustang algorithm also required two separate runs, instead of the single optimization run used by MOOGLE.

Second BWR Optimization Problem

The second BWR optimization demonstrates the MOOGLE algorithm's ability to show how the addition of rod types affects the results of the optimization. In this case, additional rod types did not significantly improve the optimization. It also shows the clear distribution of how each rod type is used within the optimization, allowing for rod designers to see what rods improve the optimization and are widely used, and which ones are rarely used or do not largely contribute to improving the solutions. Being able to determine rods of value and rods that do not improve the

optimization allows rod designers to reduce manufacturing costs by not using the fewest number of rod types and not including results that do not improve the optimization.

Overall Conclusions

The MOOGLE algorithm has been demonstrated as a powerful tool for the multi-objective optimization of PWR fuel assemblies and BWR fuel bundles. It improves upon the field of nuclear fuel management by providing designers with a wide array of valuable solutions for use in nuclear power reactors. Additionally, it allows designers to visualize the economic tradeoffs between improved performance and manufacturability through the addition of additional fuel rod types.

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APPENDIX

The number of generations over which all sensitivity analysis optimization cases were run can be found in Table A-0-1.

Table A-0-1: Number of Generations for Sensitivity Analysis Cases

Analysis Name	Case Number					
	1	2	3	4	5	Average
Base	66	71	58	52	62	62
First Selection Weight	59	60	56	79	72	65
Second Selection Weight	53	76	69	70	73	68
Third Selection Weight	48	61	50	48	62	54
Fourth Selection Weight	62	86	79	54	74	71
Fifth Selection Weight	61	57	56	56	61	58
Sixth Selection Weight	55	61	55	83	64	64
First Small Population	47	47	47	47	47	47
Second Small Population	76	45	64	92	86	73
First Alternate Mutation	81	55	66	54	78	61
Second Alternate Mutation	53	47	59	49	58	53
Large Power Bin Size	62	62	62	62	62	62
Large Peak Kinf Bin Size	62	62	62	62	62	62
Large End Kinf Bin Size	62	62	62	62	62	62

Table A-0-1 shows that the average number of solutions for the base case was 62. The case with the shortest average number of generations was the first small population test. This is because Equation 3.2 was used to calculate the maximum number of generations allowed, making the maximum number of generations 47. This indicates that the first small population test potentially suffered from premature convergence. The smallest average number of generations using equation 2.2, the normal method for determining the maximum number of generations was the second alternate mutation rate test.

The case that required the highest average number of generations was the second small population test. This makes sense, as extra generations are required to compensate for the lack of

solutions in the optimization population. The case with the second highest average number of generations was the fourth selection weight case.

The average final population metrics averaged over the five runs for each analysis are presented in Table A-0-2. The average minimum values for the final population objectives may be found in Table A-0-3. Table A-0-4 presents the average maximum values of the optimization objectives for the final population for each of the sensitivity analysis cases.

Table A-0-2: Averaged Average Final Population Metrics for Sensitivity Analysis

Analysis Name	Peak Pin Power	Peak Kinf	EOC Kinf
Base	1.112	1.199	1.072
First Selection Weight	1.111	1.199	1.072
Second Selection Weight	1.112	1.197	1.071
Third Selection Weight	1.113	1.201	1.073
Fourth Selection Weight	1.112	1.197	1.071
Fifth Selection Weight	1.112	1.199	1.072
Sixth Selection Weight	1.112	1.199	1.072
First Small Population	1.114	1.205	1.072
Second Small Population	1.114	1.200	1.079
First Alternate Mutation	1.113	1.198	1.072
Second Alternate Mutation	1.112	1.200	1.072
Large Power Bin Size	1.091	1.179	1.067
Large Peak Kinf Bin Size	1.105	1.133	1.070
Large End Kinf Bin Size	1.107	1.197	1.082

The solution space for the base and sensitivity analysis test cases are presented in Figure A-1 through Figure A-6. Each figure presents the average number of solutions produced per bin, and the error in that average. Note that the bin sizes have been altered for readability and differ from the bin sizes used in the optimization.

Table A-0-3: Average Minimum Final Population Metrics for Sensitivity Analysis

Analysis Name	Peak Pin Power	Peak Kinf	EOC Kinf
Base	1.047	1.042	1.035
First Selection Weight	1.047	1.039	1.033
Second Selection Weight	1.045	1.039	1.032
Third Selection Weight	1.046	1.042	1.034
Fourth Selection Weight	1.047	1.042	1.033
Fifth Selection Weight	1.047	1.036	1.033
Sixth Selection Weight	1.045	1.039	1.034
First Small Population	1.047	1.054	1.038
Second Small Population	1.047	1.047	1.036
First Alternate Mutation	1.045	1.040	1.033
Second Alternate Mutation	1.045	1.044	1.034
Large Power Bin Size	1.050	1.041	1.030
Large Peak Kinf Bin Size	1.051	1.039	1.033
Large End Kinf Bin Size	1.046	1.037	1.033

Table A-0-4: Average Maximum Final Population Metrics for Sensitivity Analysis

Analysis Name	Peak Pin Power	Peak Kinf	EOC Kinf
Base	1.150	1.318	1.097
First Selection Weight	1.150	1.318	1.093
Second Selection Weight	1.150	1.318	1.094
Third Selection Weight	1.150	1.318	1.094
Fourth Selection Weight	1.150	1.319	1.094
Fifth Selection Weight	1.150	1.319	1.094
Sixth Selection Weight	1.150	1.318	1.094
First Small Population	1.150	1.317	1.098
Second Small Population	1.150	1.317	1.093
First Alternate Mutation	1.150	1.319	1.094
Second Alternate Mutation	1.150	1.318	1.095
Large Power Bin Size	1.143	1.317	1.093
Large Peak Kinf Bin Size	1.145	1.279	1.092
Large End Kinf Bin Size	1.149	1.319	1.094

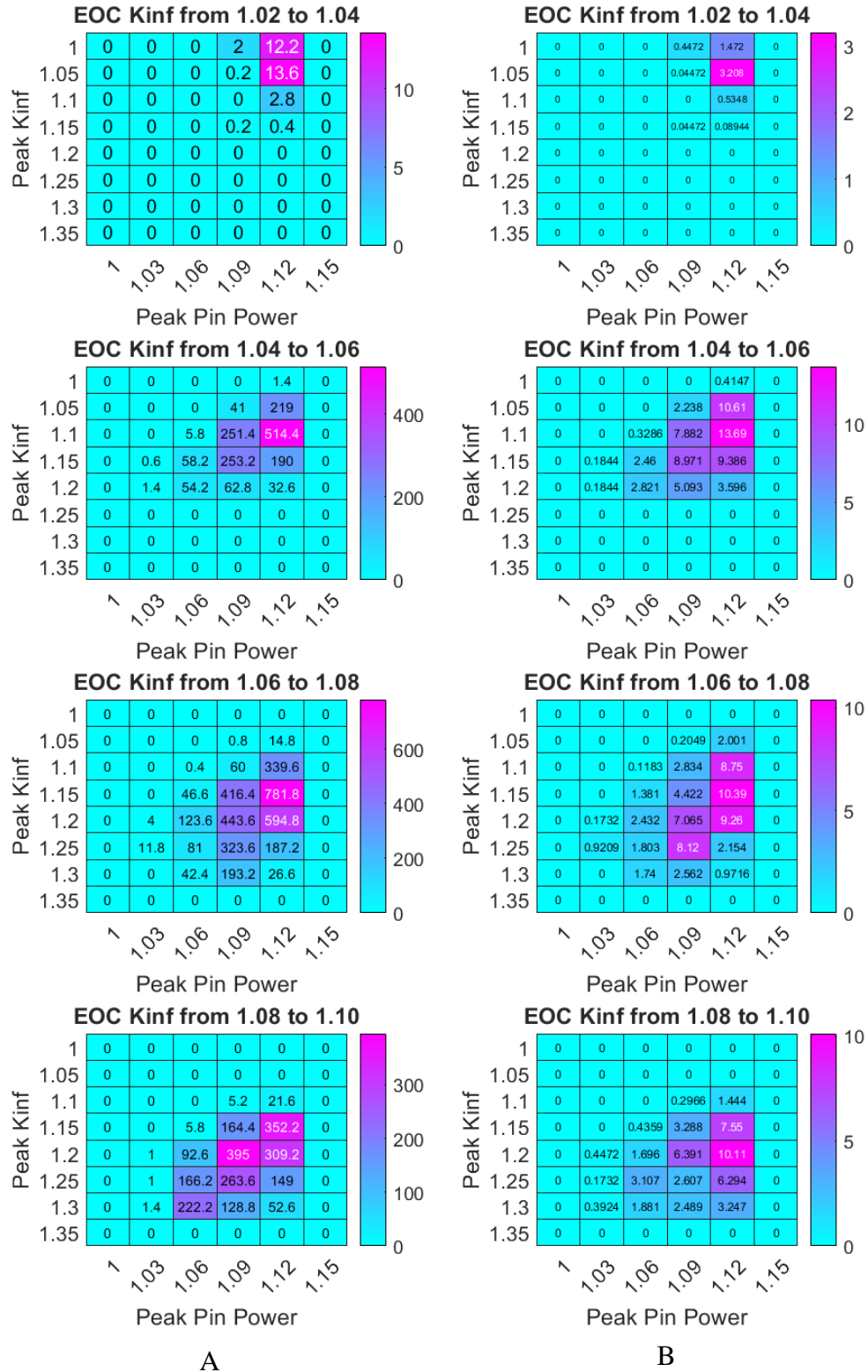


Figure A-0-1: Selection Weight One Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

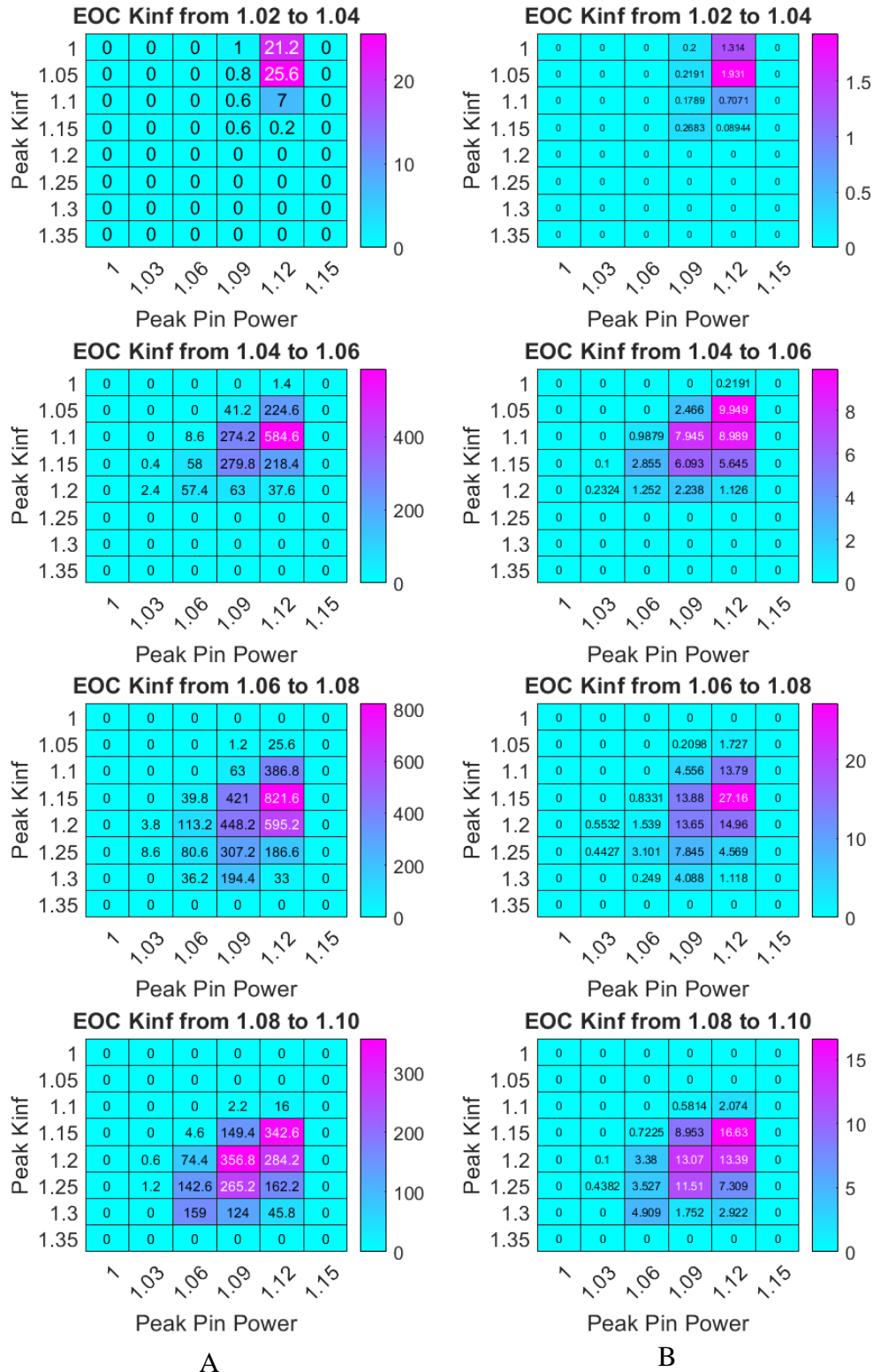


Figure A-0-2: Selection Weight Two Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

