Reserve System with Beneficiary-Share Guarantee[*]

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Abstract

We study allocation problems with reserve systems under minimum beneficiary-share guarantees—requirements that targeted matches constitute at least a specified percentage of total matches. While such mandates promote targeted matches, they inherently conflict with maximizing total matches. We characterize the complete non-domination frontier using minimal cycles, where each point represents an allocation that cannot increase targeted matches without sacrificing total matches. Our main results: (i) the frontier exhibits concave structure with monotonically decreasing slope, (ii) traversing from maximum targeted matches to maximum total matches reduces matches by at most half, (iii) the Repeated Hungarian Algorithm computes all frontier points in polynomial time, and (iv) mechanisms with beneficiary-share guarantees can respect category-dependent priority orderings but necessarily violate path-independence. These results enable rigorous evaluation of beneficiary-share policies across diverse allocation contexts.

JEL Classification: D45, D47, I14

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1 Introduction

Reserve systems with minimum beneficiary-share guarantees—requirements that targeted matches constitute at least a specified percentage of total matches—are pervasive in modern allocation problems. From vaccine distribution during health crises to university admissions, from disability employment mandates to broadcasting content regulations, policymakers frequently require that targeted matches constitute at least a specified percentage of total matches.[1] While such mandates aim to ensure representation for priority groups and address historical inequities, they create an inherent trade-off: guaranteeing minimum shares for specific beneficiaries necessarily constrains the matching process, potentially reducing the total number of successful allocations. This tension manifests when reserved positions go unfilled due to a lack of qualified candidates from targeted groups, while non-targeted candidates who could have been matched are excluded.[2] Despite the ubiquity of such reserve systems, we lack a framework for understanding the complete spectrum of achievable outcomes and the precise nature of trade-offs between beneficiary representation and total match maximization.

We study allocation problems where the social planner aims to prioritize certain matches while the matching entities themselves remain indifferent among acceptable candidates. We characterize this framework by distinguishing between two key concepts: candidates whom matching entities consider *eligible* represent the complete set

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[1]Examples include: COVID-19 vaccine distribution requiring proportional allocation to minority groups (CDC, 2021); Indian universities reserving 2–5% for athletes and disadvantaged groups (Delhi University, 2025); Germany's 5% disability employment quota (iGlobal Law, 2013) and U.S. federal contractors' 7% requirement (DPI Staffing, 2013); and 35–55% local content requirements in Canadian and Australian broadcasting (Conversation, 2016).

[2]Common failures include vaccine expiration in priority categories while other regions face shortages (CDC, 2021), vacant reserved university seats, firms paying non-compliance penalties rather than meeting disability targets (iGlobal Law, 2013), and broadcasters producing substandard "quota quickies" to meet requirements (UNSW, 2023).

of acceptable matches from the entity's perspective, while matches the social planner wishes to promote for each entity are those deemed *beneficial* to that entity from a societal standpoint. However, when social planners impose these additional prioritization constraints, matching entities typically achieve fewer total matches than they would under their own preferences (see Example 1). This creates a fundamental trade-off: improving match quality from the social planner's perspective often reduces match quantity from the entities' operational perspective. Our focus on maximizing total matches—what Ashlagi *et al.* (2020) term "allocative efficiency" in their study of school choice with distributional constraints—reflects the primary concern in many reserve systems: ensuring that positions do not go unfilled.[3]

The existing literature typically addresses this tension through lexicographic approaches that prioritize one objective over the other: either maximizing the targeted matches among all matchings that achieve the maximum total number of matches, or conversely, maximizing total matches among those that reach the maximum number of targeted matches (Evren, 2023). We introduce the flexibility of allowing the planner to specify a target percentage of beneficiary matches within the total matching. This percentage-based framework encompasses lexicographic approaches as special cases.[4]

We consider a two-sided market where individuals on one side seek to be matched with entities on the other—such as vaccines, kindergartens, institutions, or enter-

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[3]Ashlagi *et al.* (2020) develop mechanisms that assign at least as many students as the optimal fractional solution (their OPT benchmark) while violating each constraint by at most $|T|$ (the number of types). Our characterization complements their approach by explicitly quantifying how much this allocative efficiency must decrease to guarantee any given beneficiary share, providing the complete frontier rather than focusing on a single operating point.

[4]For any matching problem, there exists a specific percentage threshold that corresponds to the "maximize beneficiary matches subject to maximum total matches" solution, and another threshold that yields the "maximize total matches subject to maximum beneficiary matches" outcome. Moreover, when we constrain solutions to lie on a Pareto-like frontier of targeted and total matches, these extreme lexicographic cases can be approximated using percentage targets of 0 and 100.

prises. Each entity can only match with certain eligible individuals, and within this eligible pool, some individuals are designated as beneficiaries—the group that policymakers particularly want to prioritize. Different entities may target different beneficiary groups, and these groups can overlap across entities. To ensure adequate access for beneficiaries, the social planner establishes a minimum threshold for the share of matches that must go to beneficiaries relative to the total number of matches made. Different entities may target different beneficiary groups, and these groups can overlap across entities.

To analyze this market, we introduce the concept of non-domination: a matching is non-dominated if no other matching achieves both more total eligible matches (e) and more beneficiary matches (b). The set of all such non-dominated matchings forms what we call the non-domination frontier—essentially the efficient boundary of possible (e, b) combinations. We show that this frontier can be characterized through a new structure we term *minimal cycles* (Definition 2). These are cycles similar to those in Top Trading Cycles (TTC) mechanisms, but with a specific property: applying a minimal cycle increases the total number of matches by one while minimizing the reduction in beneficiary matches (see Theorem 1).

The non-domination frontier follows a predictable pattern: it forms a concave curve where each additional eligible match comes at an increasing cost in beneficiary matches—a classic case of diminishing returns (Theorem 2). Perhaps most strikingly, we prove that prioritizing beneficiaries never reduces total matching capacity by more than half. Specifically, when we switch from maximizing all eligible matches to maximizing beneficiary matches, the total number of matches falls by at most 50%, and this bound cannot be improved (Proposition 1). These structural properties hold universally, regardless of the specific market data. This means policymakers can understand the fundamental trade-offs of beneficiary-share requirements even before

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collecting detailed information about their particular matching market.

We develop the Repeated Hungarian Algorithm (RHA) to compute all frontier points efficiently, with a runtime of $O(n^4)$ for n individuals (Algorithm 2, Theorem 3). This transforms our theoretical framework into a practical tool capable of solving real-world allocation problems at scale.

Our analysis reveals an important insight about beneficiary-share requirements: strictly enforcing them can actually lead to dominated outcomes. When a matching exactly meets the beneficiary-share target, it often lies below the non-domination frontier—meaning we could serve more people overall without reducing beneficiary access (Example 3). This motivates our approach of "approximate" compliance: we find the frontier matching that exceeds the beneficiary-share target by the smallest amount. Crucially, any such frontier matching dominates all matchings that meet the target exactly, delivering better outcomes for both beneficiaries and non-beneficiaries (Proposition 2).

We can extend this framework to respect priority orderings while maintaining approximate beneficiary-share compliance on the frontier (Proposition 3). However, there's an inherent limitation: these mechanisms cannot satisfy path-independence—the property that the final matching remains the same whether we consider all candidates at once or first select from subgroups and then choose from those selected candidates. This impossibility holds even without priority constraints, highlighting a fundamental tension between staying on the non-domination frontier and maintaining this procedural consistency (Theorem 4).

Our framework provides a principled approach to understanding the fundamental trade-offs inherent in allocation policies that prioritize specific groups. Across diverse contexts—from disability employment requirements, to corporate board gender mandates, to broadcasting content regulations, policymakers must balance representation

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goals against overall efficiency.[5] The non-domination frontier we characterize reveals the precise nature of these trade-offs: how much total matching capacity must be sacrificed to achieve any given beneficiary-share target. Our finding that this sacrifice never exceeds 50% of total matches provides a crucial benchmark for policy design. This allows policymakers to assess, before implementation, whether a proposed beneficiary-share requirement will maintain viability or risk driving participants away from the market altogether. Rather than discovering these trade-offs through costly trial and error, our framework enables informed policy decisions that balance equity objectives with practical sustainability.

Related Literature. Our work advances the literature on reserve systems and choice rules by fully characterizing the trade-off frontier between beneficiary representation and total match capacity, building on recent theoretical developments and practical applications in market design.

Reserve systems originated with Hafalir *et al.* (2013), who demonstrated that (minority) reserve categories could implement affirmative action in school choice more effectively than (majority) quota-based approaches (Kojima (2012)).

The theory of reserve systems emerged from Hafalir *et al.* (2013), who demonstrated how reserve categories could effectively implement affirmative action in school choice, addressing limitations of quota-based systems shown by Kojima (2012). Sönmez and Yenmez (2022) expanded this framework to handle overlapping reserves and developed the meritorious horizontal choice rule. During the COVID-19 pandemic, Pathak *et al.* (2023b) demonstrated how reserves could balance multiple ethical principles in medical resource allocation. Most recently, Evren (2023) proposed the

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[5]Examples include: companies choosing between meeting 1.5–7% disability targets or paying substantial fines (iGlobal Law, 2013); firms facing 33–40% board gender quotas that may compromise optimal composition or prompt delisting (Smith & Von Essen, 2025); and broadcasters producing low-quality "quota quickies" to meet 35–60% local content requirements (UNSW, 2023).

Threshold Reserve Model and Smart Pipeline Matching Mechanism, achieving the max-in-max property (see Remark 1) while maintaining independent priority orderings across categories. Our work extends this line of research by fully characterizing the non-domination frontier, revealing all feasible trade-offs between beneficiary representation and total match capacity.