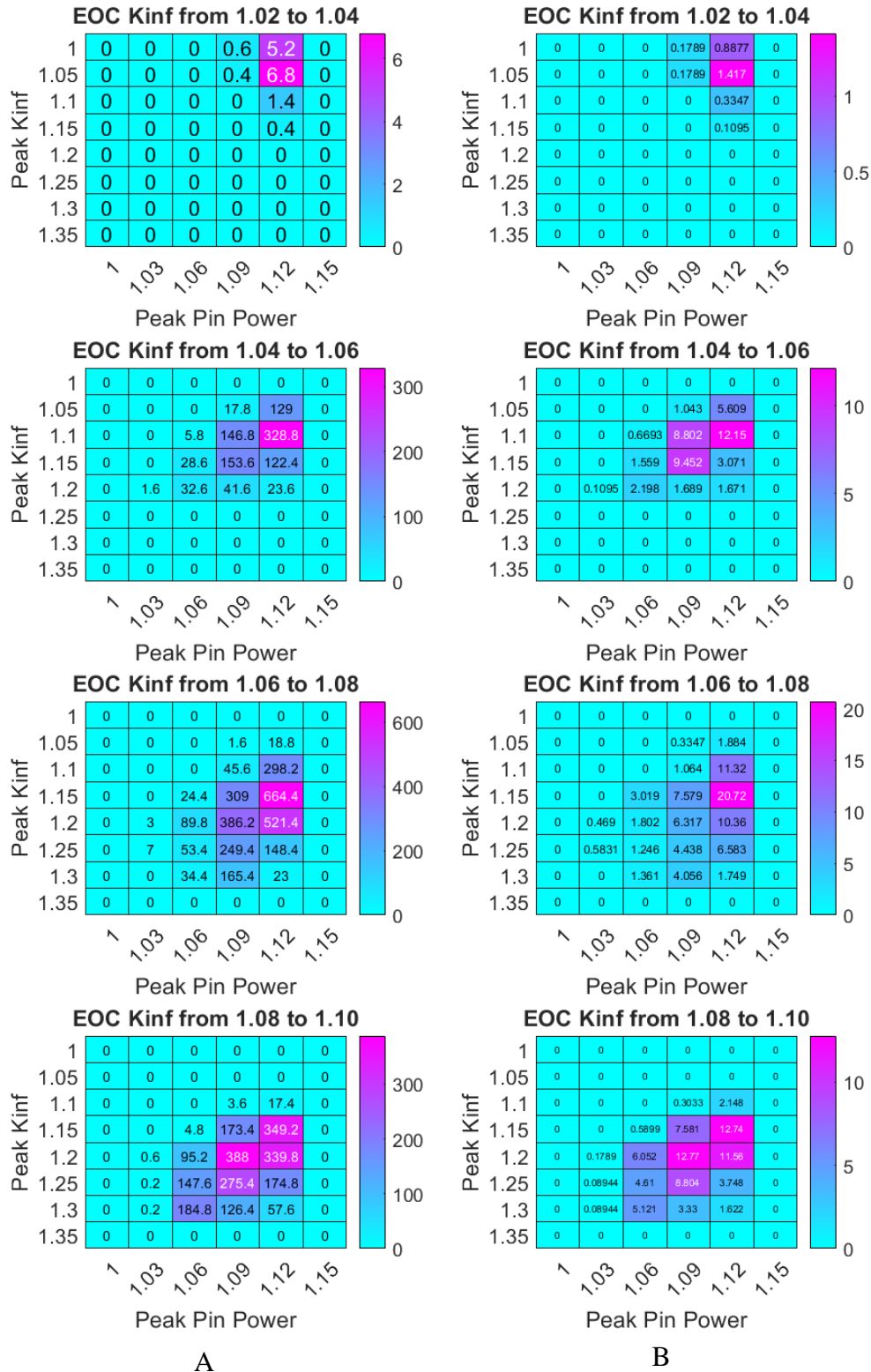


Figure A-0-3: Selection Weight Three Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

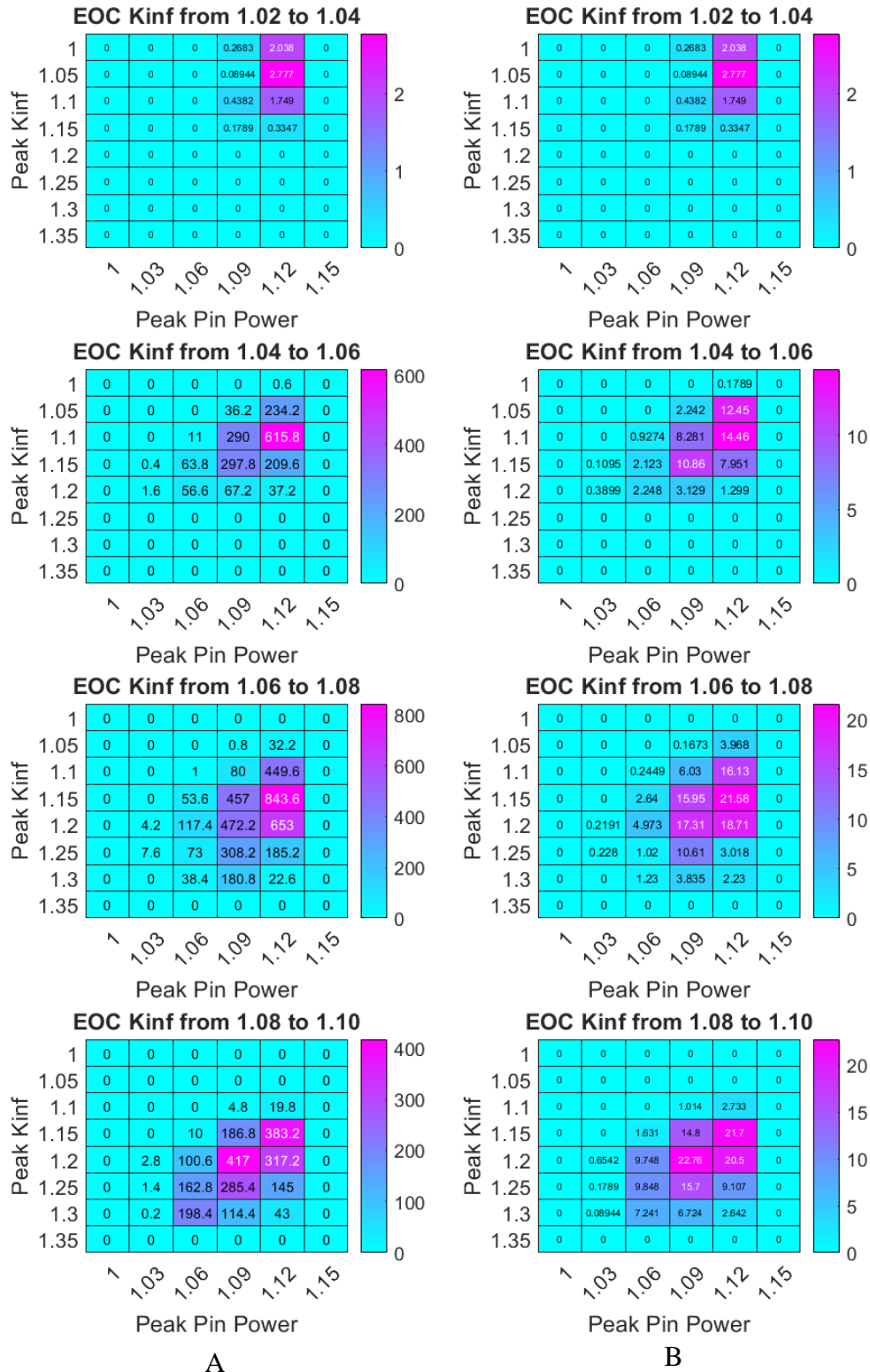


Figure A-0-4: Selection Weight Four Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

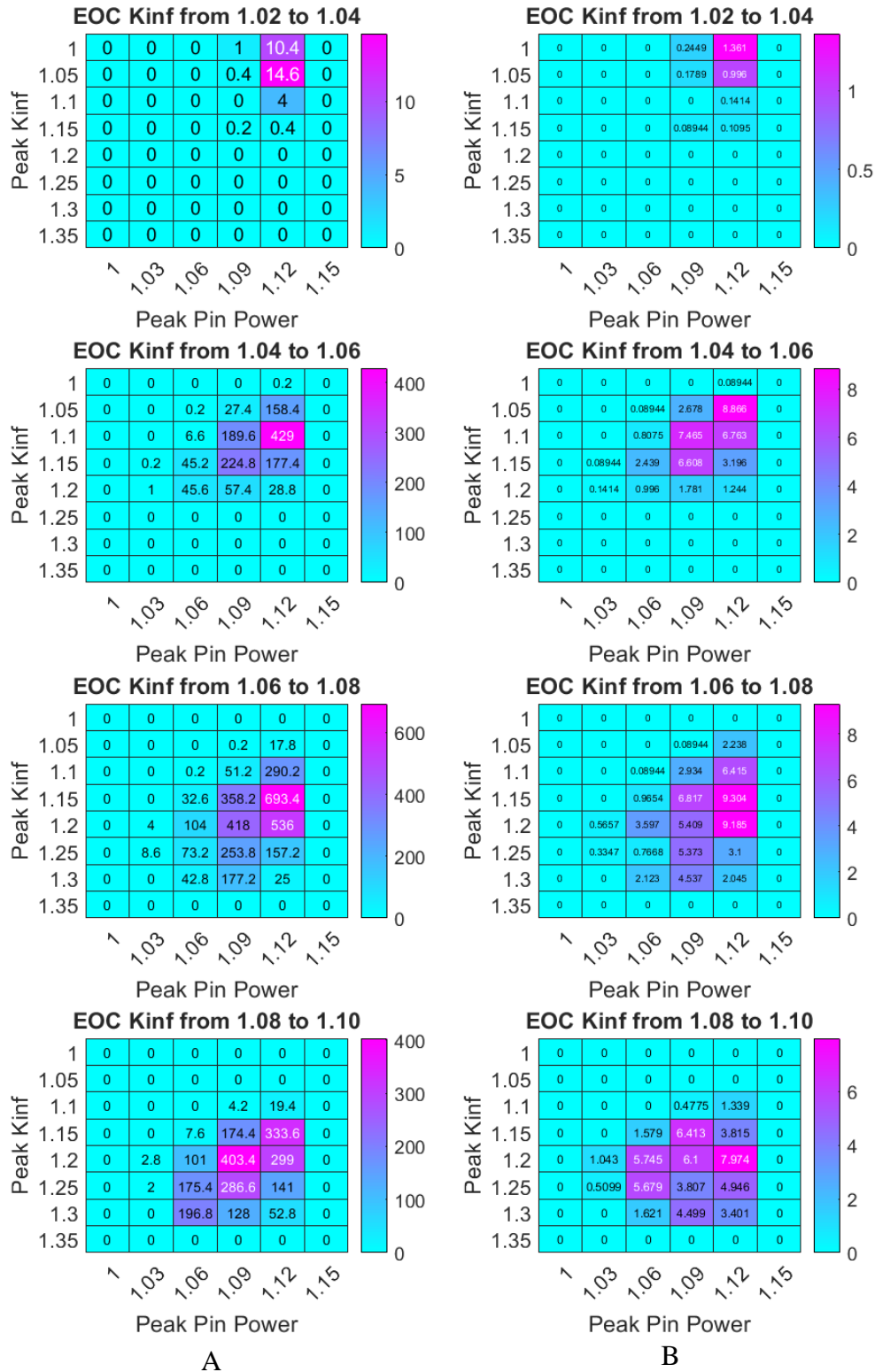


Figure A-0-5: Selection Weight Five Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

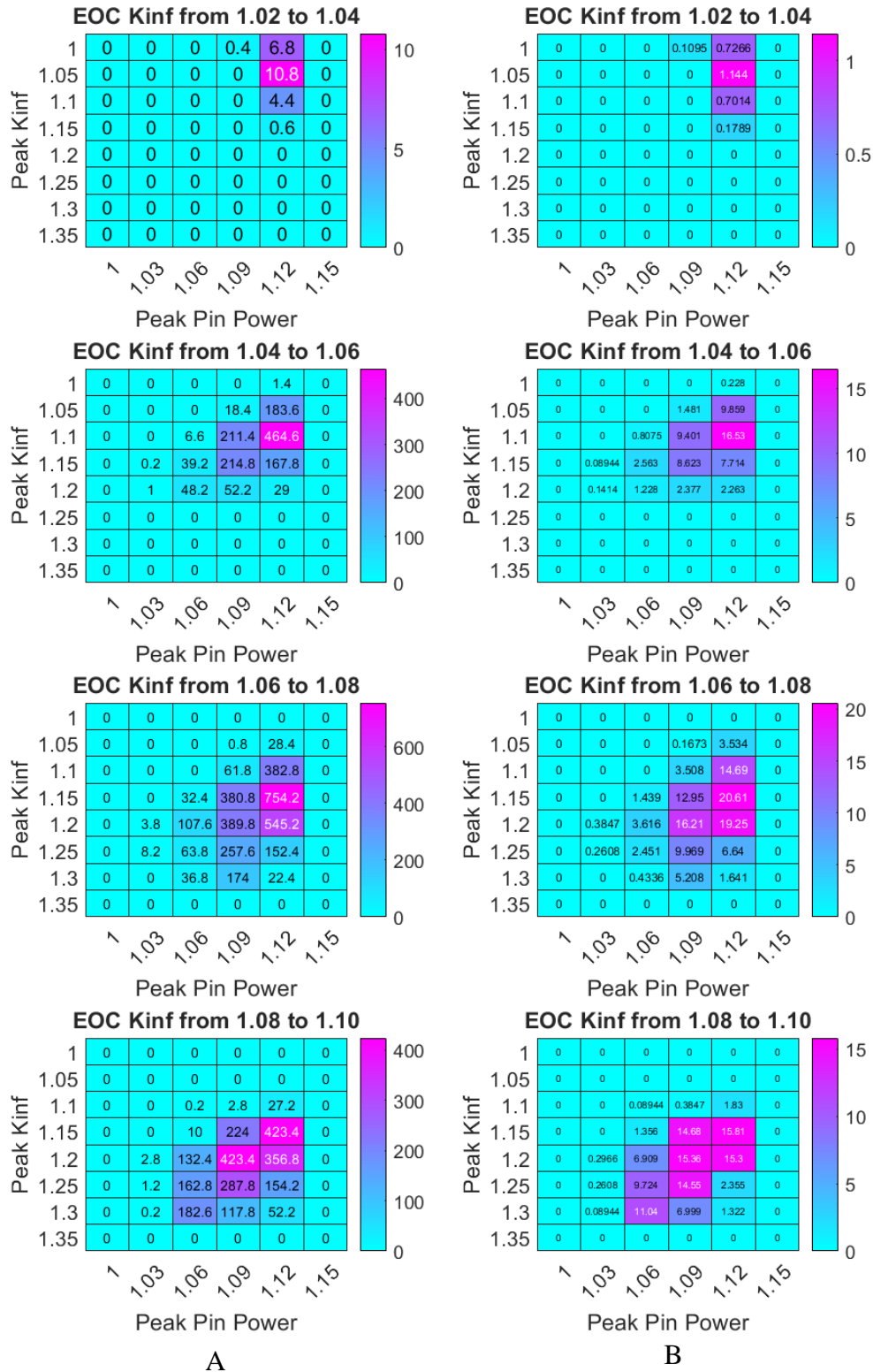


Figure A-0-6: Selection Weight Six Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