Real-world implementations reveal the complexity of reserve systems—from Boston's school walk zones (Dur *et al.*, 2018) to H-1B visa reforms (Pathak *et al.*, 2025)—highlighting the importance of understanding feasible outcomes before policy deployment. Pathak *et al.* (2023a) demonstrate through incentivized experiments that 40% of participants fail to appreciate how processing order affects reserve system outcomes, mistakenly treating minimum guarantees (reserves processed first) as equivalent to over-and-above allocations (reserves processed last).[6] Experience with Indian colleges' affirmative action policies reinforces this lesson, prompting several theoretical advances: Manocha and Turhan (2025) extended gradual matching to complex affirmative action settings, while Aygün and Turhan (2017), Aygün and Turhan (2020), and Aygün and Turhan (2022) examined large-scale implementations, dynamic reserves, and de-reservation through choice rules. Our frontier characterization directly addresses these implementation concerns by revealing the precise trade-offs policymakers face. Specifically, we prove that transitioning from maximum eligibility to maximum beneficiary matching reduces eligible matches by at most 50%, quantifying this fundamental constraint for policy design.

Our work connects to the broader literature on choice rule design, which encompasses characterizing substitutability (Aygün and Sönmez, 2013), developing affirmative action schemes (Echenique and Yenmez, 2015; Imamura, 2025), preserving

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[6]This misunderstanding persists even among educated participants, suggesting that subtle features of reserve systems—like the distinction between minimum guarantees and additional seats—are systematically overlooked by stakeholders who must approve and oversee these policies.

substitutability under slot-specific priorities (Kominers and Sönmez, 2016), and incorporating diverse policy objectives (Doğan *et al.*, 2025; Yokote *et al.*, 2023). Doğan *et al.* (2025) recently emphasized the importance of path-independent choice rules (Chambers and Yenmez, 2017; Plott, 1973) in market design. We demonstrate that pursuing non-domination while approximately maintaining beneficiary-share guarantees necessarily yields choice rules that violate substitutability—and therefore path-independence—revealing an inherent tension between these desirable properties.

Nguyen and Vohra (2019) examined how much proportionality must be sacrificed to achieve stability, treating proportionality as a soft constraint and deriving bounds on necessary violations. While they quantify stability's cost in terms of proportionality violations, we measure the cost in total match capacity. Moreover, our setup differs from standard approaches in that beneficiary status is category-specific: the same individual may be a beneficiary for some categories but not others.

The paper is organized as follows. Section 2 presents the model and defines the frontier concept. Section 3 characterizes the frontier and introduces our Repeated Hungarian Algorithm with complexity analysis. Section 4 examines key allocation criteria. Section 5 concludes. Omitted proofs appear in the appendix.

2 Model

Following Pathak *et al.* (2023b), we model vaccine allocation using a reserve system with beneficiary-share guarantees comprising:

1. A finite set of categories $\mathcal{C} = \{c_1, c_2, ...\}$,

2. A finite set of patients $\mathcal{P} = \{p_1, p_2, ...\}$,

3. Eligible patient sets $\mathcal{E} = (E_c)_{c \in \mathcal{C}}$ where $E_c \subseteq \mathcal{P}$,

4. Beneficiary patient sets $\mathcal{B} = (B_c)_{c \in \mathcal{C}}$ where $B_c \subseteq E_c \subseteq \mathcal{P}$,

5. Category quotas $\mathbf{q} = (q_p)_{p \in \mathcal{C}} \in \mathbb{N}^{|\mathcal{C}|}$,

6. A beneficiary-share guarantee $\beta^* \in [0, 1]$.

We call tuples $(\mathcal{C}, \mathcal{P}, \mathbf{q}, \mathcal{E}, \mathcal{B})$ and $(\mathcal{C}, \mathcal{P}, \mathbf{q}, \mathcal{E}, \mathcal{B}, \beta^*)$ an **instance** and a **problem** respectively. For any instance, a correspondence $\mu : \mathcal{C} \cup \mathcal{P} \rightrightarrows \mathcal{C} \cup \mathcal{P} \cup \{\emptyset\}$ is a **matching** if: (i) each patient matches to at most one category ($|\mu(p)| \leq 1$ for all $p \in \mathcal{P}$); (ii) each category's assignments respect its quota ($|\mu(c)| \leq q_c$ for all $c \in \mathcal{C}$); and (iii) assignments are consistent ($\mu(p) = \{c\}$ if and only if $p \in \mu(c)$). When unambiguous, we write $\mu(p) = c$ if position p is matched to category c, and $\mu(p) = \emptyset$ if p is unmatched. A matching μ is **eligible** if $\mu(p) = c \in \mathcal{C} \implies p \in E_c$. We consider only eligible matchings unless stated otherwise.

For matching μ, we define **beneficiary matches** as $B(\mu) = \{(p, c) \mid p \in \mathcal{P}, c \in \mathcal{C}, p \in \mu(c) \cap B_c\}$, and for category c, $B_\mu(c) = \{(p, c) \mid p \in \mu(c) \cap B_c\}$. Similarly, **eligible matches** are $E(\mu) = \{(p, c) \mid p \in \mathcal{P}, c \in \mathcal{C}, p \in \mu(c) \cap E_c\}$, and $E_\mu(c) = \{(p, c) \mid p \in \mu(c) \cap E_c\}$. When context is clear, we use these terms to refer to either the sets or their cardinalities, use "targeted matches" interchangeably with "beneficiary matches", and use "total matches" interchangeably with "eligible matches".

For any non-empty matching μ, its **beneficiary-share** is $\beta(\mu) = \frac{|B(\mu)|}{|E(\mu)|}$. The policymaker mandates that beneficiary matches constitute at least $\beta^* \times 100\%$ of eligible matches, requiring $\beta(\mu) \geq \beta^*$.

A **mechanism** $\varphi : (\mathcal{C}, \mathcal{P}, \mathbf{q}, \mathcal{E}, \mathcal{B}, \beta^*) \mapsto \mu$ is a function which takes a problem $(\mathcal{C}, \mathcal{P}, \mathbf{q}, \mathcal{E}, \mathcal{B}, \beta^*)$ as input and outputs an eligible matching μ.

2.1 The Frontier

Two competing objectives arise in allocation: maximizing eligible matches for broad access versus maximizing beneficiary matches for targeted priorities. These goals typically conflict, requiring trade-offs between coverage and targeting.

To address this tension, Evren (2023) proposed **max-in-max**, which lexicographically prioritizes objectives: selecting the matching with maximum beneficiary matches among those maximizing eligible matches.

However, lexicographic maximization can entirely neglect one objective:

Example 1. *Consider patients $\mathcal{P} = p_1, p_2$ and categories $\mathcal{C} = c_1, c_2$. Patient p_1 is eligible for both categories and a beneficiary of c_2; patient p_2 is eligible only for c_2. The unique eligible-maximizing matching assigns $\mu(p_1) = c_1$ and $\mu(p_2) = c_2$, yielding zero beneficiary matches.*[7,8]

While lexicographic solutions prove problematic, the underlying principle remains appealing: conditional on eligible matches, maximize beneficiary matches; conditional on beneficiary matches, maximize eligible matches. We formalize this idea in the following definition.

Definition 1 (Domination and Frontier). *For any instance, a matching μ is **dominated** by matching μ' if:*

$$|E(\mu')| \geq |E(\mu)| \quad and \quad |B(\mu')| \geq |B(\mu)|,$$

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[7]Although patient p_1 is a beneficiary for c_2, their match to c_1 in the eligible-maximizing allocation does not count as a beneficiary match—beneficiary status only applies when matched to the designated category. In vaccine allocation, this captures the policy goal of prioritizing local frontline workers (medical staff, first responders) for their own district's vaccine supply. A frontline worker from District A receiving District B's vaccine dose represents a successful match but not a beneficiary match, as it fails to achieve the intended local protection priority.

[8]The cost of prioritizing total matches can be severe: our construction in Example 4 shows that maximizing eligible matches first can sacrifice arbitrarily many beneficiary matches—the loss grows unboundedly with market size.

with at least one strict inequality.[9] By definition, domination is a transitive relation. A matching is non-dominated if no other matching dominates it. A mechanism φ is **non-dominated** if it always produces non-dominated matchings. The **non-domination frontier** is:

$$F = \{(|E(\mu)|, |B(\mu)|) \in \mathbb{N}^2 : \mu \text{ is non-dominated }\}.$$

A non-dominated matching μ **corresponds to** point $(e, b) \in F$ if $|E(\mu)| = e$ and $|B(\mu)| = b$.

Remark 1. *The max-in-max solution (Evren, 2023) lies on the frontier but captures only one extreme point.*

Non-domination provides both a normative criterion and a practical framework for understanding trade-offs between eligible and beneficiary matches. The non-domination frontier, combined with a ray at the angle corresponding to the beneficiary-share guarantee, delimits feasible allocations. Section 3 characterizes the frontier and develops algorithms for its computation. Section 4 examines how non-domination interacts with other key allocation criteria.

3 Characterization and Computation of Frontier

We characterize the non-domination frontier and present a polynomial-time algorithm for its computation.

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[9]Unlike the roommate problem domination in Molis and Veszteg (2024), where matchings dominate via blocking pair chains, our definition operates at the aggregate level and allows indifference.

3.1 Cycle Characterization

We characterize the frontier using **minimal cycles** that link consecutive frontier points.

Without loss of generality, assume unit quotas, allowing us to write $\mu(c) = \{p\}$ as $\mu(c) = p$ and $\mu(c) = \{\emptyset\}$ as $\mu(c) = \emptyset$ (with slight abuse of notation). We call unit-quota categories seats. For non-dominated matching μ, the **associated graph** $G_\mu(\mathcal{P}, \mathcal{C}, E_\mu)$ is a directed bipartite graph with patients $\mathcal{P}$ and categories $\mathcal{C}$ as vertex sets.