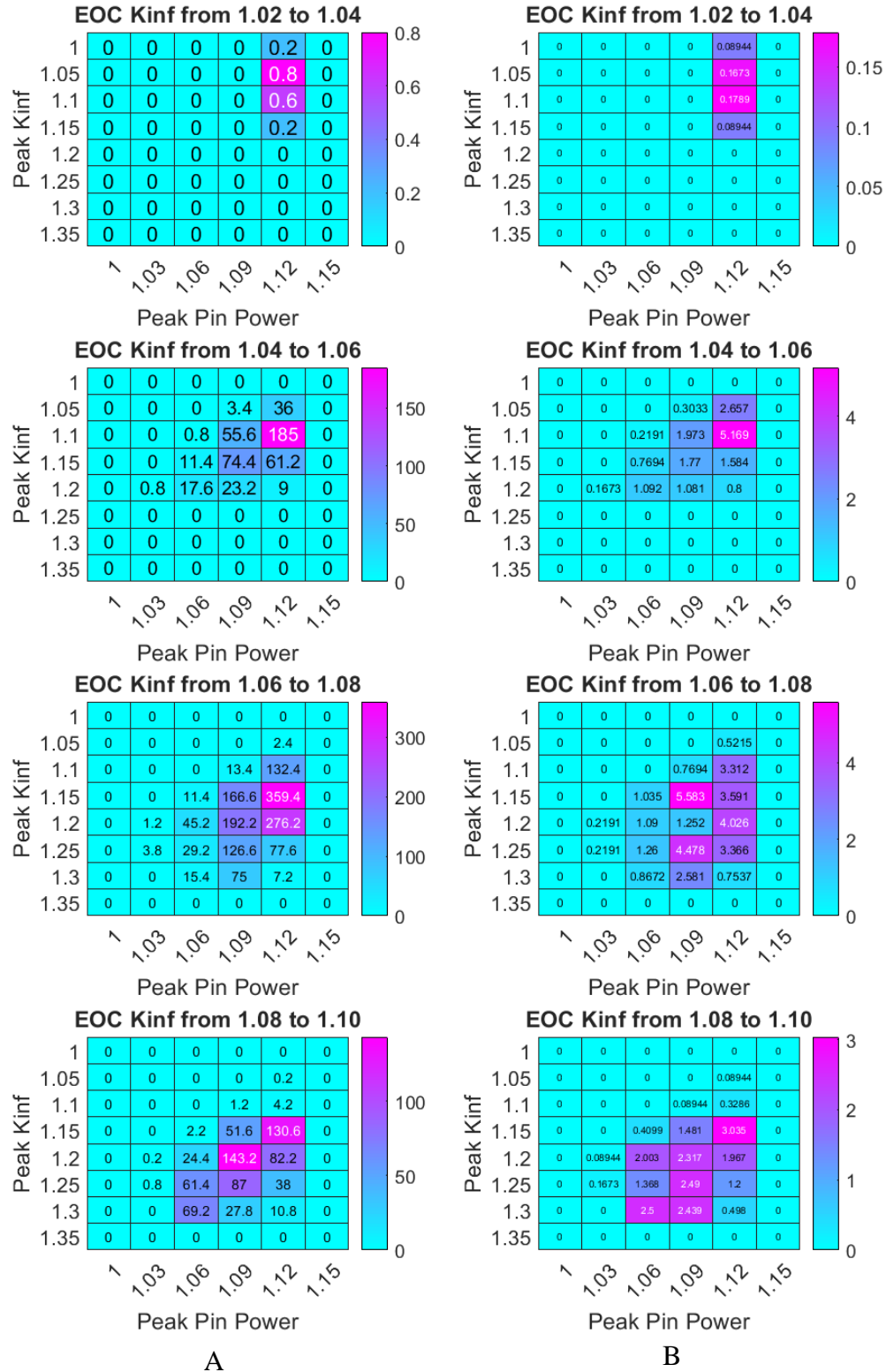


Figure A-0-7: Small Population One Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

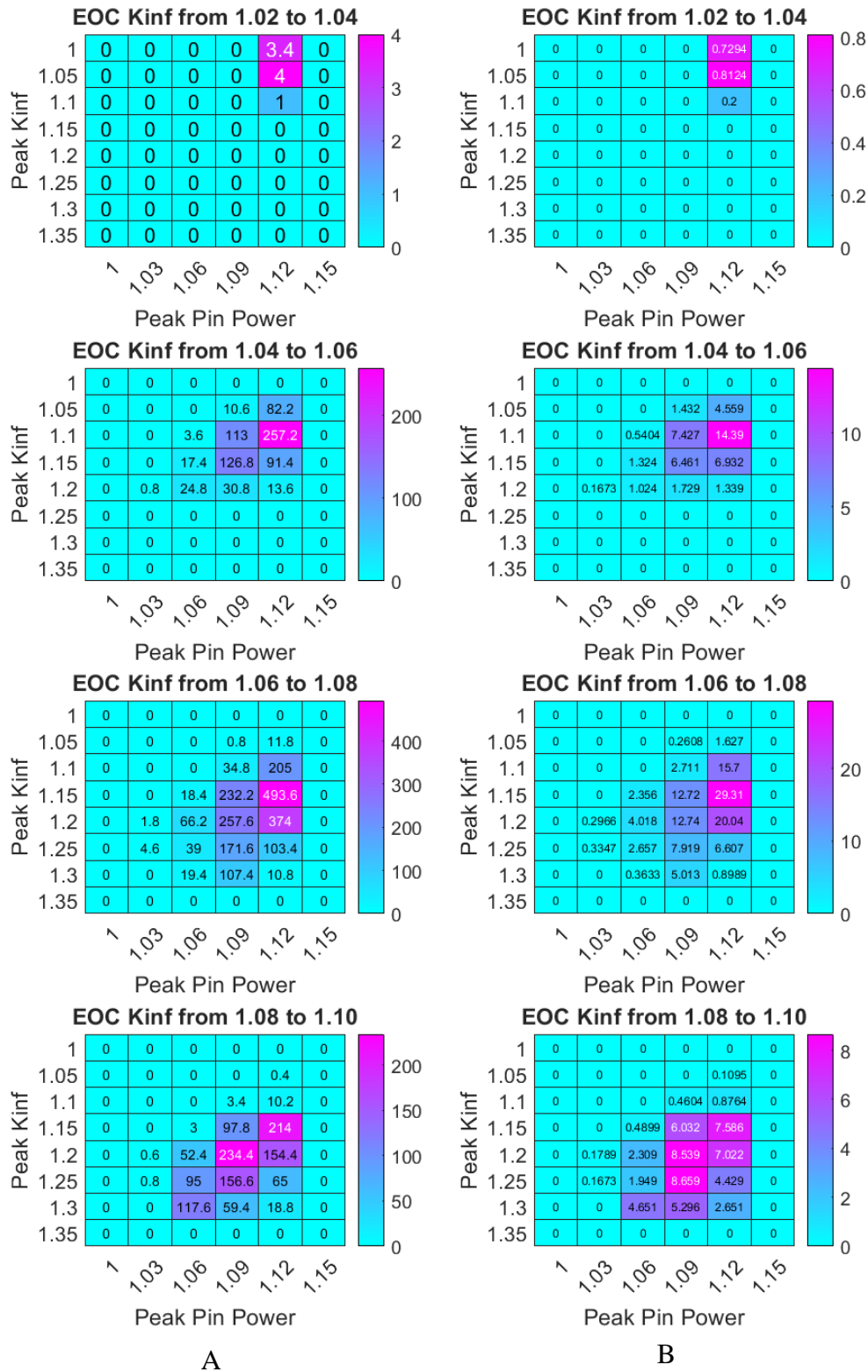


Figure A-0-8: Small Population Two Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

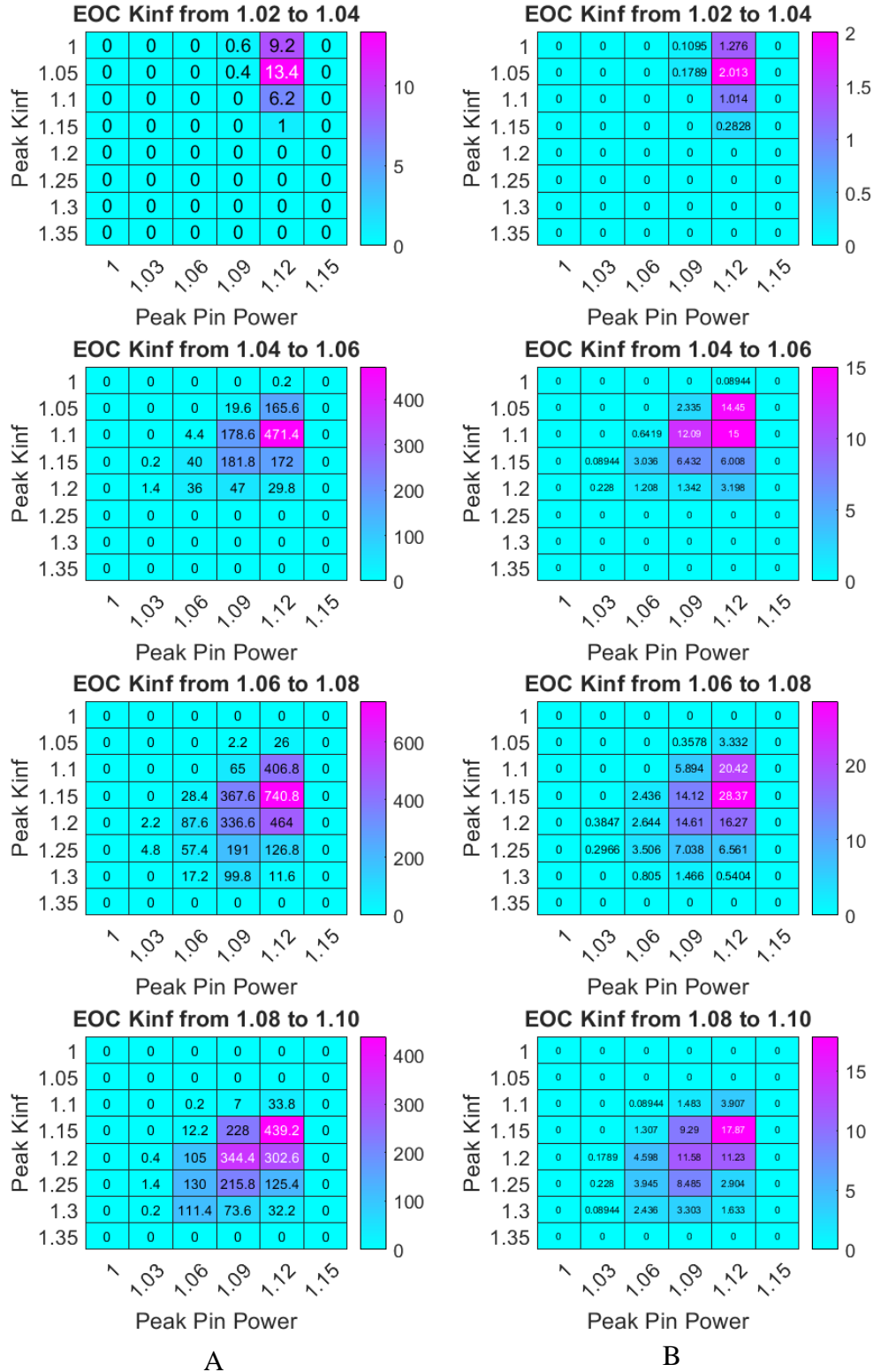


Figure A-0-9: First Alternate Mutation Rate One Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

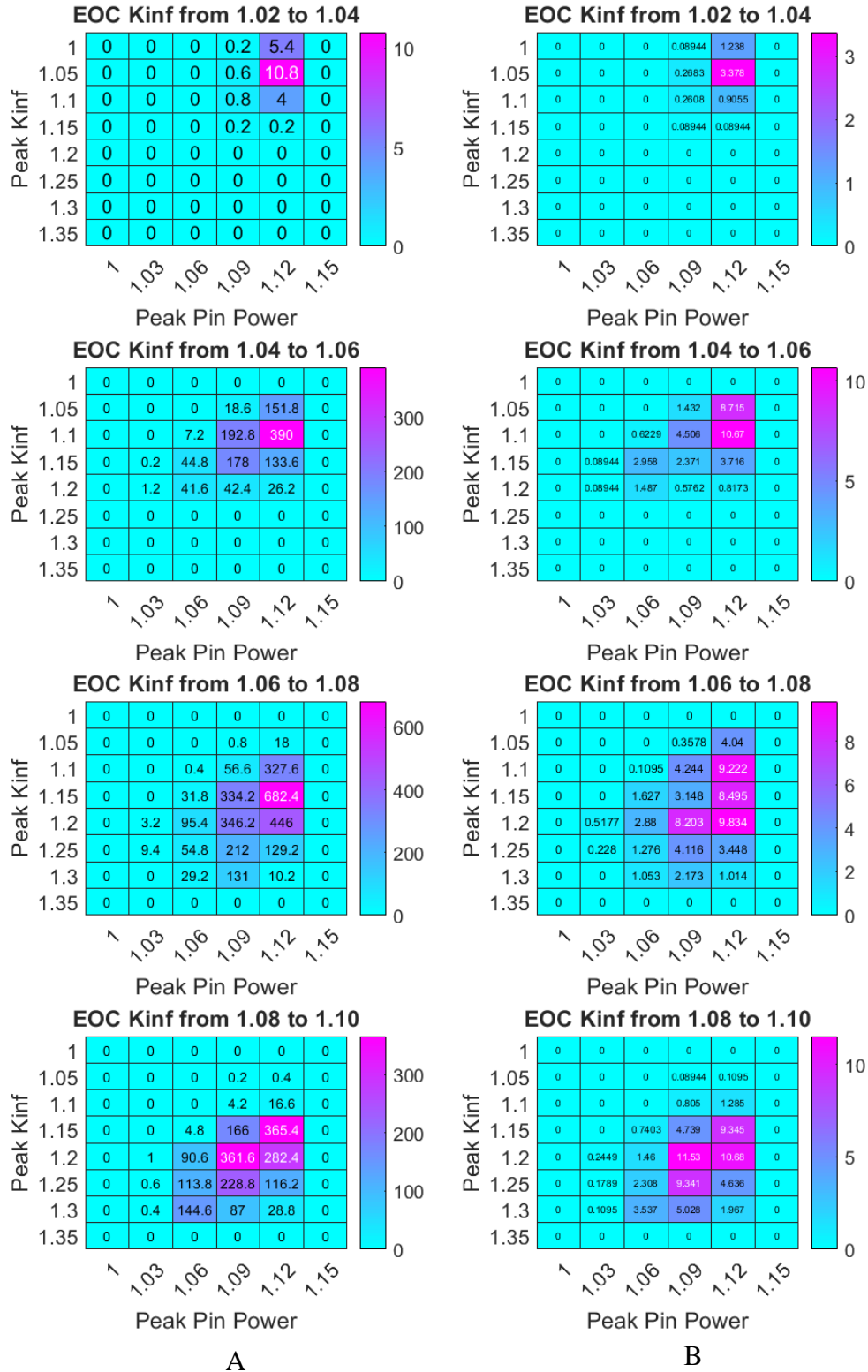


Figure A-0-10: Second Alternate Mutation Rate Two Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

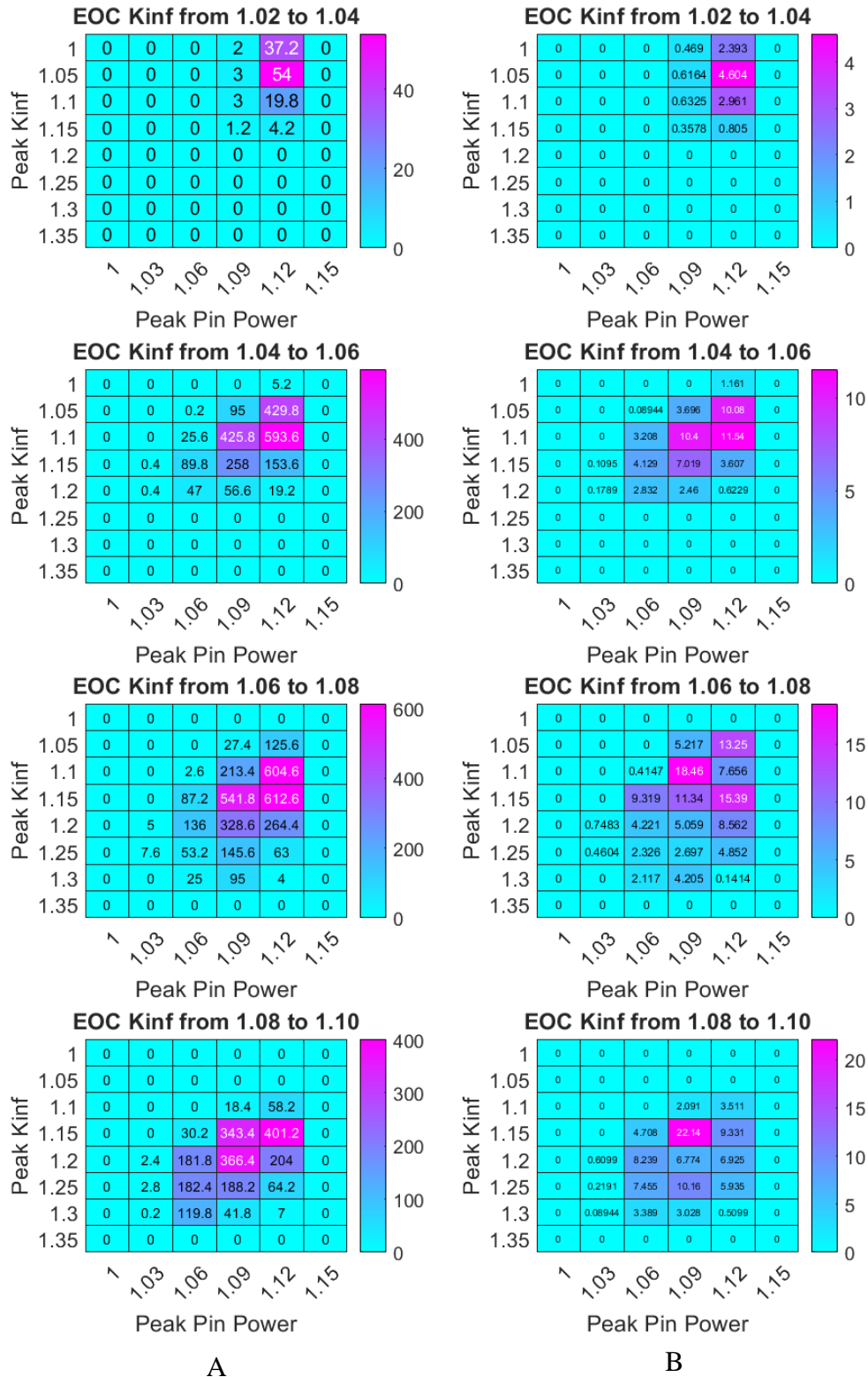


Figure A-0-11: Large PPF Bin Size Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

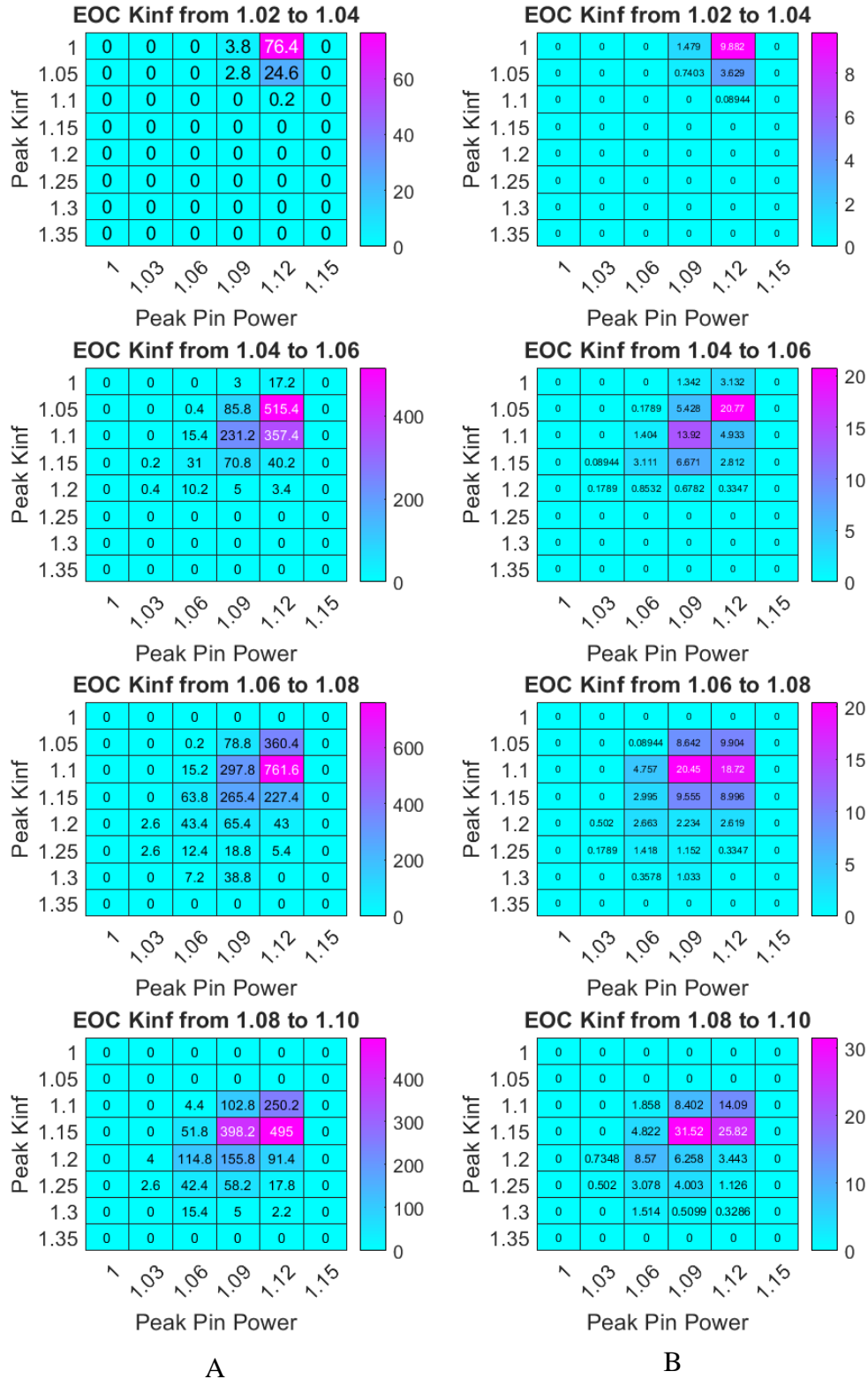


Figure A-0-12: Large Peak Kinf Bin Size Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

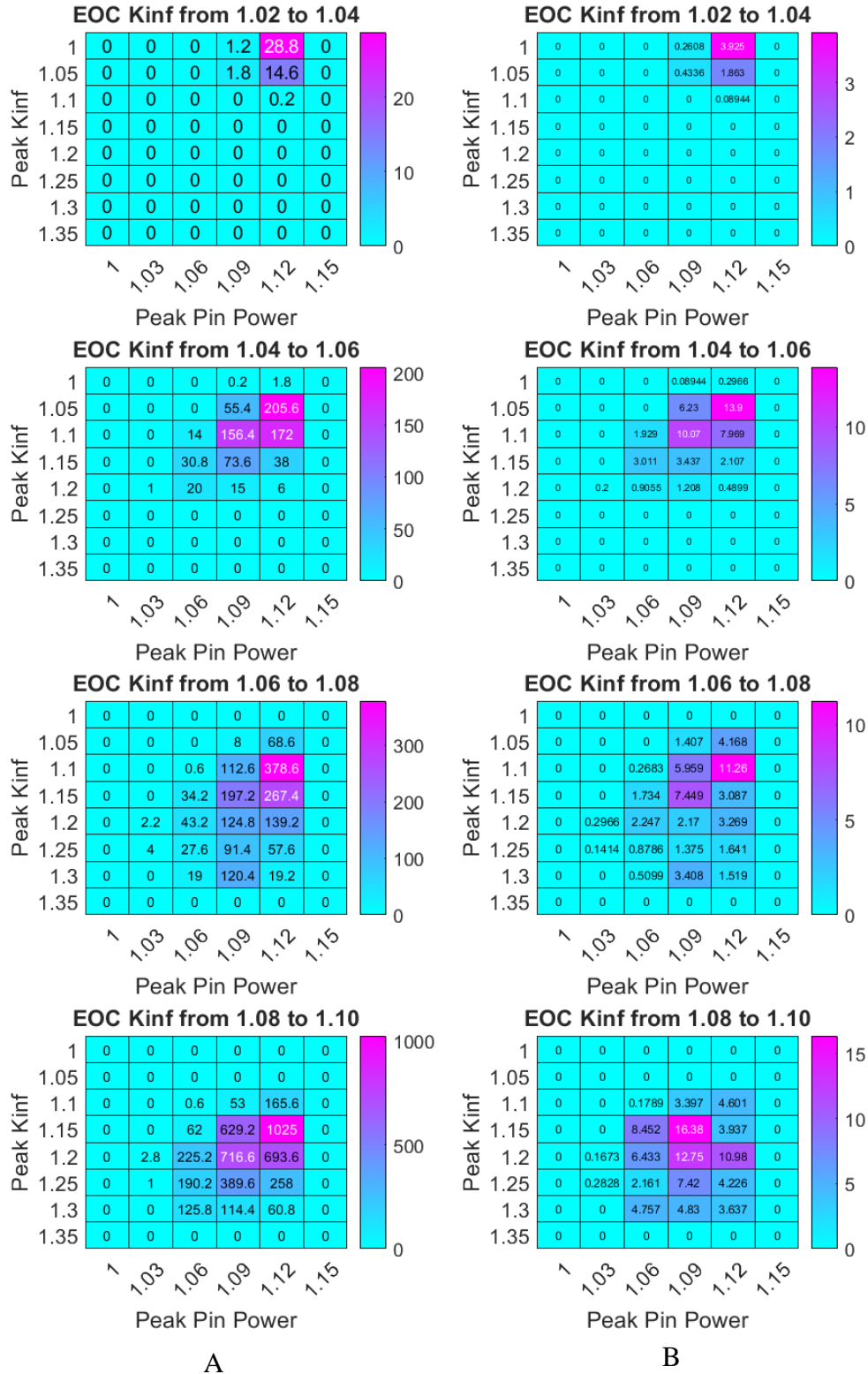


Figure A-0-13: Large EOC Kinf Bin Size Solution Space Results. A: Average number of solutions per bin in the solution space. B: Error in the average number of solutions per bin.

Table A-5 gives the average distances between the individual optimization runs and the optimal solution front for the selection weight cases. Figure A-14 compares the solution front and solution spaces of the first select weight and base cases, and Figure A-15 compares the solution front and solution spaces of the second select weight and base cases. Figure A-16 compares the solution front and solution spaces of the third select weight and base cases. Figure A-17 compares the solution front and solution spaces of the fourth select weight and base cases. Figure A-18 compares the solution front and solution spaces of the fifth select weight and base cases. Figure A-19 compares the solution front and solution spaces of the sixth select weight and base cases.