The edge set E_μ contains: an edge from p to c if $p \in E_c$ and $\mu(p) \neq c$; an edge from c to p if $\mu(c) = p$ or $\mu(p) = \mu(c) = \emptyset$.

A **cycle** in G_μ is a sequence $\mathbf{c} = (p_1, c_1, \ldots, p_n, c_n, p_1)$ where consecutive vertices are connected by directed edges. Cycle $\mathbf{c}$ is **applicable** if p_1 and c_n are the unique unmatched patient and seat under μ, respectively.

Applying an applicable cycle $\mathbf{c}$ (in G_μ) to μ reassigns each patient p_k to category c_k, yielding matching $\mathbf{c}(\mu)$ where:

$$\mathbf{c}(\mu)(p) = \begin{cases} \mu(p) & \text{if } p \notin \mathbf{c} \\ c_k & \text{if } p = p_k \in \mathbf{c} \text{ for some } k. \end{cases}$$

The resulting matching remains eligible by construction. Consider the following example:

Example 2. *Consider patients* $\mathcal{P} = \{p_1, p_2, p_3\}$ *and categories* $\mathcal{C} = \{c_1, c_2, c_3\}$ *with unit quotas. The eligibility sets are:*

- $E_{c_1} = \{p_1, p_2\}$

- $E_{c_2} = \{p_2, p_3\}$

- $E_{c_3} = \{p_1\}$

Under matching μ: $\mu(p_1) = c_1$, $\mu(p_2) = c_2$, $\mu(p_3) = \emptyset$.

The cycle $\boldsymbol{c} = (p_3, c_2, p_2, c_1, p_1, c_3, p_3)$ is applicable since p_3 and c_3 are the unique unmatched patient and category, respectively.
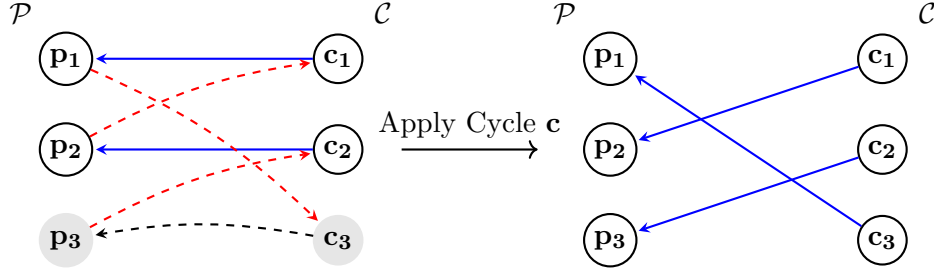

Figure 1: Left: Original associated graph G_μ. Right: New matching after applying cycle c. Blue: matching edges ($c \to p$), Red dashed: eligibility edges ($p \to c$), Black dashed: unmatched edge ($c \to p$).

Applying cycle $\boldsymbol{c}$ yields: $\mathbf{c}(\mu)(p_1) = c_3$, $\mathbf{c}(\mu)(p_2) = c_1$, $\mathbf{c}(\mu)(p_3) = c_2$, demonstrating how cycles transform matchings while preserving eligibility.

While the above definitions are standard in the matching literature, we now introduce **minimal cycles**, which are tailored to our two-tier environment and characterize the non-domination frontier.

Definition 2. *The **beneficiary loss** of applying applicable cycle $\mathbf{c}$ to non-dominated matching μ is $\Delta_{\mathbf{c}} = |B(\mu)| - |B(\mathbf{c}(\mu))| > 0$. An applicable cycle is **minimal** if it achieves the smallest beneficiary loss among all applicable cycles in G_μ.*
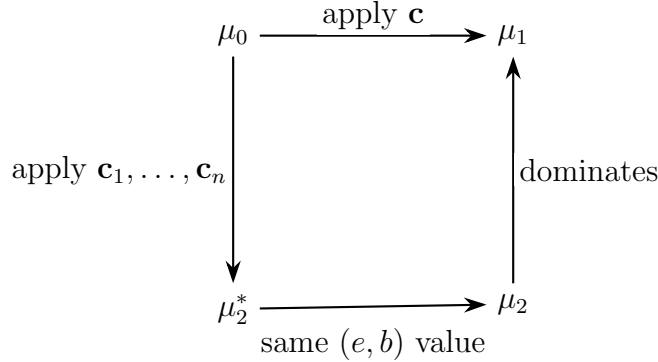
Minimal cycles connect consecutive frontier points:

Theorem 1. *Applying any minimal cycle $\mathbf{c}$ to any non-dominated matching μ_0 yields a non-dominated matching $\mu_1 = \mathbf{c}(\mu_0)$.*

Proof. We prove by contradiction. Suppose μ_1 is dominated, then it must be dominated by some non-dominated matching μ_2 with $|E(\mu_2)| \geq |E(\mu_1)|$. As μ_1 is achieved by applying $\mathbf{c}$ to μ_0, $|E(\mu_1)| = |E(\mu_0)| + 1$. Therefore, $|E(\mu_2)| \geq |E(\mu_1)| > |E(\mu_0)|$.

We require the following result:

Lemma 1. *For frontier points $f_1 = (e_1, b_1), f_2 = (e_1 - k, b_2)$ where $k \in \mathbb{N}$, and any non-dominated matching μ_2 corresponding to f_2, there exist k disjoint applicable cycles in G_{μ_2} that transform μ_2 to a non-dominated matching corresponding to f_1. Each cycle has strictly positive beneficiary loss.*

By Lemma 1, there exists μ_2^* with the same eligible and beneficiary match counts as μ_2, obtained by applying disjoint applicable cycles $\mathbf{c}_1, \ldots, \mathbf{c}_n$ to μ_0, each with strictly positive beneficiary loss. Thus μ_2^* also dominates μ_1. The relationships are illustrated below:

$$
\begin{array}{ccc}
\mu_0 & \xrightarrow{\text{apply } \mathbf{c}} & \mu_1 \\
\Big\downarrow{\scriptstyle\text{apply } \mathbf{c}_1, \ldots, \mathbf{c}_n} & & \Big\uparrow{\scriptstyle\text{dominates}} \\
\mu_2^* & \xrightarrow[\text{same } (e, b) \text{ value}]{} & \mu_2
\end{array}
$$

If $|E(\mu_2^*)| > |E(\mu_1)|$, then $n \geq 2$. This yields $|B(\mu_2^*)| = |B(\mu_0)| - \sum_{j=1}^{n} \Delta_{\mathbf{c}_j} < |B(\mu_0)| - \Delta_{\mathbf{c}_1} \leq |B(\mu_0)| - \Delta_{\mathbf{c}} = |B(\mu_1)|$, contradicting that μ_2^* dominates μ_1.

If $|E(\mu_2^*)| = |E(\mu_1)|$, then $n = 1$ and $|B(\mu_2^*)| > |B(\mu_1)|$. But this means $\Delta_{\mathbf{c}_1} < \Delta_{\mathbf{c}}$, contradicting the minimality of $\mathbf{c}$.

Therefore, μ_1 is non-dominated. $\qquad\square$

After applying a minimal cycle to a non-dominated matching, the resulting matching has exactly one additional eligible match, corresponding to the next consecutive point on the frontier. Can we find the entire non-domination frontier by starting from an appropriate matching? The natural candidates are the frontier's endpoints.

A matching is **max-bene then max-elig** if it maximizes eligible matches among all matchings that maximize beneficiary matches. Let μ_{BE} denote the set of such matchings:

$$\mu_{\text{BE}} = \underset{\mu \in \mathcal{M}}{\arg\max} |E(\mu)| \quad \text{where} \quad \mathcal{M} = \underset{\mu}{\arg\max} |B(\mu)|.$$

While μ_{BE} may contain multiple matchings, they share identical properties in our setting. We abuse notation and let μ_{BE} denote an arbitrary fixed element from this set.

Analogously, a **max-elig then max-bene** matching μ_{EB} maximizes beneficiary matches among all matchings that maximize eligible matches. This corresponds to the solution in Evren (2023).

These matchings correspond to the frontier's endpoints. Since the frontier captures the complete trade-off between maximizing total matches and maximizing target matches, the endpoints represent the extremes of prioritizing each goal.

The following theorem establishes that repeatedly applying minimal cycles to μ_{BE} generates all frontier points:

Theorem 2. *Starting from μ_{BE} and iteratively applying minimal cycles until no applicable cycles remain generates matchings corresponding to all frontier points. The frontier is dense in eligible matches: it contains points for every integer value of total matches from $|E(\mu_{BE})|$ to $|E(\mu_{EB})|$. Moreover, beneficiary loss increases weakly along this sequence, yielding a frontier with a negative, decreasing slope.*

Proof. By Lemma 1, every non-dominated matching except μ_{EB} has an applicable

cycle. By Theorem 1, applying a minimal cycle to a non-dominated matching yields another non-dominated matching with one additional eligible match. Since no other non-dominated matching can exist between these two matchings, they are consecutive points on the frontier. Combined the above arguments, repeatedly applying minimal cycles generates all non-dominated matchings. Consequently, the frontier contains a point for every feasible integer value of total matches between $E(\mu_{BE})$ and $E(\mu_{(}EB))$.

For the concavity of the frontier, consider the non-trivial case with three consecutive frontier points $(e_1, b_1), (e_1 + 1, b_2), (e_1 + 2, b_3)$ and any non-dominated matching μ_1 corresponding to (e_1, b_1). By Lemma 1, there exist disjoint applicable cycles $\mathbf{c}_1, \mathbf{c}_2$ in G_{μ_1} such that $b_3 = b_1 - \Delta_{\mathbf{c}_1} - \Delta_{\mathbf{c}_2}$. By Theorem 1, there exists a minimal cycle $\mathbf{c}_3$ in G_{μ_1} with $b_2 = b_1 - \Delta_{\mathbf{c}_3}$ where $\Delta_{\mathbf{c}_3} \leq \min\{\Delta_{\mathbf{c}_1}, \Delta_{\mathbf{c}_2}\}$ (because it is minimal). Therefore, $b_2 - b_3 = \Delta_{\mathbf{c}_1} + \Delta_{\mathbf{c}_2} - \Delta_{\mathbf{c}_3} \geq \Delta_{\mathbf{c}_3} = b_1 - b_2$. $\qquad\square$

With this result, we can quantify the worst-case resource sacrifice when prioritizing beneficiary matches.

Proposition 1. *For any instance* $(\mathcal{C}, \mathcal{P}, \boldsymbol{q}, \mathcal{E}, \mathcal{B})$:

$$\frac{|E(\mu_{\text{EB}})| - |E(\mu_{\text{BE}})|}{|\mathcal{P}|} \leq \frac{|E(\mu_{\text{EB}})| - |E(\mu_{\text{BE}})|}{min(|\mathcal{P}|, \sum_i q_i)} \leq \frac{|E(\mu_{\text{EB}})| - |E(\mu_{\text{BE}})|}{|E(\mu_{EB})|} \leq \frac{1}{2}.$$

This bound is tight: Example 1 achieves $\frac{|E(\mu_{\text{EB}})| - |E(\mu_{\text{BE}})|}{|\mathcal{P}|} = \frac{1}{2}$.

Proof. Let $K = |E(\mu_{\text{EB}})| - |E(\mu_{\text{BE}})|$. By Lemma 1, there exist K disjoint applicable cycles transforming μ_{BE} to some max-elig then max-bene matching μ_1. Each cycle contains at least two patients—a single-patient cycle would allow increasing eligible matches without changing other matches, contradicting that μ_{BE} is non-dominated.

Therefore, μ_1 matches at least $2K$ distinct patients, yielding:

$$\frac{|E(\mu_{\text{EB}})| - |E(\mu_{\text{BE}})|}{|E(\mu_{EB})|} \leq \frac{1}{2}.$$

The result follows since $|\mathcal{P}| \geq \min(|\mathcal{P}|, \sum_i q_i) \geq |E(\mu_{EB})|$. $\qquad\square$

This bound has profound policy implications: among non-dominated matchings, at most half the matched positions can be sacrificed under *any* policy prioritizing targeted matches—whether through quotas, beneficiary-share guarantees, or weighted objectives combining total and targeted matches.

3.2 Repeated Hungarian Algorithm

While directly identifying minimal cycles to calculate the frontier becomes computationally challenging as the number of patients and seats grows, the characterization enabled by these cycles allows for a novel approach to frontier calculation,[10] through repeated application of the Hungarian algorithm.

While identifying minimal cycles becomes computationally challenging as the number of patients and seats grows, our characterization enables a novel frontier calculation through repeated application of the Hungarian algorithm.

From Theorem 2, the non-domination frontier has decreasing slope and hence is concave. To find all frontier points, we first identify kinks where the slope changes, then exploit density to fill intermediate points by linear interpolation.[11]

To find all the kinks, we employ the Hungarian algorithm, typically used to com-

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[10]Alternatively, consider it as a linear programming problem: loop over the number of total matches e, maximize the number of beneficiary matches subject to the number of total matches being greater or equal than the current e.

[11]That is, since the frontier is dense in eligible matches, we fill in intermediate points at every unit interval in eligible matches by extending the same slope between them.

pute a maximum-weight matching in a bipartite graph (Kuhn, 1955a,b).[12] Our bipartite graph has patients $\mathcal{P}$ on one side, categories $\mathcal{C}$ on the other, with edges connecting eligible patient-category pairs regardless of beneficiary status. Edge weights determine which frontier kink is identified—the algorithm finds points where supporting lines of different slopes meet the frontier.[13]

The complete algorithm follows:

Algorithm 2 Repeated Hungarian Algorithm (RHA)

1: Initialize frontier $\leftarrow \emptyset$
2: Set $n \leftarrow \max(|\mathcal{P}|, \sum_i q_i)$
3: Set $m \leftarrow 0$ *(Counter of kinks)*
4: **for** $k \leftarrow 1$ to n **do**
5:     Assign weights:
6:         Eligible but not beneficiary: $w_{\text{elig}} \leftarrow 1$
7:         Beneficiary: $w_{\text{bene}} \leftarrow 1 + \frac{1}{k} + \frac{1}{n^2}$
8:     Run Hungarian algorithm to maximize $w_{\text{elig}} \cdot |E(\mu) - B(\mu)| + w_{\text{bene}} \cdot |B(\mu)|$
9:     Compute $e \leftarrow |E(\mu)|$
10:     Compute $b \leftarrow |B(\mu)|$
11:     **if** $m = 0$ or $(e, b) \neq (e_m, b_m)$ **then**
12:         $m \leftarrow m + 1$
13:         $(e_m, b_m) \leftarrow (e, b)$ *(Add kink (e, b) to frontier)*
14:     **end if**
15: **end for**
16: **for** $k \leftarrow 1$ to $m - 1$ **do**
17:     *(Insert intermediate points between kink (e_k, b_k) and kink (e_{k+1}, b_{k+1}))*
18:     **for** $j \leftarrow 1$ to $e_{k+1} - e_k - 1$ **do**
19:         Add $(e_k + j, b_{k+1} + j \cdot (b_k - b_{k+1})/(e_{k+1} - e_k))$ to frontier
20:     **end for**
21: **end for**

To establish correctness of this algorithm, note that by Theorem 2, the frontier F

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[12]While the classical Hungarian algorithm formulation assumes equal-sized partitions, the standard solution for unbalanced cases involves adding dummy vertices connected by zero-weight edges to create an equivalent balanced bipartite graph, thus enabling the algorithm's application.

[13]A supporting line touches the frontier at exactly one point.

for any instance takes the form:

$$F = \left\{ (e, b), (e - 1, b + \Delta b_1), \ldots, \left(e - K, b + \sum_{i=1}^{K} \Delta b_i \right) \right\}$$

where $K = |E(\mu_{EB})| - |E(\mu_{BE})|$. This frontier contains $K+1$ points. The starting point (e, b) corresponds to μ_{EB}, while the endpoint $(e - K, b + \sum_{i=1}^{K} \Delta b_i)$ corresponds to μ_{BE}. The beneficiary differences satisfy $\Delta b_1 \geq \Delta b_2 \geq \cdots \geq \Delta b_K \geq 1$.

Point j is a kink when $\Delta b_j \neq \Delta b_{j+1}$. At kink $(e - j, b + \sum_{i=1}^{j} \Delta b_i)$, the marginal trade-off changes from Δb_j to Δb_{j+1} beneficiary matches per eligible match. This point lies on the supporting line with slope in $(-\Delta b_j, -\Delta b_{j+1})$, which corresponds to beneficiary weight $w_B = 1 + \frac{1}{\Delta b_j} + \frac{1}{n^2}$ in the algorithm.

Lemma 2. *The Repeated Hungarian Algorithm (RHA) satisfies:*

1. *In the first loop, the first and last iterations compute μ_{BE} and μ_{EB} respectively.*

2. *For any interior frontier point $f_j = (e - j, b + \sum_{i=1}^{j} \Delta b_i)$ (excluding endpoints) with $\Delta b_j > \Delta b_{j+1}$, the RHA computes this point in iteration Δb_j of the first loop.*

We now establish the algorithm's properties.

Theorem 3. *The Repeated Hungarian Algorithm (RHA) satisfies:*

1. ***Completeness***: *RHA generates the entire non-domination frontier.*

2. ***Computational Complexity***: *RHA runs in $O(n^4)$ time, where $n = max(|\mathcal{P}|, \sum_i q_i)$.*

Proof. For completeness, Lemma 2 establishes that the first loop identifies all kinks (points where slope changes) and both endpoints. Any remaining frontier points lie on constant-slope segments and are filled by linear interpolation in the second loop.

The complexity bound follows from the first loop, which runs at most n iterations (since $\Delta b_i \geq 1$ and there are at most n possible values), with each iteration executing the Hungarian algorithm in $O(n^3)$ time (Kuhn, 1955a). The second loop performs only linear interpolation in $O(n)$ time. Thus, the total complexity is $O(n^4)$.   □

Remark 2. *Frontier concavity is essential for our approach. Suppose the frontier is not concave (but is still dense in eligibility), that is, there exists three hypothetical points $f_1 = (e, b)$, $f_2 = (e-1, b+\Delta b_1)$, and $f_3 = (e-2, b+\Delta b_1+\Delta b_2)$ with $\Delta b_1 < \Delta b_2$. To identify f_2 in RHA, there exists beneficiary weight $w \in \mathbb{R}^2_{++}$ at which f_2 exceeds both f_1 and f_3 in weighted value, requiring*

$$w(\Delta b_1) - 1 > 0 \quad and \quad 1 - w(\Delta b_2) > 0.$$

These inequalities cannot hold simultaneously when $\Delta b_1 < \Delta b_2$. Thus, without concavity, RHA cannot identify all the kinks and fails to generate the complete frontier.

4   Compatibility with Design Objectives

This section examines how the non-domination frontier interacts with key allocation criteria that arise in practice. We first address the tension between achieving beneficiary-share guarantees and maintaining non-dominated allocations-the rigorous enforcement of beneficiary-share might harm the underlying policy goal. We then explore two important considerations: whether the framework can accommodate priority orderings (as commonly required in school choice and medical allocation), and whether the resulting choice rules can satisfy path-independence, a foundational property for stable market design.