Table A-5: Average Distance Comparison of Selection Weight Cases

Case Name	Case Part	Average Distance for EOC Kinf Range				
		1.02 – 1.04	1.04 – 1.06	1.06 – 1.08	1.08 – 1.10	Total
First Selection Weight	Test	8.41	9.18	14.00	21.31	52.89
	Base	10.97	10.87	11.20	14.77	47.81
	Difference	-2.56	-1.69	2.79	6.53	5.08
Second Selection Weight	Test	4.78	9.77	13.60	23.13	51.28
	Base	6.93	11.04	12.23	14.88	45.08
	Difference	-2.15	-1.27	1.37	8.26	6.20
Third Selection Weight	Test	3.89	11.55	16.55	19.90	51.89
	Base	4.52	9.96	15.12	14.95	44.56
	Difference	-0.63	1.59	1.43	4.95	7.34
Fourth Selection Weight	Test	11.01	10.20	13.71	22.75	57.67
	Base	14.26	10.24	14.56	15.49	54.55
	Difference	-3.25	-0.04	-0.85	7.26	3.12
Fifth Selection Weight	Test	4.90	11.49	15.62	22.03	54.04
	Base	5.14	12.55	14.77	14.26	46.72
	Difference	-0.24	-1.06	0.85	7.76	7.31
Sixth Selection Weight	Test	4.23	11.08	13.31	19.71	48.32
	Base	5.07	9.97	12.94	14.78	42.78
	Difference	-0.85	1.10	0.36	4.92	5.54

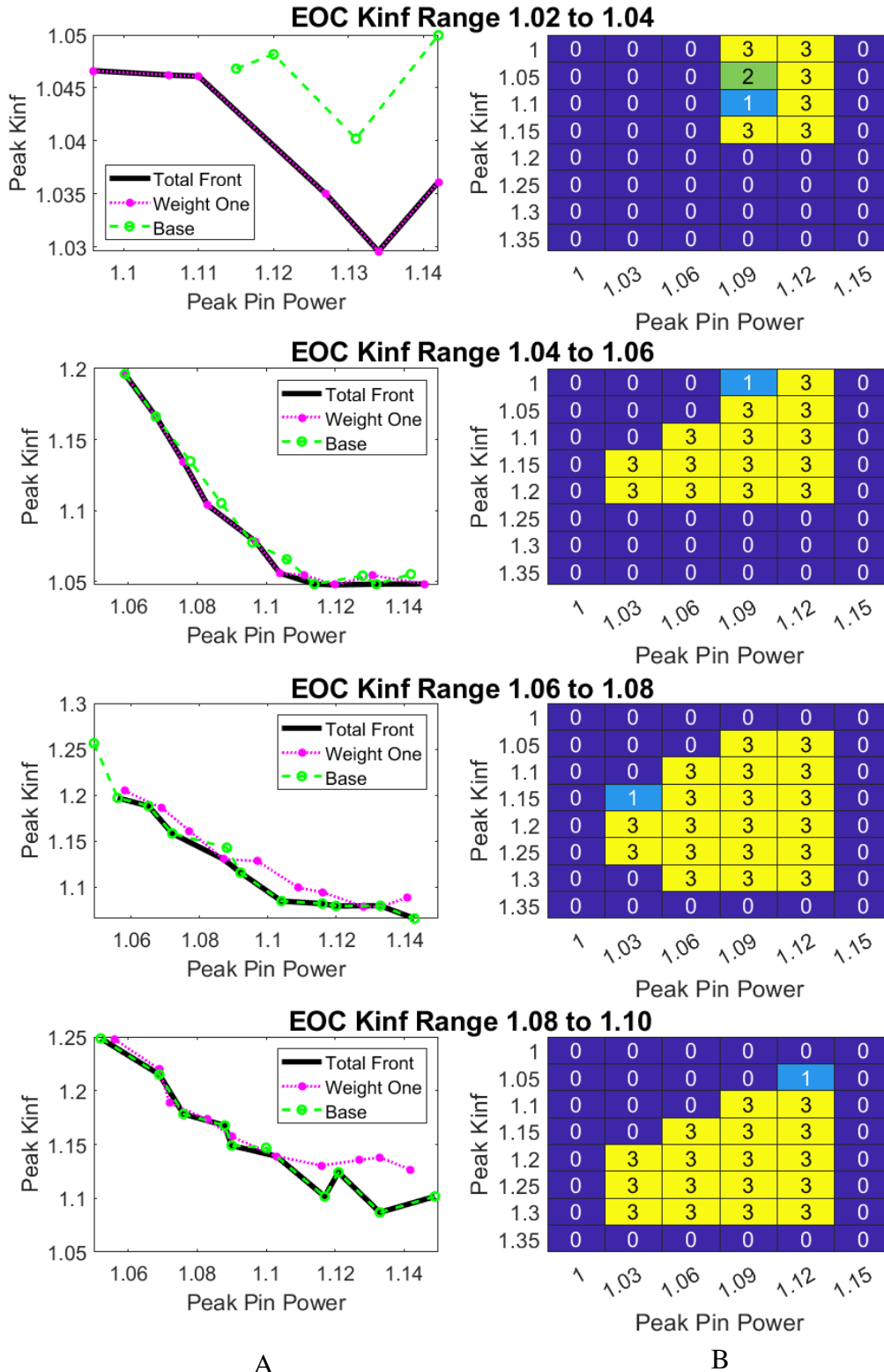


Figure A-0-14: Solution Front and Solution space comparison between base and first select weight test cases. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.

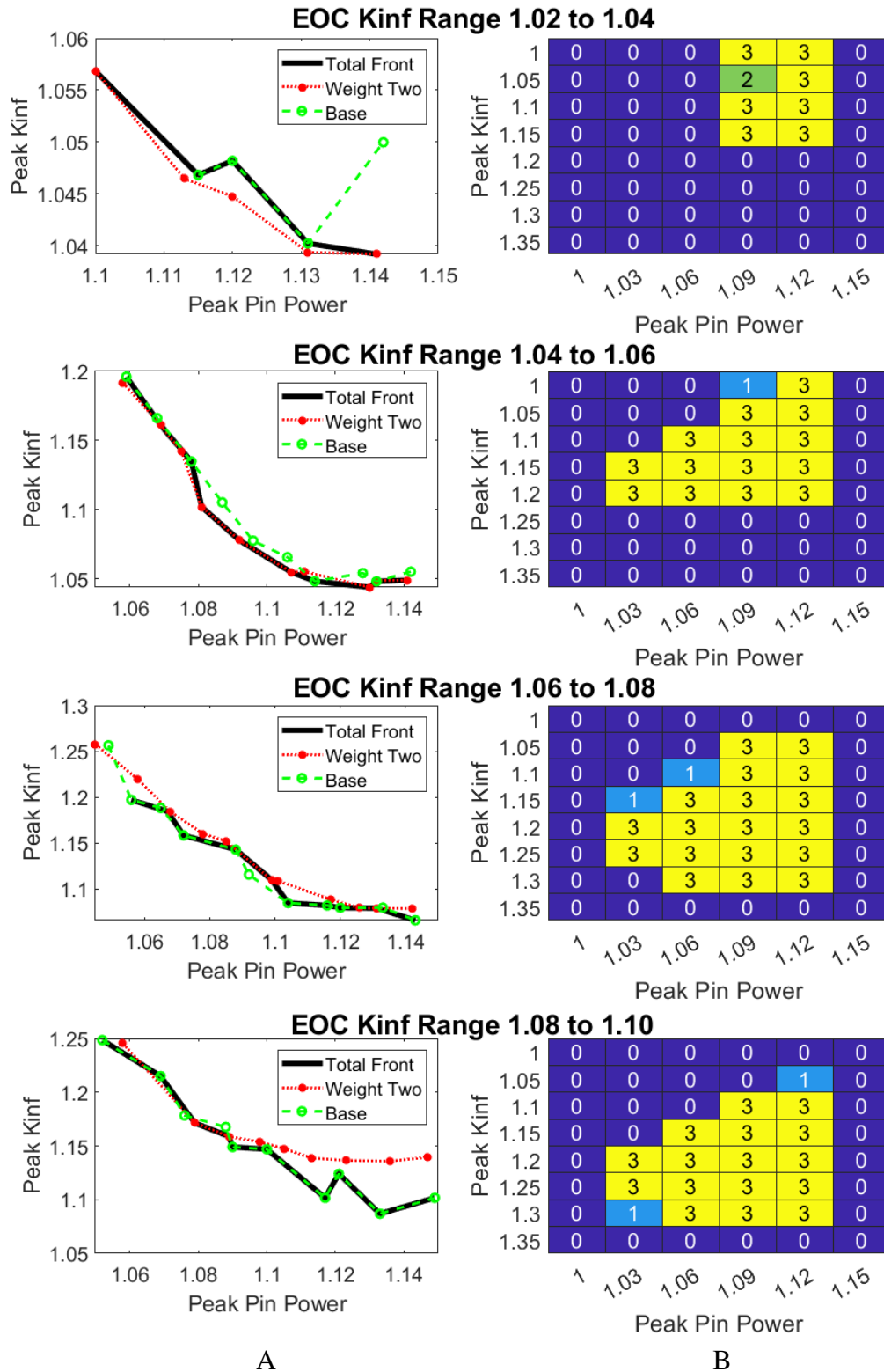
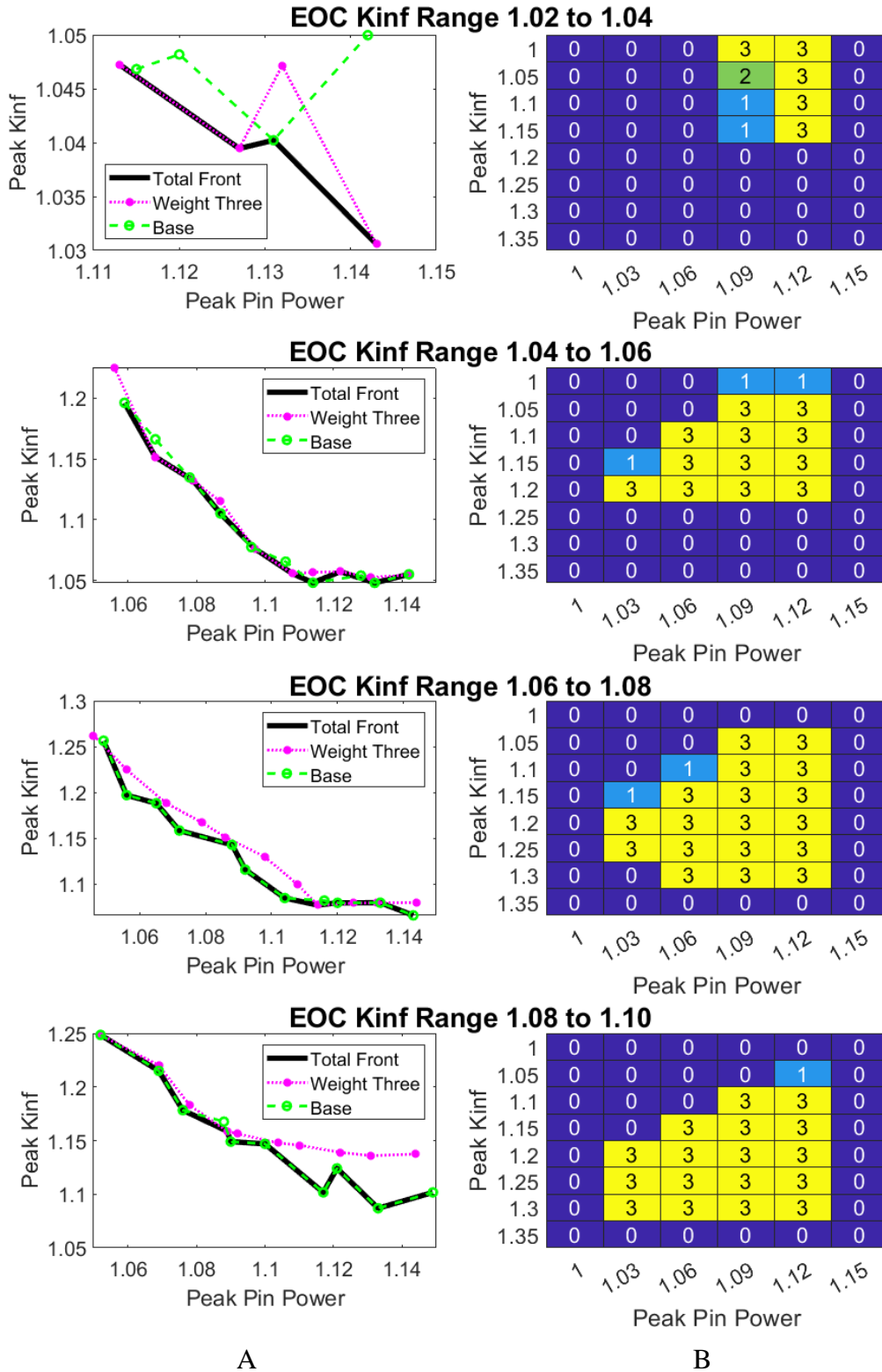


Figure A-0-15: Solution Front and Solution space comparison between base and second select weight test cases. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.