4.1 Beneficiary-share guarantee and non-domination

Given a problem $(\mathcal{C}, \mathcal{P}, \mathbf{q}, \mathcal{E}, \mathcal{B}, \beta^*)$, we say a non-empty matching μ **respects beneficiary-share guarantee** if it satisfies:

$$\beta(\mu) = \frac{|B(\mu)|}{|E(\mu)|} \geq \beta^*,$$

meaning beneficiary matches constitute at least β^* proportion of total matches.

A mechanism φ **respects beneficiary-share guarantee** if for any problem with at least one non-empty beneficiary set, the mechanism chooses a matching that respects beneficiary-share guarantee.[14]

While such mechanisms exist, the beneficiary-share guarantee fundamentally conflicts with non-domination, as the following example demonstrates.

Example 3. *Consider a problem with patients $\mathcal{P} = \{p_1, p_2\}$ and categories $\mathcal{C} = \{c_1, c_2\}$ with $q_{c_1} = q_{c_2} = 1$, and beneficiary-share guarantee $\beta^* = 0.7$. Patient p_1 is a beneficiary of c_1 but not eligible for c_2, while patient p_2 is eligible for c_2 but not a beneficiary.*

To respect the beneficiary-share guarantee, any mechanism must choose matching μ with $\mu(p_1) = c_1$ and $\mu(p_2) = \emptyset$, yielding $\beta(\mu) = 1$. The alternative matching μ' with $\mu'(p_1) = c_1$ and $\mu'(p_2) = c_2$ violates the guarantee since $\beta(\mu') = 0.5 < 0.7$.

However, μ' dominates μ by achieving $(|E(\mu')|, |B(\mu')|) = (2,1)$ versus $(|E(\mu)|, |B(\mu)|) = (1,1)$. In this case, the beneficiary-share guarantee forces selection of a dominated matching.

Example 3 demonstrates a critical policy limitation: mandating too high a beneficiary-

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[14]For any problem with at least one non-empty beneficiary set, a matching respecting the beneficiary-share guarantee exists: simply match only within this beneficiary set, achieving $\beta(\mu) = 1 \geq \beta^*$. Thus, mechanisms respecting the beneficiary-share guarantee exist.

share guarantee can force selection of a matching dominated by μ_{BE}. This domination is unjustifiable—while the beneficiary-share guarantee aims to increase targeted matches, the resulting matching achieves no more targeted matches than μ_{BE} while strictly fewer total matches.

With this consideration, when non-domination conflicts with the beneficiary-share guarantee, we prioritize non-domination. We formalize this through the following concept: given a problem, a matching μ **respects the beneficiary-share guarantee approximately on the frontier** if:

- When $\beta^* < \beta(\mu_{BE})$: μ achieves the beneficiary-share closest to β^* among all non-dominated matchings satisfying $\beta(\mu) \geq \beta^*$.

- When $\beta^* \geq \beta(\mu_{BE})$: μ is a max-bene then max-elig matching.

A mechanism **respects the beneficiary-share guarantee approximately on the frontier** if it always selects such a matching.[15,16] Such mechanisms always exist by construction.

The following result further justifies this solution concept: when we could choose a dominated matching μ achieving exactly β^*, selecting instead a matching that respects the beneficiary-share guarantee approximately on the frontier yields a matching that dominates μ.

Proposition 2. *For any problem* $(\mathcal{C}, \mathcal{P}, \boldsymbol{q}, \mathcal{E}, \mathcal{B}, \beta^*)$, *let* μ^* *be a matching that respects the beneficiary-share guarantee approximately on the frontier. If* $\beta(\mu^*) \neq \beta^*$, *then* μ^* *dominates any matching with beneficiary-share* β^*.

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[15]By definition, $\beta(\mu_{BE}) = 0$ when all beneficiary sets are empty.

[16]Our solution concept satisfies constrained Pareto optimality for individual welfare. A matching μ is Pareto dominated by μ' if: (i) every participant matched in μ remains matched in μ' (i.e., $\mu(p) \neq \emptyset \implies \mu'(p) \neq \emptyset$), and (ii) at least one previously unmatched participant becomes matched (i.e., $\exists p' \in \mathcal{P}$ such that $\mu(p') = \emptyset$ but $\mu'(p') \neq \emptyset$). Since frontier matchings maximize total matches subject to the beneficiary-share guarantee, they cannot be Pareto dominated by any other matching that respects the same guarantee—any additional match would violate the beneficiary-share constraint.

Proof. Consider the non-trivial case where a matching with beneficiary-share β^* exists but all the frontier points do not achieve the exact β^*. Let μ' be a matching with $\beta(\mu') = \beta^*$ that maximizes $|E(\mu)|$ among all matchings achieving beneficiary-share β^*. Then μ' dominates all other matchings with the same beneficiary-share but fewer total matches. To prove the proposition, it suffices to show that μ^* dominates μ'. We consider two cases.

Case 1: $|E(\mu')| < |E(\mu_{BE})|$. Since μ^* is non-dominated and μ_{BE} is the non-dominated matching with the least eligible matches, we have $|E(\mu^*)| \geq |E(\mu_{BE})| > |E(\mu')|$. If $\beta(\mu^*) > \beta(\mu')$, then $|B(\mu^*)| > |B(\mu')|$, so μ^* clearly dominates μ'. If instead $\beta(\mu^*) < \beta(\mu')$, then by definition μ^* is a max-bene then max-elig matching, implying $|B(\mu^*)| \geq |B(\mu')|$. Combined with $|E(\mu^*)| > |E(\mu')|$, we have that μ^* dominates μ'.

Case 2: $|E(\mu')| \geq E(\mu_{BE})$. By Theorem 2, there exists a non-dominated matching μ'' with $|E(\mu'')| = |E(\mu')|$ and $|B(\mu'')| > |B(\mu')|$, implying $\beta(\mu'') > \beta(\mu') = \beta^*$. Since μ^* respects the beneficiary-share guarantee approximately on the frontier and $\beta(\mu^*) \neq \beta^*$, we must have $\beta(\mu^*) > \beta^* = \beta(\mu')$ and $|E(\mu^*)| \geq |E(\mu'')| = |E(\mu')|$. This implies $|B(\mu^*)| = \beta(\mu^*)|E(\mu^*)| > |B(\mu')|$. Therefore, μ^* dominates μ'.

In both cases, μ^* dominates μ', completing the proof. $\square$

4.2 Respecting Priority

In many real-world allocation systems, reserves operate alongside priority orderings of patients. This subsection extends our model to incorporate such priorities. Following Pathak *et al.* (2023b), we allow category-specific priorities while requiring beneficiary patients to rank above non-beneficiary patients within each category.

Formally, a list of strict total orders on $\mathcal{P}$, denoted $\pi = (\pi_c)_{c \in \mathcal{C}}$, is a **priority**

order if for any category c:

- For any $(p, j) \in B_c \times (E_c \setminus B_c)$: $p\pi_c j$ (beneficiaries rank above non-beneficiaries)

- For any $(j, k) \in E_c \times (\mathcal{P} \setminus E_c)$: $j\pi_c k$ (eligible patients rank above ineligible patients)

We call the vector $(\mathcal{C}, \mathcal{P}, \mathbf{q}, \mathcal{E}, \mathcal{B}, \beta^*, \pi)$ a **problem with order**. With slight abuse of notation, we retain our terminology for mechanisms, matchings, and respecting the beneficiary-share guarantee approximately on the frontier when applied to problems with order.

Given a problem with order, a matching μ **respects priority** if for every category c and patients $p, p' \in \mathcal{P}$:

$$\mu(p) = c \text{ and } \mu(j) = \emptyset \implies p\pi_c p'.$$

This condition ensures no unassigned patient has higher priority than an assigned patient for the same category, preventing justified envy. This definition aligns with priority-respecting matching in Pathak *et al.* (2023b). A mechanism φ **respects priority** if for any problem with order $(\mathcal{C}, \mathcal{P}, \mathbf{q}, \mathcal{E}, \mathcal{B}, \beta^*, \pi)$, the mechanism's output respects priority.

The following result establishes that respecting priority is compatible with respecting the beneficiary-share guarantee approximately on the frontier.

Proposition 3. *There exists a mechanism that respects priority and respects beneficiary-share guarantee approximately on the frontier.*

Proof. For any eligible matching μ, define its **rank sum** as $R(\mu) = \sum_{\mu(p)=c} R_c(p)$ where $R_c(p)$ denotes the position of patient p in category c's priority order π_c (with $R_c(p) = 1$ for the highest-priority patient).

Consider any point (e, b) on the frontier. Among all matchings achieving this point, the matching with minimum rank sum must respect priority. To see why, suppose matching μ achieves (e, b) with minimum rank sum but violates priority: for some category c, we have $\mu(p) = c$ and $\mu(p') = \emptyset$ with $p' \pi_c p$. Then swapping assignments to set $\mu'(p') = c$ and $\mu'(p) = \emptyset$ would yield another matching achieving (e, b) with strictly lower rank sum, contradicting minimality.

Therefore, our mechanism operates as follows: First, identify the frontier point (e^*, b^*) corresponding to a matching that respects the beneficiary-share guarantee approximately on the frontier. Then, among all matchings achieving (e^*, b^*), select one minimizing the rank sum. This matching respects both priority and the beneficiary-share guarantee approximately on the frontier. $\square$

4.3 Path-independence

This subsection analyzes path-independence, a fundamental property of choice rules. We first define the choice rule induced by a mechanism.

Given a problem $(\mathcal{C}, \mathcal{P}, \mathbf{q}, \mathcal{E}, \mathcal{B}, \beta^*)$, the **choice rule** C induced by mechanism φ is a function from $2^{\mathcal{P}}$ to $2^{\mathcal{P}}$ such that for any $X \in 2^{\mathcal{P}}$:

$$C(X) = \{p \in X : \varphi(\mathcal{C}, X, \mathbf{q}, \mathcal{E}, \mathcal{B}, \beta^*)(p) \neq \emptyset\}$$

That is, $C(X)$ consists of all patients in X who receive assignments when the mechanism is applied to patient set X.

Given a problem, a choice rule C is **path-independent** if for all $X, X' \in 2^{\mathcal{P}}$:

$$C(X \cup X') = C(C(X) \cup X').$$

This property ensures that choosing from a union can be done sequentially: first choose from X, then combine those chosen with X' and choose again, yields the same result as choosing directly from $X \cup X'$. Path-independence plays a fundamental role in market design, particularly for choice rule-based deferred acceptance mechanisms (Doğan *et al.*, 2025). A mechanism is **path-independent** if the choice rule it induces is path-independent for every problem.

Theorem 4. *There does not exist a mechanism that is path-independent and respects beneficiary-share guarantee approximately on the frontier.*

Proof. Consider a problem where $\mathcal{P} = \{p_1, p_2, p_3, p_4, p_5, p_6\}$, $\mathcal{C} = \{c_1, c_2, c_3, c_4, c_5\}$, each with capacity 1, and $\beta^* = 0.2$. The eligibility and beneficiary relations are given in the following table, where boxed entries indicate beneficiaries of the corresponding categories:

	c_1	c_2	c_3	c_4	c_5
	$\boxed{p_1}$	p_2	p_3	$\boxed{p_6}$	p_1
	p_2	p_3	p_5	p_4	

Consider $X = \{p_1, p_2, p_3, p_4, p_5\}$. The non-dominated matchings for the subproblem $(\mathcal{C}, X, \mathbf{q}, \mathcal{E}, \mathcal{B}, \succ, \beta^*)$ with patient set X are:

$$B = 1, \ E = 4, \ \beta = 0.25 : \{(c_1, \boxed{p_1}), (c_2, p_2), (c_3, p_3), (c_4, p_4), (c_5, \emptyset)\},$$
$$\{(c_1, \boxed{p_1}), (c_2, p_2), (c_3, p_5), (c_4, p_4), (c_5, \emptyset)\},$$
$$\text{and } \{(c_1, \boxed{p_1}), (c_2, p_3), (c_3, p_5), (c_4, p_4), (c_5, \emptyset)\}.$$
$$B = 0, \ E = 5, \ \beta = 0 : \{(c_1, p_2), (c_2, p_3), (c_3, p_5), (c_4, p_4), (c_5, p_1)\}.$$

Since $\beta^* = 0.2$ and the first three matchings achieve $\beta = 0.25 > \beta^*$, any mecha-

nism respecting the beneficiary-share guarantee approximately on the frontier must select one of these three matchings. Therefore, $C(X) \in \{\{p_1, p_2, p_3, p_4\}, \{p_1, p_2, p_4, p_5\}, \{p_1, p_3, p_4, p_5\}\}$

Now consider the full patient set $\mathcal{P} = X \cup \{p_6\}$. The frontier becomes:

$$B = 2, \ E = 4, \ \beta = 0.5 : \{(c_1, \boxed{p_1}), (c_2, p_2), (c_3, p_3), (c_4, \boxed{p_6}), (c_5, \emptyset)\},$$
$$\{(c_1, \boxed{p_1}), (c_2, p_2), (c_3, p_5), (c_4, \boxed{p_6}), (c_5, \emptyset)\},$$
$$\text{and } \{(c_1, \boxed{p_1}), (c_2, p_3), (c_3, p_5), (c_4, \boxed{p_6}), (c_5, \emptyset)\}.$$
$$B = 1, \ E = 5, \ \beta = 0.2 : \{(c_1, p_2), (c_2, p_3), (c_3, p_5), (c_4, \boxed{p_6}), (c_5, p_1)\}.$$

Since the matching with $\beta = 0.2$ exactly achieves β^*, the mechanism must select it. Thus $C(\mathcal{P}) = \{p_1, p_2, p_3, p_5, p_6\}$.

However, for any possible $C(\cdot)$, we have:

$$C(\{p_1, p_2, p_3, p_4, p_5, p_6\}) \cap \{p_1, p_2, p_3, p_4, p_5\} = \{p_1, p_2, p_3, p_5\} \nsubseteq C(\{p_1, p_2, p_3, p_4, p_5\}),$$

which violates path-independence.[17] $\qquad\square$

5 Conclusion

We characterize the non-domination frontier between total matches and beneficiary matches through the novel concept of minimal cycles. Our analysis reveals that the frontier exhibits a concave structure with increasing marginal costs—each addi-

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[17]The example in the proof actually demonstrates a violation of the *substitutability* (see recent discussion in Bando *et al.*, 2025), which states that if $X' \subseteq X$, then $C(X) \cap X' \subseteq C(X')$. In our example, we have $X \subseteq \mathcal{P}$ with $C(\mathcal{P}) \cap X = p_1, p_2, p_3, p_5 \nsubseteq C(X)$ for any valid $C(X)$. Since our mechanism violates substitutability, it necessarily violates path-independence (Aizerman and Malishevski, 1981). The violation occurs because after patient p_6 enters, the new chosen matching is obtained from substituting the matching with $B = 0, E = 5$ with the new patient, instead from substituting the matching with $B = 1, E = 4$ which is chosen without p_6.

tional eligible match requires progressively larger sacrifices in beneficiary matches. We establish that the relative efficiency loss from beneficiary-share requirements is bounded by $\frac{1}{2}$, and this bound is tight. The Repeated Hungarian Algorithm we develop generates all frontier points in polynomial time ($O(n^4)$), providing practitioners with a computationally tractable tool. Our framework demonstrates that respecting beneficiary-share guarantees approximately on the frontier is compatible with priority considerations but fundamentally incompatible with path-independence choice rules.

While our analysis focuses on settings with a single beneficiary category, the minimal cycle approach naturally extends to richer environments. Multiple overlapping beneficiary requirements—such as simultaneous quotas for different demographic groups in school allocation—present interesting directions for future work. Our characterization moves beyond traditional lexicographic approaches, offering guidance for balancing competing objectives. The minimal cycle construction we introduce provides a new analytical tool for matching theory that may prove valuable in broader reserve system design.

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A   Appendix

A.1   Example 4

While it may seem natural to first maximize the total number of matches and then maximize beneficiary matches among those solutions, this lexicographic approach can lead to poor outcomes for beneficiaries. We demonstrate that prioritizing total matches can result in an arbitrarily large loss of beneficiary matches compared to directly maximizing beneficiary matches.

Example 4. *Consider the following market instance with parameter $K \in \mathbb{Z}^+$:*

- *$\mathcal{P} = \{p_1, p_2, \ldots, p_{K+2}\}$.*

- *$\mathcal{C} = \{c_1, c_2, \ldots, c_{K+2}\}$, each with a unit quota.*

The beneficiary and eligibility sets are defined as follows:

$$B_{c_n} = \{p_n\} \quad \text{for } n = 1, 2, \ldots, K+1, \qquad B_{c_{K+2}} = \emptyset,$$

$$E_{c_n} = \{p_n, p_{n-1}\} \quad \text{for } n = 2, \ldots, K+1, \qquad E_{c_1} = \{p_1, p_{K+2}\}, \quad E_{c_{K+2}} = \{p_{K+1}\}.$$

In this construction:

- *A **max-bene matching** μ_1 can assign each participant p_n $(1 \leq n \leq K+1)$ to their unique beneficiary category c_n, achieving $|B(\mu_1)| = K+1$ beneficiary matches, with p_{K+2} remaining unmatched.*

- *A **max-elig-then-max-bene matching** μ_2 must first maximize total matches. To match all $K+2$ participants, it must assign p_{K+2} to c_1 (its only eligible category), which displaces p_1 to c_2, which displaces p_2 to c_3, and so on, creating*

a chain reaction. The resulting matching assigns p_{K+1} to c_{K+2} and achieves $|E(\mu_2)| = K + 2$ total matches but $|B(\mu_2)| = 0$ beneficiary matches.

The difference in beneficiary matches is $|B(\mu_1)| - |B(\mu_2)| = K + 1$. Since K can be chosen arbitrarily large, this demonstrates that the lexicographic approach of first maximizing eligible matches can sacrifice an unbounded number of beneficiary matches.

A.2 Proof of Lemma 1

To prove Lemma 1 we need the following lemma:

Lemma A1. *Given a matching μ_2 corresponding to $f_2 = (e_2, b_2)$ on the frontier, for any $f_1 = (e_1, b_1)$ with $e_1 > e_2$ on the frontier, there exists a matching μ^* corresponding to f_1 such that any patient matched in μ_2 is still matched in μ^*.*

Proof. Let μ_1 be any non-dominated matching corresponding to frontier point $f_1 = (e_1, b_1)$, with $e_1 - e_2 = k \in \mathbb{N}_+$. We will construct a matching μ^* from μ_1 such that any patient matched in μ_2 is still matched in μ^* and μ^* corresponds to f_1.