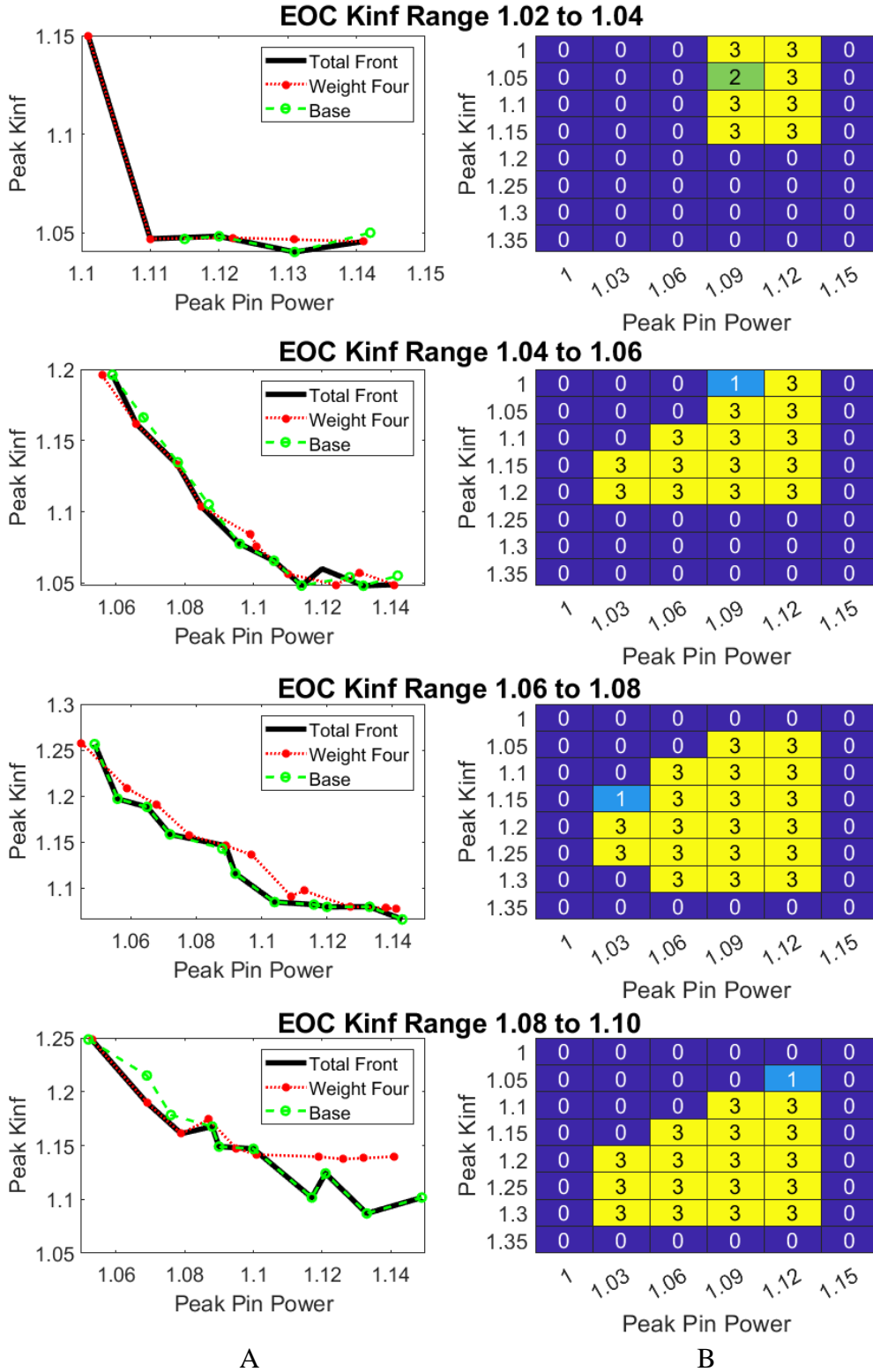


Figure A-0-17: Solution Front and Solution space comparison between base and fourth select weight test cases. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.

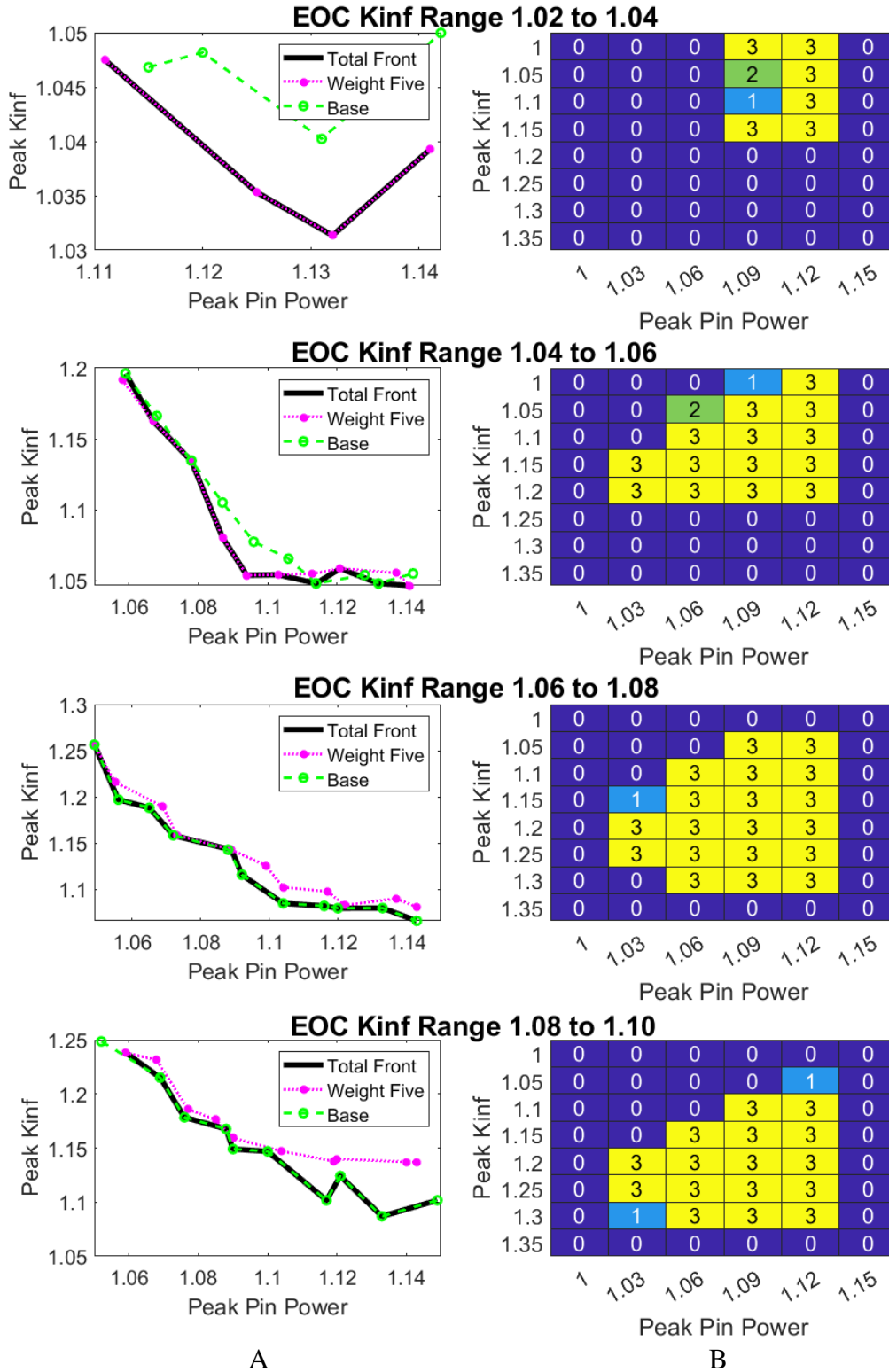


Figure A-0-18: Solution Front and Solution space comparison between base and fifth select weight test cases. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.

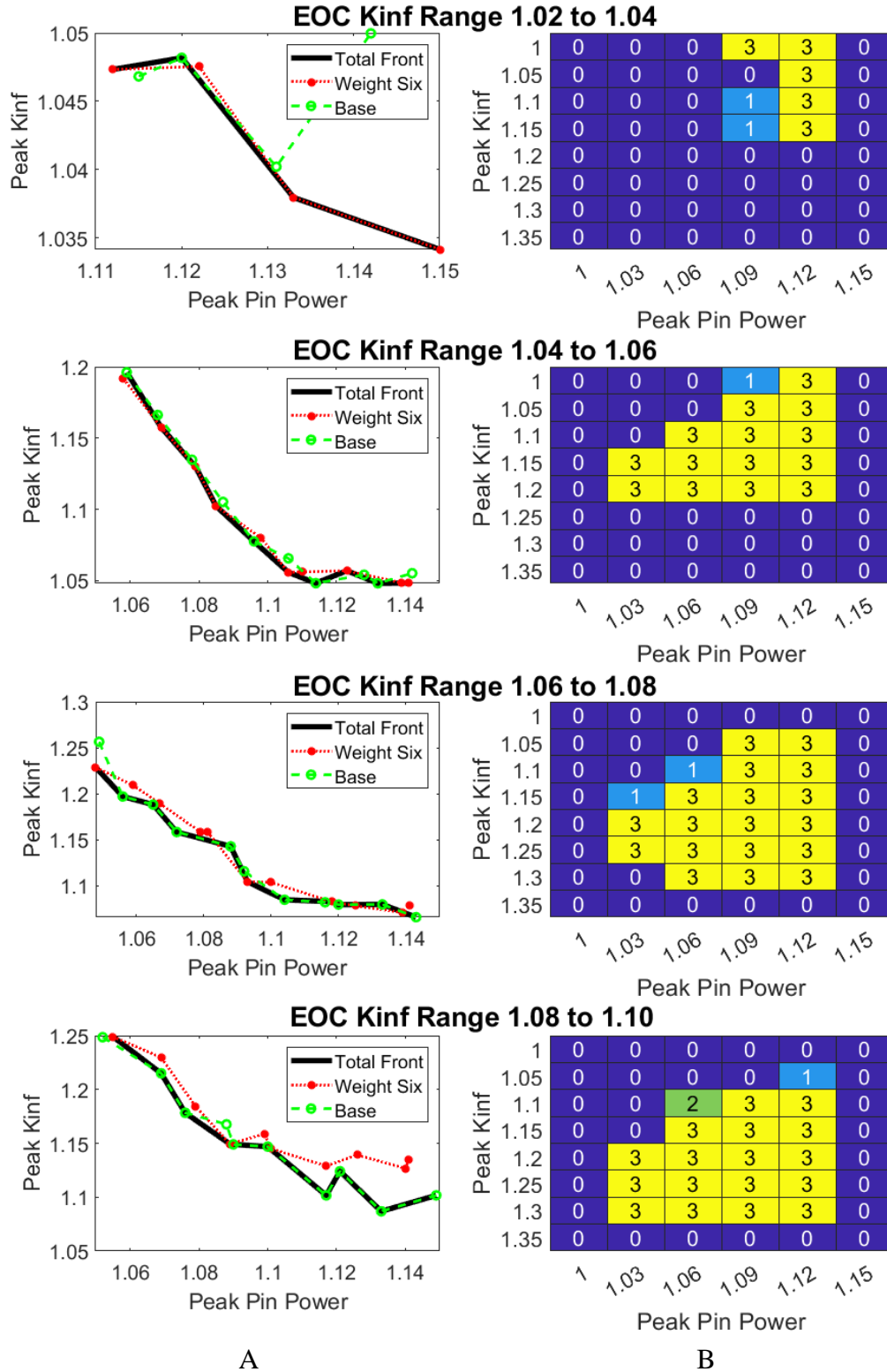


Figure A-0-19: Solution Front and Solution space comparison between base and sixth select weight test cases. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.

As previously indicated in Table A-0-2 through Table A-0-4, there are not large differences in the final population metrics between the six weight selection cases and the base case. The total distances in Table A- for the base case are less than the distances for the selection weight test cases. The distances between the test cases and the optimal curve are less than the distance between the base and optimal case for lower EOC Kinf values but are significantly greater at the highest EOC Kinf. Figure A-12 through Figure A-19 confirms that at lower EOC values the optimal solution front is mostly composed of values from the test cases. Optimal solution fronts at higher EOC kinf values mostly use solutions from the base case. Additionally, these figures indicate the base optimization searches a wider area of the solution space than any of the selection weight test cases. Many of the bins explored only by the base case are found in the upper left-hand corner. This is the area where the solution fronts are located.

Table A-6 gives the average distances between the individual optimization runs and the optimal solution front for the population size test cases. Figure A-20 compares the solution front and solution spaces of the first population size test and base cases, and Figure A-21 compares the solution front and solution spaces of the second population size test and base cases.

Table A-6: Average Distance Comparison of Small Population Cases

Case Name	Case Part	Average Distance for EOC Kinf Range				
		1.02 – 1.04	1.04 – 1.06	1.06 – 1.08	1.08 – 1.10	Total
First Small Population	Test	10.10	16.50	25.39	20.79	72.78
	Base	3.78	9.73	14.62	16.60	44.73
	Difference	6.32	6.78	10.76	4.19	28.05
Second Small Population	Test	4.48	14.57	19.78	15.40	54.22
	Base	3.78	10.38	15.96	18.52	48.64
	Difference	0.70	4.19	3.82	-3.12	6.20

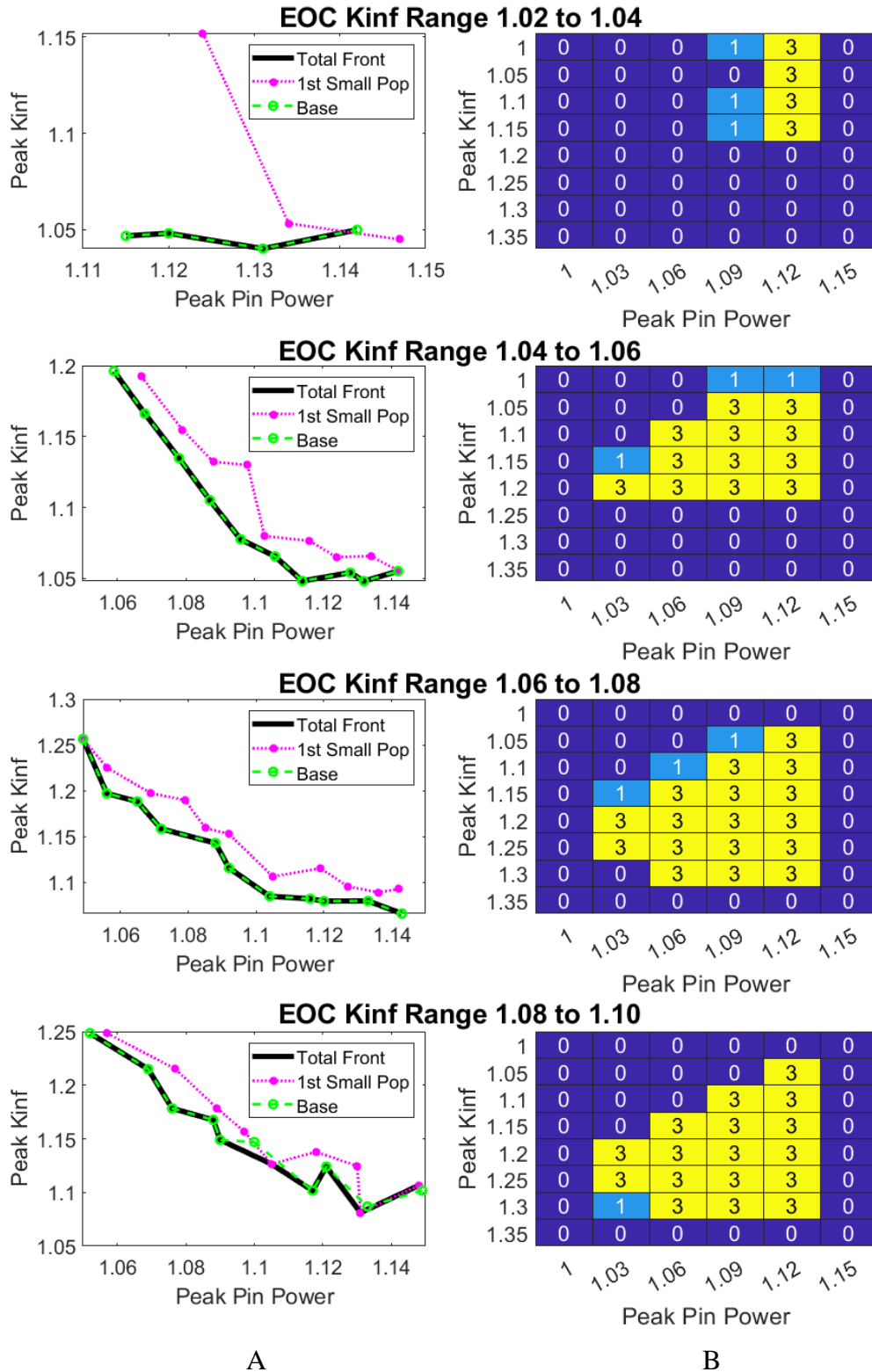


Figure A-0-20: Solution Front and Solution space comparison between base and first small population test cases. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.