Let A and D be the sets of matched patients in μ_2 and μ_1, respectively. We partition A into three disjoint sets A_1, A_2, A_3 such that:

$$A_1 = \{p \in A : \mu_1(p) = \mu_2(p)\}, \quad A_2 = \{p \in A : \mu_1(p) \neq \emptyset, \mu_1(p) \neq \mu_2(p)\}, \text{ and}$$

$$A_3 = \{p \in A : \mu_1(p) = \emptyset\}.$$

Intuitively, we want to replace the patients in μ_1 that are only matched in μ_1 ($p \in D \backslash A$) with patients that are only matched in μ_2 ($p \in A_3$). With eligibility constraints, we cannot do this one-to-one exchange directly. So instead, we first match all the

patients in A_3, then unmatch patients in $D \setminus A$ to restore the (e_1, b_1) requirement.
See the following diagram.

$$\mu_1 \xrightarrow[\text{step 1}]{\text{Match all patients in } A_3} \mu' \xrightarrow[\text{step 2}]{\text{Unmatch patients in } D \setminus A} \mu^*.$$

Step 1. For each patient $p_0 \in A_3$, we construct a sequence starting with p_0,
where each subsequent patient is matched in μ_1 to the previous patient's seat in μ_2,
until the sequence ends with an unmatched seat in μ_1 or an unmatched patient in μ_2.
Formally, the process is as follows.

As μ_1 is non-dominated, seat $\mu_2(p_0)$ must be occupied in μ_1 by some patient in
D, let $p_1 = \mu_1(\mu_2(p_0))$ and add p_1 to the sequence. If $\mu_2(p_1) = \emptyset$, then terminate the
sequence with $p_1 \in D \setminus A$. Else, if $\mu_1(\mu_2(p_1)) = \emptyset$, then terminate the sequence with
$p_1 \in A_2$; if $\mu_1(\mu_2(p_1)) \neq \emptyset$, add $p_2 = \mu_1(\mu_2(p_1))$ to the sequence and continue this
process.

Since $\mathbf{q}$ is finite and all seats are visited at most once, the process ends with a
finite sequence $(p_0, p_1, \ldots, p_N)$ satisfying: for every $1 \leq m \leq N$, $\mu_1(p_m) = \mu_2(p_{m-1})$;
all intermediate patients p_n for $1 \leq n < N$ belong to A_2; and the terminal patient p_N
is either in $D \setminus A$ with $\mu_2(p_N) = \emptyset$, or in A_2 with $\mu_1(\mu_2(p_N)) = \emptyset$. We call the latter
case a **type 1** sequence, and the former a **type 2** sequence.

Given any sequence $\mathbf{s} = (p_0, p_1, \ldots, p_N)$, define the process of rematching the
patients in $\mathbf{s}$ to their seats in μ_2 and keeping other patients' seats in μ_1 unchanged as
$R_s(\mu_1)$. Concretely, for any given sequence $\mathbf{s} = (p_0, p_1, \ldots, p_N)$,

$$R_s(\mu_1)(p) = \begin{cases} \mu_2(p), & \text{if } p \in \mathbf{s}, \\ \mu_1(p), & \text{if } p \notin \mathbf{s}. \end{cases}$$

The new matching $R_s(\mu_1)$ is eligible and satisfies the quota constraint. Note that for

any sequence $\mathbf{s}$ of type 1, we have $E(R_s(\mu_1)) = E(\mu_1) \cup \{p_0\}$ and thus $|E(R_s(\mu_1))| = |E(\mu_1)| + 1$, which combined with the non-domination of μ_1 means $|B(R_s(\mu_1))| < |B(\mu_1)|$.

For any $\mathbf{s}'$ of type 2, $E(R_{s'}(\mu_1)) = E(\mu_1) \cup \{p_0\} - \{p_N\}$ and thus $|E(R_{s'}(\mu_1))| = |E(\mu_1)|$. We claim that $|B(R_{s'}(\mu_1))| = |B(\mu_1)|$. Suppose not. If $|B(R_{s'}(\mu_1))| > |B(\mu_1)|$, then μ_1 is dominated by $R_{s'}(\mu_1)$. If instead $|B(\mu_1)| > |B(R_{s'}(\mu_1))|$, re-match the patients in $\mathbf{s}'$ to their seats in μ_1 and keep other patients' seats in μ_2 unchanged—the new matching will dominate μ_2.

By construction, the sequences initialized by distinct patients in A_3 are disjoint. Suppose there are k_1 type 1 sequences and k_2 type 2 sequences, then $k_1 + k_2 = |A_3|$. Denote the sequences as $\mathbf{s}_1, \mathbf{s}_2, \cdots, \mathbf{s}_{|A_3|}$. Rematch all the patients in all the sequences to their seats in μ_2 and keep other patients' seats in μ_1 unchanged, we obtain a new matching $\mu' = R_{s_1}(R_{s_2}(\cdots(R_{s_{|A_3|}}(\mu_1))))$.

Let F be the set of matched patients in μ' and $A_2' = \{p \in A : p$ belongs to some sequence$\}$, then

1. All patients in A are matched in μ': $A \subset F \subseteq D \cup A_3$, and $|F \setminus A| = |F| - |A| = k_1 + |D| - |A| = k_1 + k$.

2. $F \setminus A \subseteq D \setminus A$.

3. Only patients in $A_2 \setminus A_2'$ and $F \setminus A$ get different seats (including $\emptyset$) in μ' than in μ_2.

4. $|E(\mu')| - |E(\mu_1)| = k_1$ and $|B(\mu')| < |B(\mu_1)|$. Let $k_3 = |B(\mu_1)| - |B(\mu')|$, then $k_3 \geq k_1$.

Step 2: With μ' and μ_2, for each patient $p_0' \in F \setminus A$, we can find a disjoint cycle that is also an applicable cycle in G_{μ_2}. We construct the cycle by constructing

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a sequence like in Step 1.

Start from any patient p'_0 in $F \setminus A$. As μ_2 is non-dominated, seat $\mu'(p'_0)$ must be taken by some patient under μ_2. Let $p'_1 = \mu_2(\mu'(p'_0))$. As all the patients in A are matched in μ', $\mu'(p'_1) \neq \emptyset$. If $\mu_2(\mu'(p'_1)) = \emptyset$, then terminate the sequence; else, let $p'_2 = \mu_2(\mu'(p'_1))$ and continue this process.

After the above process, we have a sequence $(p'_0, p'_1..., p'_N)$ where $\mu'(p'_m) = \mu_2(p'_{m+1})$ for all $0 \leq m < N$ and $\mu_2(\mu'(p'_N)) = \emptyset$. Each patient p'_m with $1 \leq m \leq N$ belongs to $A_2 \setminus A'_2$, since $\mu'(p'_m) \neq \mu_2(p'_m)$ and $\mu_2(p'_m) \neq \emptyset$.

Given any sequence generated above $(p'_0, p'_1..., p'_N)$, we construct an applicable cycle in G_{μ_2} by linking patient p'_m to seat $\mu'(p'_m)$ and seat $\mu'(p'_m)$ to patient p'_{m+1} for $0 \leq m \leq N-1$, then linking patient p'_N to seat $\mu'(p'_N)$ and seat $\mu'(p'_N)$ to patient p'_0. The applicable cycles constructed from different sequences are disjoint. Denote these cycles as $\mathbf{c}_1, \mathbf{c}_2, \ldots \mathbf{c}_{k+k_1}$, ordered such that $\Delta_{\mathbf{c}_1} \leq \Delta_{\mathbf{c}_2} \leq \cdots \leq \Delta_{\mathbf{c}_{k+k_1}}$. Moreover, we have $\Delta_{c_1} > 0$; otherwise, applying $\mathbf{c}_1$ to μ_2 would yield a matching that dominates μ_2. Therefore, all these disjoint applicable cycles have positive beneficiary loss.

We claim that $\sum_{i=1}^{k_1} \Delta_{\mathbf{c}_i} = k_3$. We prove this by contradiction, considering two cases.

Case 1. Suppose $\sum_{i=1}^{k_1} \Delta_{\mathbf{c}_i} > k_3$. If we rematch the seats involved in these k_1 cycles to their patients (or $\emptyset$) in μ_2 while keeping other seats' patients as in μ', the resulting matching would have e_1 eligible matches and $b_1 - k_3 + \sum_{i=1}^{k_1} \Delta_{\mathbf{c}_i} > b_1$ beneficiary matches, which dominates μ_1, a contradiction.

Case 2. Suppose $\sum_{i=1}^{k_1} \Delta_{\mathbf{c}_i} < k_3$.

First, rematch the seats involved in all type 1 sequences to their patients (or to $\emptyset$) in μ_1 and keep other seats' patients in μ_2. Denote the resulting matching as μ_t.

Second, rematch the seats involved in the cycles $\mathbf{c}_1, \mathbf{c}_2, \ldots, \mathbf{c}_{k_1}$ to their patients (or to $\emptyset$) as in μ' and keep all other seats' patients in μ_t. Note that this second rematch does not affect any seat or patient that was modified in the first rematch, because the sequences constructed in Step 1 and the applicable cycles are disjoint: if $p \in A$ lies in some cycle $\mathbf{c}$, then by the generating process of $\mathbf{c}$, $\mu'(p) \neq \mu_2(p)$; if p belongs to some sequence $\mathbf{s}$, then by the construction of μ', $\mu'(p) = \mu_2(p)$.

The resulting matching has $e_2 - k_1 + k_1 = e_2$ eligible matches and $b_2 + k_3 - \sum_{i=1}^{k_1} \Delta_{\mathbf{c}_i} > b_2$ beneficiary matches, thus dominating μ_2, a contradiction.

Now we construct μ^*. Rematch all the seats involved in the cycles $\mathbf{c}_1, \ldots, \mathbf{c}_{k_1}$ to their patients in μ_2 and keep other seats' patients in μ'. We call this process the reverse application of the applicable cycles. We claim the resulting matching μ^* satisfies the requirements. Since $\sum_{i=1}^{k_1} \Delta_{\mathbf{c}_i} = k_3$, we have $|B(\mu^*)| = |B(\mu_1)| = b_1$. The fact that $|E(\mu')| - |E(\mu_1)| = k_1$ and that μ^* is obtained by reversely applying k_1 applicable cycles implies $|E(\mu^*)| = |E(\mu_1)| = e_1$. To show that μ^* matches all the matched patients in μ_2, note that μ' has all the patients in A matched, and the reverse application of applicable cycles in Step 2 only unmatches patients in $F \setminus A$. $\qquad\square$

Proof of Lemma 1. In this proof, we use some notation from the proof of Lemma A1.

By Lemma A1, there exists a matching μ^* corresponding to f_1 such that any matched patient in μ_2 is still matched in μ^*. Partition $\mathcal{C}$ into five subsets $C_1, \cdots, C_5$, separately containing: seats of patients in the k_1 type-1 sequences; seats in the k disjoint applicable cycles that have not been used in constructing μ^*; seats in the k_1 disjoint applicable cycles that have been used in constructing μ^*; seats of patients in the k_2 type-2 sequences; and all other seats. The partition is shown below.

$$\text{Partition } \mathcal{C} \text{ into} \begin{cases} C_1 : & \text{seats of patients in the } k_1 \text{ type-1 sequences,} \\[1em] C_2 : & \text{seats in the } k \text{ disjoint applicable cycles not used in constructing } \mu^*, \\[1em] C_3 : & \text{seats in the } k_1 \text{ disjoint applicable cycles used in constructing } \mu^*, \\[1em] C_4 : & \text{seats of patients in the } k_2 \text{ type-2 sequences,} \\[1em] C_5 : & \text{other seats.} \end{cases}$$

By construction, the seats in C_1, C_3, C_4 are all matched to the same patients in μ^* and μ_2, while the seats in C_2 and C_5 are all matched to the same patients(or are both unmatched) in μ^* and μ_1.

Apply the k disjoint applicable cycles that have not been used in constructing μ^*, proved in Lemma A1 to have positive beneficiary loss, to μ_2, and denote the resulting matching as μ_3. Then μ_3 matches seats in C_1, C_3, C_4, C_5 to the same patients as in μ_2, and seats in C_2 to the same patients as in μ_1. We will show that μ_3 corresponds to (e_1, b_1).

As μ^* corresponds to (e_1, b_1), and μ^* and μ_3 differ only in the matches of seats in C_5, it suffices to show that μ_1 and μ_2 have the same numbers of eligible and beneficiary matches when restricted to seats in C_5.

For simplicity, we will refer to seats of patients in sequences as seats belonging to those sequences.

Consider any patient involved in a cycle or sequence. If this patient is matched in both μ_1 and μ_2, then in each matching it must be matched to a seat belonging to the same cycle or sequence. Additionally, patients matched only in μ_2 belong to sequences, while patients matched only in μ_1 belong to cycles. As a consequence,

any patient matched to a seat in C_5 under μ_1 must also be matched to a seat in C_5 under μ_2. Therefore, when restricted to C_5, both matchings have the same number of eligible matches and match the same set of patients.

We claim they also have the same number of beneficiary matches. Suppose for contradiction, without loss of generality, μ_1 has more beneficiary matches than μ_2 when restricted to C_5. Consider the matching obtained by rematching the seats in C_5 according to μ_1 while keeping all other seats' matches as in μ_2. This new matching would dominate μ_2, contradicting its non-domination. Therefore, μ_1 and μ_2 have the same number of beneficiary matches when restricted to C_5, which implies that μ_3 corresponds to (e_1, b_1), completing the proof. $\qquad\square$

A.3   Proof of Lemma 2

Proof. Note that given a weight, a dominated matching will have a smaller weight sum than the matching that dominates it. Thus only non-dominated matchings can achieve maximum weight matching in any iteration of the first loop of Algorithm 2. It suffices to show that in each iteration, the stated non-dominated matching has a higher weight sum than all other non-dominated matchings.

Proof of Claim 1.

Consider the first and the last iterations of the first loop of Algorithm 2. In the first iteration ($k = 1$), the weights are

$$w_{\text{elig}} = 1, \qquad w_{\text{bene}} = 1 + \frac{1}{1} + \frac{1}{n^2} = 2 + \frac{1}{n^2}.$$

The weight sum of any max-bene then max-elig matching μ is

$$(e - K) + \left(b + \sum_{i=1}^{K} \Delta b_i\right)\left(1 + \frac{1}{n^2}\right).$$

Meanwhile, the weight sum of any other non-dominated matching corresponding to point $(e - T, \sum_{i=1}^{T} \Delta b_i)$ for $0 \leq T < K$ is

$$(e - T) + (b + \sum_{i=1}^{T} \Delta b_i)(1 + \frac{1}{n^2}).$$

Since $\Delta b_i \geq 1$ for all $i \in \{1, \ldots K\}$ by [Theorem 2](), the difference is

$$(\sum_{i=T+1}^{K} \Delta b_i)(1 + \frac{1}{n^2}) - (K - T) > 0.$$

Therefore, any max-bene then max-elig matching has a higher weight sum than other non-dominated matchings (under this weight), so one of the max-bene then max-elig matching will be chosen in the first iteration.

In the last iteration $(k = n)$ the weights are

$$w_{\text{elig}} = 1, \qquad w_{\text{bene}} = 1 + \frac{1}{n} + \frac{1}{n^2}.$$

The weight sum of any max-elig then max-bene matching is

$$e + \left(\frac{1}{n} + \frac{1}{n^2}\right) b.$$

The weight sum of any other non-dominated matching corresponding to $(e - T, \sum_{i=1}^{T} \Delta b_i)$ for $1 \leq T \leq K$ is

$$(e - T) + \left(b + \sum_{i=1}^{T} \Delta b_i \right) \left(\frac{1}{n} + \frac{1}{n^2} \right).$$

Since $\sum_{i=1}^{T} \Delta b_i \leq e - T \leq n - T$ and $T \geq 1$, the difference is

$$T - \left(\sum_{i=1}^{T} \Delta b_i \right) \left(\frac{1}{n} + \frac{1}{n^2} \right) \geq T - (n-T) \left(\frac{1}{n} + \frac{1}{n^2} \right) = T \left(1 + \frac{1}{n} + \frac{1}{n^2} \right) - \left(1 + \frac{1}{n} \right) > 0.$$

Therefore, any max-elig then max-bene matching achieves a higher weight sum than other non-dominated matchings (under this weight), so one of the max-elig then max-bene matching will be chosen in the last iteration.

Proof of Claim 2.

Fix a kink $f_j = (e - j, b + \sum_{i=1}^{j} \Delta b_i)$ on the frontier such that $\Delta b_j > \Delta b_{j+1}$. We show that RHA computes its (e, b) values in the Δb_j-th iteration.

In the Δb_j-th iteration, the weights are

$$w_{\text{elig}} = 1, \qquad w_{\text{bene}} = 1 + \frac{1}{\Delta b_j} + \frac{1}{n^2}.$$

We show that any matching corresponding to f_j has a higher weight sum than any matching corresponding to another frontier point f_t. We consider two cases.

Case 1. $t < j$. The difference in weight sums between f_j and f_t is

$$\left(\frac{1}{\Delta b_j} + \frac{1}{n^2} \right) \sum_{i=t+1}^{j} \Delta b_i - (j - t) \geq \left(\frac{1}{\Delta b_j} + \frac{1}{n^2} \right) (j - t) \Delta b_j - (j - t) = (j - t) \frac{\Delta b_j}{n^2} > 0.$$

Thus, any frontier point f_t with $t < j$ will not be chosen in the Δb_j-th iteration.

Case 2. $t > j$ First consider $t = j + 1$. The difference in weight sum between f_j

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and f_{j+1} is

$$1 - \left(\frac{1}{\Delta b_j} + \frac{1}{n^2} \right) \Delta b_{j+1}.$$

Since $\frac{1}{n^2} < \frac{1}{\Delta b_j^2} < \frac{1}{\Delta b_j \Delta b_{j+1}}$ and $\Delta b_j > \Delta b_{j+1}$, we have

$$1 - \left(\frac{1}{\Delta b_j} + \frac{1}{n^2} \right) \Delta b_{j+1} > 1 - \left(\frac{1}{\Delta b_j} + \frac{1}{\Delta b_j \Delta b_{j+1}} \right) \Delta b_{j+1} = \frac{\Delta b_j - \Delta b_{j+1} - 1}{\Delta b_j} \geq 0. \tag{1}$$

Thus, the frontier point f_{j+1} will not be chosen in the Δb_j-th iteration.

For any $t > j + 1$, the difference in weight sums between f_j and f_t is

$$(t - j) - \left(\frac{1}{\Delta b_j} + \frac{1}{n^2} \right) \sum_{i=j+1}^{t} \Delta b_i.$$

Since $\Delta b_{j+1} \geq \Delta b_{j+2} \geq \cdots \Delta b_t$, we have $\sum_{i=j+1}^{t} \Delta b_i \leq (t - j)\Delta b_{j+1}$. Combined with Equation 1, this gives

$$(t - j) - \left(\frac{1}{\Delta b_j} + \frac{1}{n^2} \right) \sum_{i=j+1}^{t} \Delta b_i \geq (t - j) - \left(\frac{1}{\Delta b_j} + \frac{1}{n^2} \right)(t - j)\Delta b_{j+1} > 0.$$

Thus, any frontier point f_t with $t > j + 1$ will not be chosen in the Δb_j-th iteration.

Therefore, the matching corresponding to f_j has the highest weight sum in the Δb_j-th iteration.

$\square$