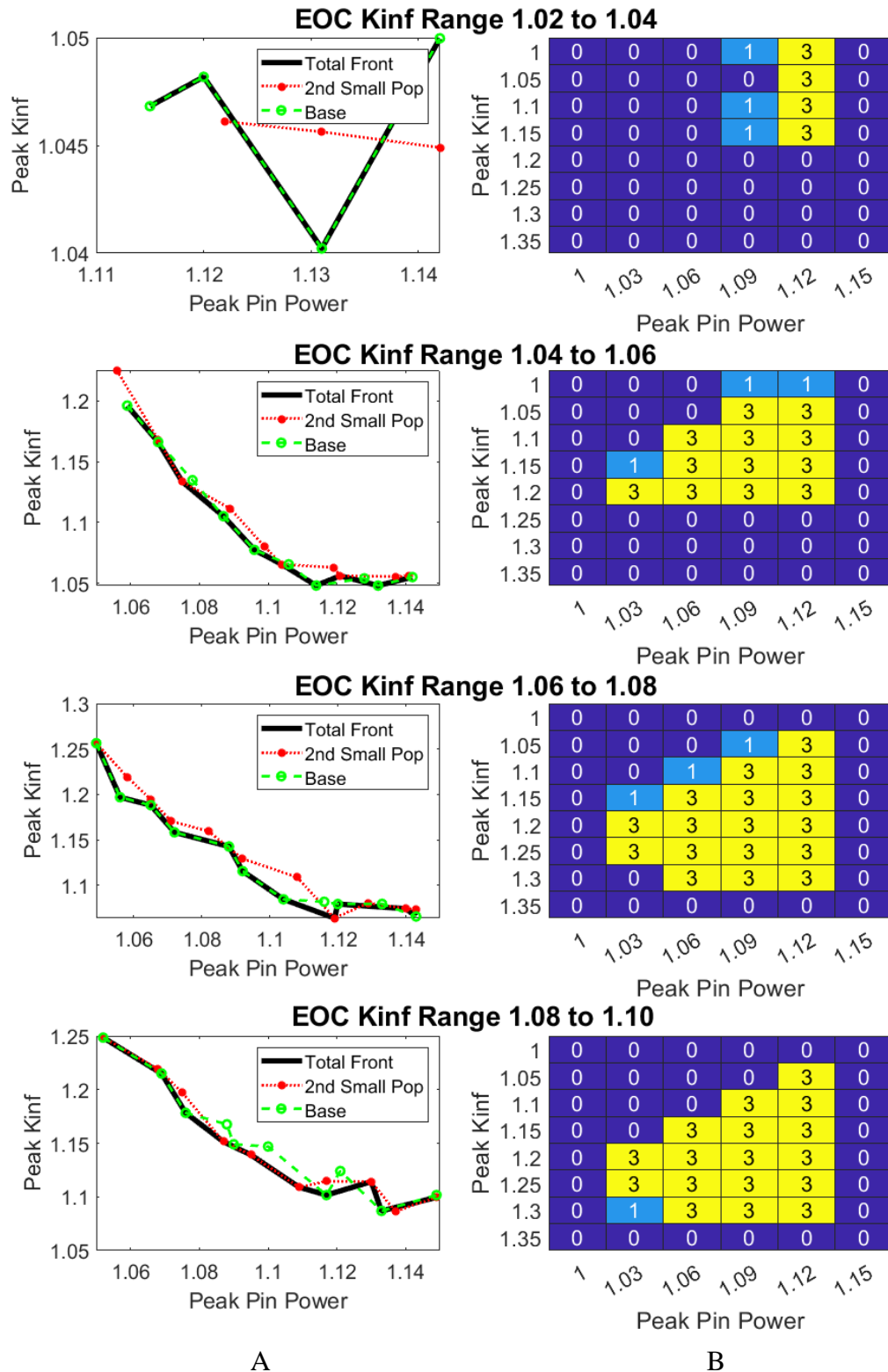


Figure A-0-21: Solution Front and Solution space comparison between base and second small population test case. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.

As shown in Table A-0-2 through Table A-0-4, the final population metrics are the same or slightly worse for the small population cases than the base case. The total distances in for the base case are less than the distances for the small population test cases. Figure A-20 and Figure A-21 show that the solution fronts are mostly composed of solutions from the base case in the small population tests. Additionally, these figures indicate the base optimization searches a wider area of the solution space than any of the small population test cases.

Table A-7 gives the average distances between the individual runs of the optimization to the optimal solution front. Figure A-22 compares the solution front and solution spaces of the first alternate mutation rate test case and base cases. Figure A-23 compares the solution front and solution spaces of the second alternate mutation rate test case and base cases.

Table A-7: Average Distance Comparison of Alternate Mutation Rate Cases

Case Name	Case Part	Average Distance for EOC Kinf Range				
		1.02 – 1.04	1.04 – 1.06	1.06 – 1.08	1.08 – 1.10	Total
First Alternate Rate	Test	6.42	12.11	14.74	22.34	55.61
	Base	8.03	10.32	14.70	15.71	48.76
	Difference	-1.61	1.79	0.04	6.63	6.85
Second Alternate Rate	Test	12.56	11.33	17.35	21.44	62.68
	Base	3.83	9.87	15.36	19.40	48.46
	Difference	8.72	1.45	1.99	2.05	14.21

As shown in Table A-0-2 through Table A-0-4, the final population metrics are similar for the alternate mutation rate cases and the base case. The total distances in for the base case are less than the distances for the alternate mutation rate test cases. Figure A-22 and Figure A-23 show that the solution fronts are mostly composed of solutions from the base case in the alternate mutation rate tests. Additionally, these figures indicate the base optimization searches a wider area of the solution space than any of the alternate mutation rate cases.

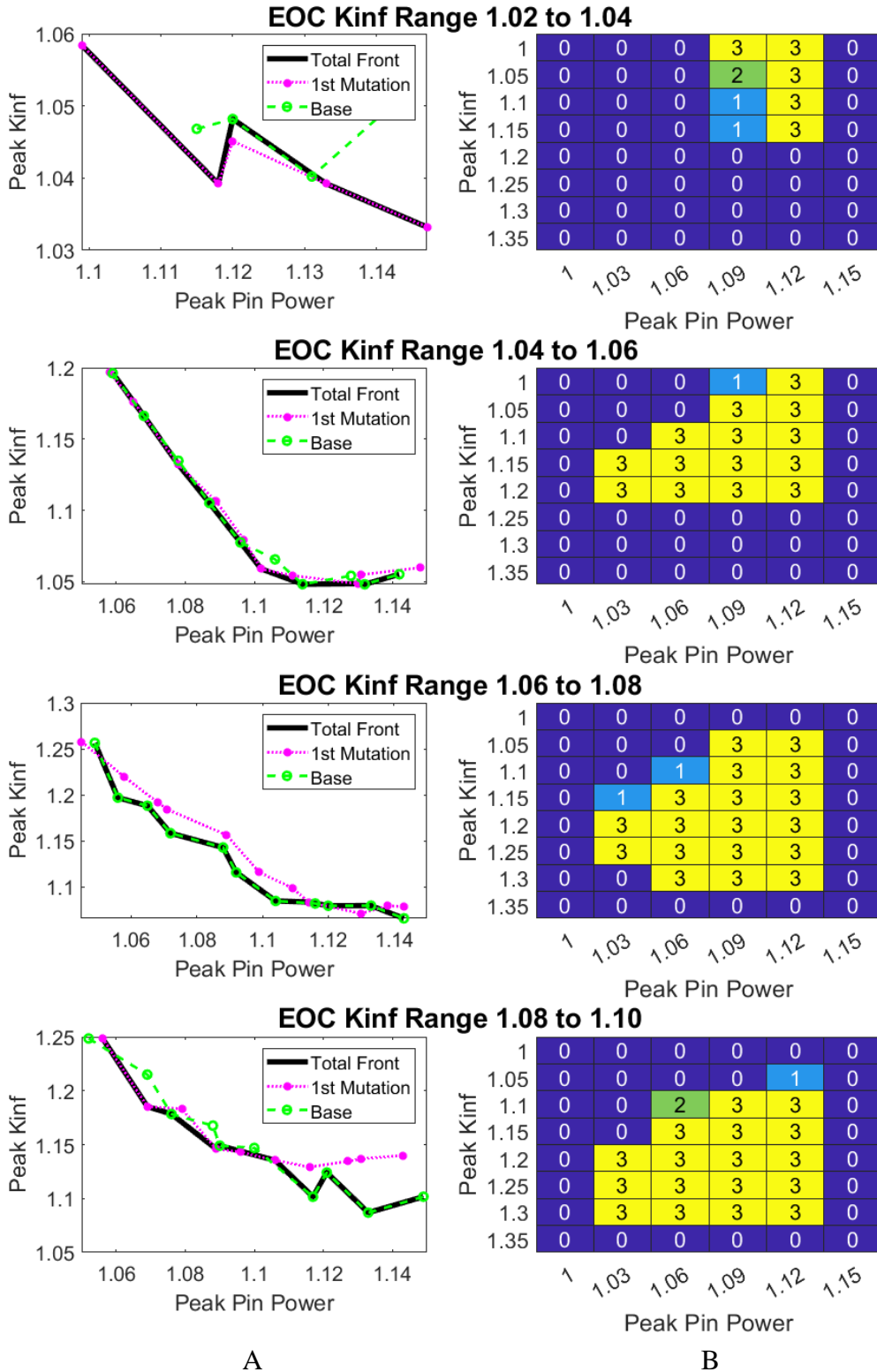


Figure A-0-22: Solution Front and Solution space comparison between base and first alternate mutation rate cases. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.

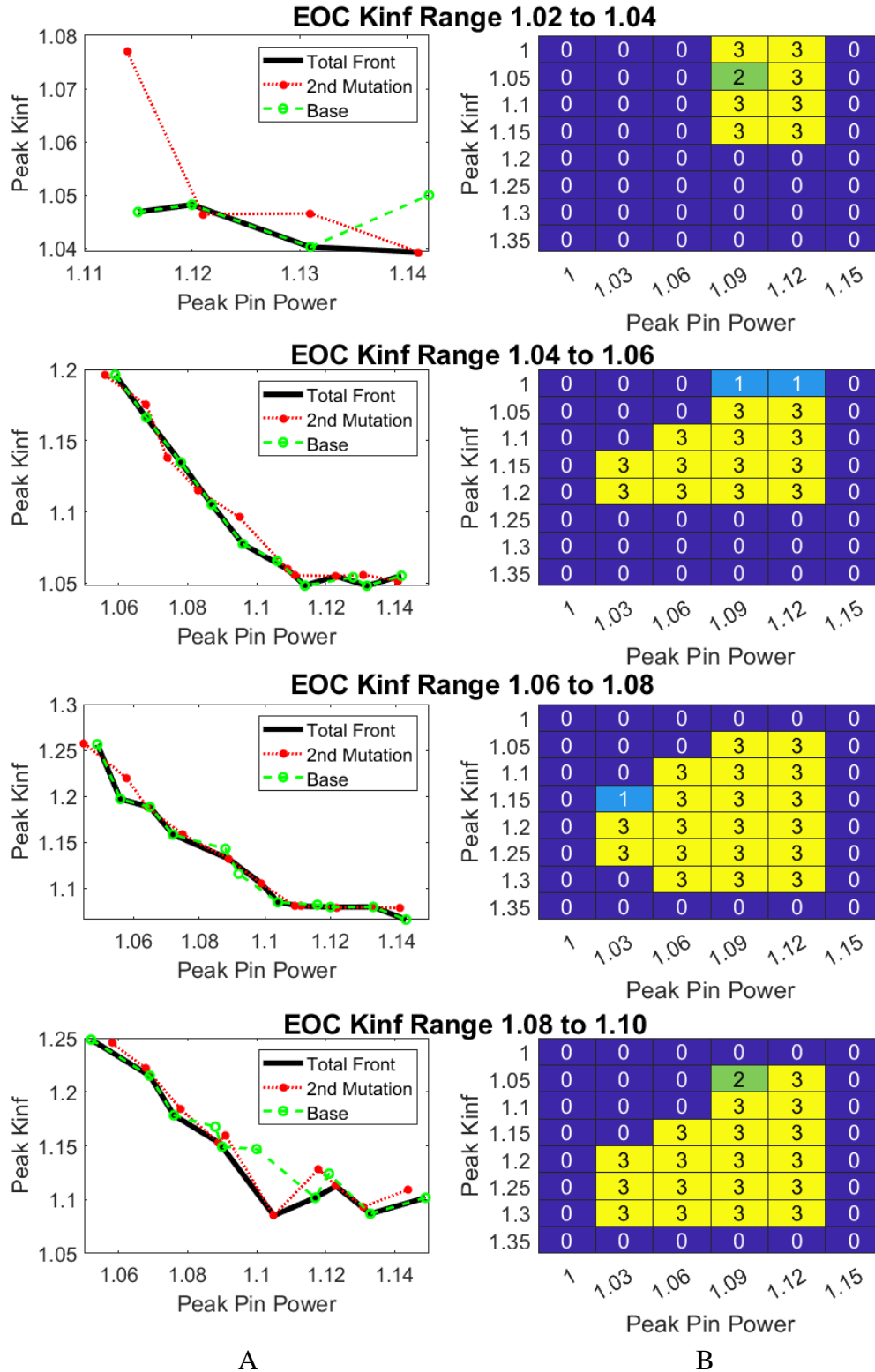


Figure A-0-23: Solution Front and Solution space comparison between base and second alternate mutation rate cases. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.

Table A-8 gives the average distances between the individual runs of the optimization to the optimal solution front for the large bin size cases. Figure A-24 compares the solution front and solution spaces of the large power bin size and base cases. Figure A-25 compares the solution front and solution spaces of the large peak kinf bin size and base cases. Figure 5-3 compares the solution front and solution spaces of the large end kinf bin size and base cases.

Table A-8: Average Distance Comparison of Large Bin Size Cases

Case Name	Case Part	Average Distance for EOC Kinf Range				
		1.02 – 1.04	1.04 – 1.06	1.06 – 1.08	1.08 – 1.10	Total
Large Power Bin Size	Test	7.67	12.11	16.48	21.22	57.48
	Base	7.38	12.04	18.30	15.60	53.32
	Difference	0.29	0.06	-1.82	5.62	4.16
Large Peak Kinf Bin Size	Test	5.93	14.62	25.82	20.49	66.86
	Base	3.78	13.29	23.20	20.06	60.33
	Difference	2.16	1.33	2.61	0.43	6.53
Large EOC Kinf Bin Size	Test	2.70	11.38	13.30	18.41	45.79
	Base	4.55	11.58	17.11	20.74	53.98
	Difference	-1.85	-0.19	-3.81	-2.33	-8.19

As shown in Table A-0-2 through Table A-0-4, the final population metrics differ from the base case, with average values being lower for the large bin size test cases than the base case. This is because solution space is larger for the base case than the large bin size test cases, so only fitter solutions will survive the binning process for the large bin size tests. The total distances in for the base case are less than the large power bin size and large peak kinf bin size. The distance for the large EOC kinf bin size is less than the distance for the base case. Figure A-24 and Figure A-25 show that the solution fronts are mostly composed of solutions from the base case, but that Figure 5-3 is most composed of solutions from the large EOC bin size case. These figures indicate the base optimization searches a wider area of the solution space than the large bin size test cases.

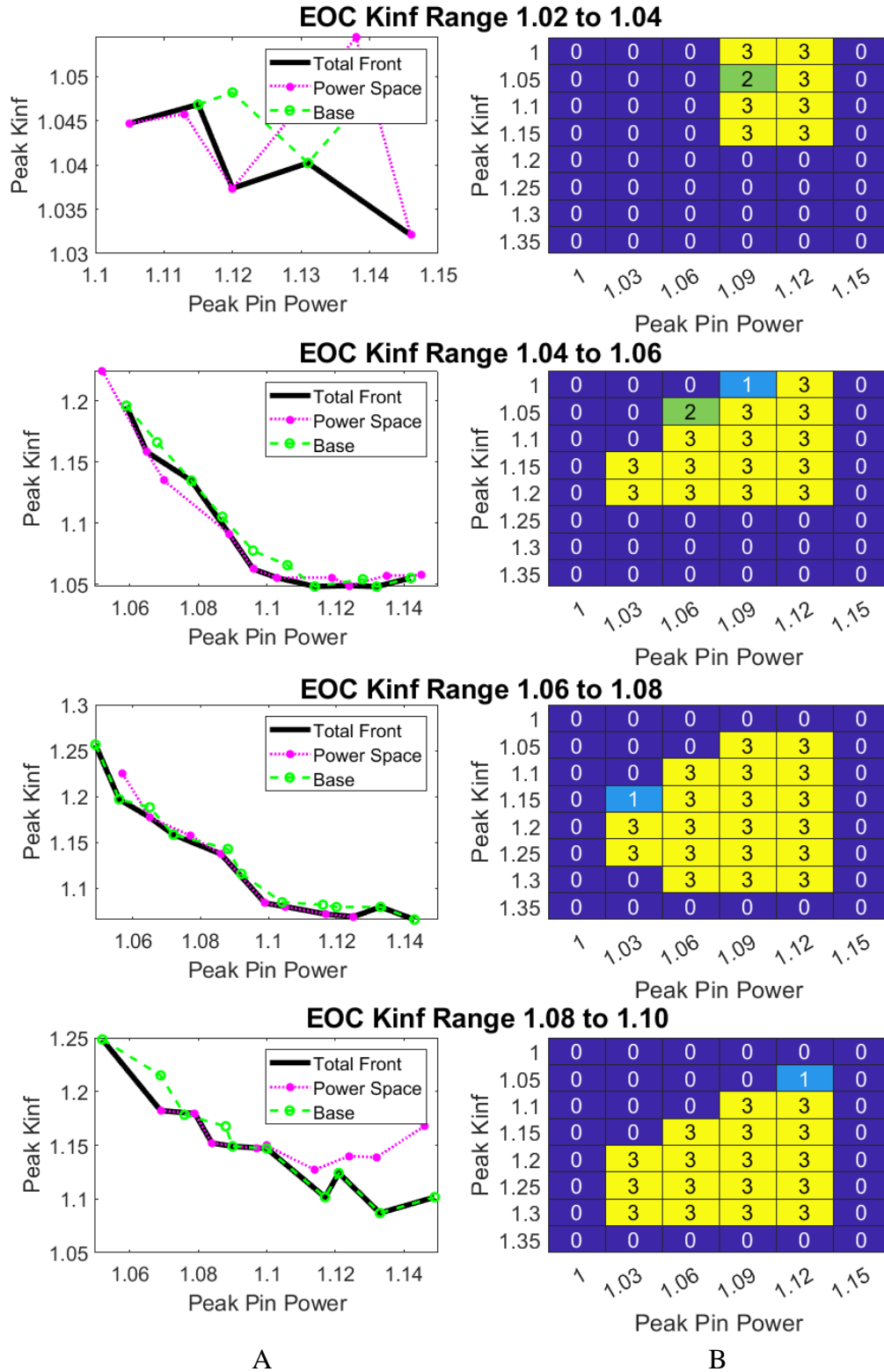


Figure A-0-24: Solution Front and Solution space comparison between base and the large PPF bin size case. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.

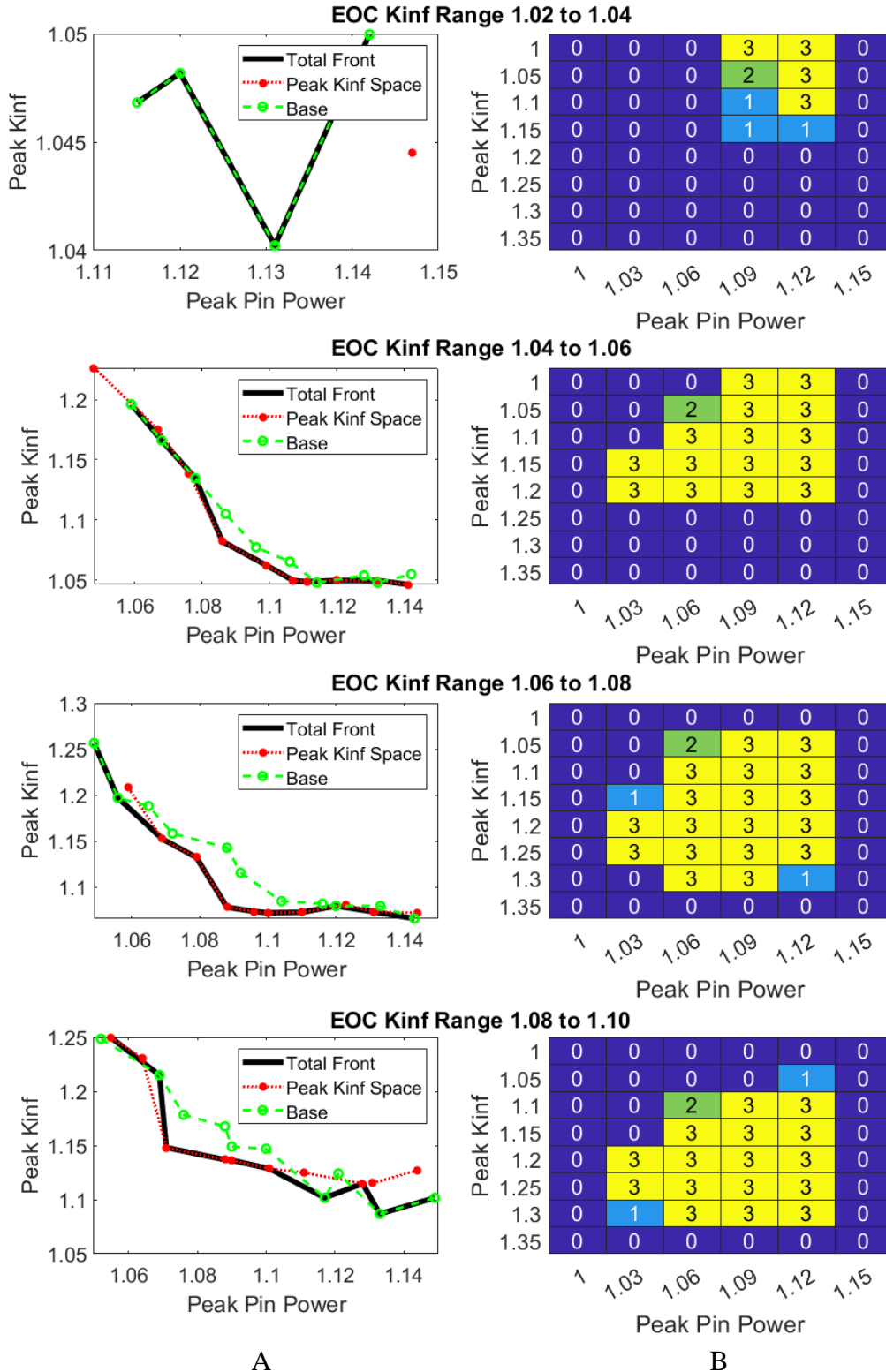
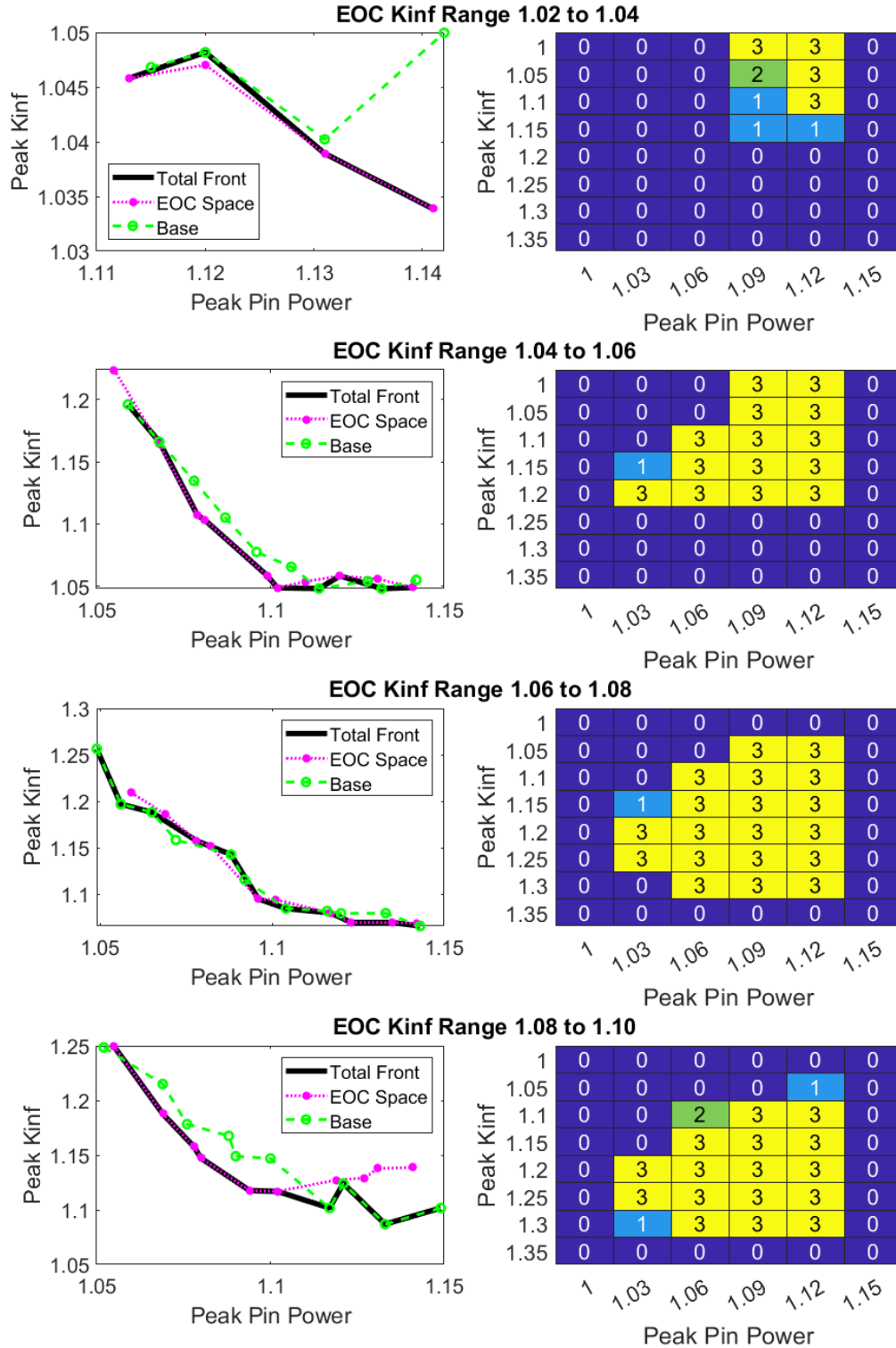


Figure A-0-25: Solution Front and Solution space comparison between base and the large peak kinf bin size. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.



A

B

Figure A-0-26: Solution Front and Solution space comparison between base and the large EOC kinf bin size. A: Solution Front. B: Solution Space. 1 indicates bin filled by base case only. 2 is filled by test case only. 3 is filled by both cases.