Online Appendix
Matching with Couples: Stability and Incentives in Large Markets

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A Theory Appendix (Not for publication)

A.1 Formal Definitions

A.1.1 Definition of Responsive Preferences

Let $h \in H$ and κ_h be a positive integer. We say that preference relation $\succeq_h$ is **responsive with capacity** κ_h if

(1) For any $D' \subseteq D$ with $|D'| \leq \kappa_h$, $d \in D \setminus D'$ and $d' \in D'$, $D' \cup d \setminus d' \succeq_h D'$ if and only if $d \succeq_h d'$,

(2) For any $D' \subseteq D$ with $|D'| \leq \kappa_h$ and $d' \in D'$, $D' \succeq_h D' \setminus d'$ if and only if $d' \succeq_h \emptyset$, and

(3) $\emptyset \succ_h D'$ for any $D' \subseteq D$ with $|D'| > \kappa_h$.

A.1.2 Definition of Individual Rationality

A matching μ is **individually rational** if

(1) $\mu(s) R_s \emptyset$ for every $s \in S$,

(2) $\mu(c) R_c (\emptyset, \emptyset)$ for every $c \in C$, and

(3) $Ch_h(\mu(h)) = \mu(h)$ for every $h \in H$.[1]

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[1] When there is a couple (f, m) with $\{f, m\} \subseteq \mu(h)$, we adopt a notational convention that $Ch_h(\mu(h))$ means $Ch_h(\mu(h) \cup (f, m) \setminus \{f, m\})$, that is, we let hospital h to consider the existing couple as a whole when choosing the most preferred subset of doctors. Similar conventions will be used elsewhere when the choice involves a couple who are matched as a whole at the given matching.

A.2 An Alternative Definition of Stability

We offer an alternative definition of stability from the one presented in the main text. This alternative definition, which we call strong stability, allows for larger coalitions to block a matching. A strongly stable matching is also stable according to the definition in the main text. In the proof of Theorem 1, we establish a more general result for strong stability, and this implies existence of a stable matching as defined in the main text.

In the definition of strong stability, we consider two cases of a block as follows:

(1) A couple-hospital pair $(c, h) \in C \times H$ is a **block** of μ if

  (a) $(h, h)P_c\mu(c)$,

  (b) $f, m \in Ch_h(\mu(h) \cup c)$ where $c = (f, m)$.

(2) A group of doctors D' and hospital h is a **block** of μ if

  (a) there is no couple (f, m) such that $\{f, m\} \subseteq D'$,

  (b) $D' \subseteq Ch_h(\mu(h) \cup D')$,[2]

  (c) for all $s \in D' \cap S$, we have $hP_s\mu(s)$,

  (d) i. for all $f \in D' \cap F$ where $c = (f, m) \in C$, $(h, h')P_c\mu(c)$ for some h' and $m \in Ch_{h'}(\mu(h') \cup m)$,

   ii. for all $m \in D' \cap M$ where $c = (f, m) \in C$, we have $(h', h)P_c\mu(c)$ for some h' and $f \in Ch_{h'}(\mu(h') \cup f)$.

A matching is **strongly stable** if it is individually rational and there is no block as defined by conditions (1) and (2) above.

This definition allows for a couple assigned to a hospital to be blocked by two doctors (who are either single or are a member of a couple). If one of the blocking doctors is a couple member, we require that the member's partner is chosen by another hospital over its assignment and that the couple together prefer this assignment to their current assignment.

The motivation for this definition is to allow certain joint deviations to happen, but rule out more complicated deviations involving larger groups. When a couple member is part of a blocking coalition of doctors D' and hospital h, our interpretation is that hospital h is the "initiating" blocker, and any hospital h' involved to satiate the other member of a couple is a passive blocker. The reason we consider this definition is to stay close to pairwise stability, but still accommodate this particular type of blocking pair is that we think that blocking coalitions of larger size are less likely to form due to coordination issues among members. This definition also keeps the notation less burdensome, but our main existence

[2]When there is a couple (f, m) with $\{f, m\} \subseteq \mu(h)$, then we adopt a notational convention that $Ch_h(\mu(h) \cup D')$ means $Ch_h(\mu(h) \cup (f, m) \setminus \{f, m\} \cup D')$, that is, we let hospital h consider the existing couple as a whole when choosing the most preferred subset of doctors. A similar convention will be used elsewhere when the choice involves a couple who are matched as a whole at the given matching.

result continues to hold when we allow larger sets of blocking coalitions to form or employ the core as our solution concept.

Since the definition of strong stability allows for coalitions of doctors who are single or couple members to be part of blocking pairs, a strongly stable matching is stable, but not vice versa. Moreover, if each hospital has one position, strong stability is equivalent to unit-capacity stability.

Finally, strong stability is equivalent to the standard definition of (pairwise) stability when there is no couple. To see this last point, first observe that condition (1) in the definition of strong stability is irrelevant if there is no couple, as are conditions (2a) and (2d). The remaining conditions (2b) and (2c) are equivalent to the nonexistence of a blocking pair under the assumption that hospital preferences are responsive. Thus this, together with individual rationality, is equivalent to the standard pairwise stability concept.[3]

A.3 Proof of Theorem 1

Let $(H, S, C, (\succeq_h)_{h\in H}, (R_i)_{i\in S\cup C})$ be a matching market.

Step 1: Doctor-Proposing Deferred Acceptance Algorithm

Apply the doctor-proposing deferred acceptance algorithm to the sub-market without couples: $(H, S, (\succeq_h)_{h\in H}, (R_s)_{s\in S})$.

Step 2: Sequential Couples Algorithm

Algorithm 1. Sequential Couples Algorithm

(1) Initialization:

Let matching μ be the output of the deferred acceptance algorithm in the sub-market without couples.

(2) *Iterate through couples*: set $C^0 = C$, $i = 0$ and $B = \emptyset$.

  (a) If C^i is empty, then go to Step 3. Otherwise, pick some couple $c = (f, m) \in C^i$. Let $C^{i+1} = C^i \backslash c$ and increment i by one.

  (b) Let couple c apply to their most preferred pair of hospitals $(h, h') \in \tilde{H} \times \tilde{H}$ that has not rejected them yet.

    i. If such a hospital (pair) does not exist, modify matching μ such that couple c is unassigned and then go to Step 2a.

[3] Ashlagi et al. (2011) consider another definition of stability, which neither implies our definition nor is implied by it. However, our main existence theorem holds for their definition as well.

ii. If such a hospital (pair) exists, then if either hospital h or hospital h' has previously been applied to by a member (or both members) of any couple different from c, then terminate the algorithm.

iii. Otherwise,

A. If $h = h' \neq \emptyset$ and $\{f, m\} \subseteq Ch_h(\mu(h) \cup c)$, then modify matching μ by assigning (f, m) to hospital h and having h reject

$$(\mu(h) \cup f \cup m) \setminus Ch_h(\mu(h) \cup c).$$

Add the rejected single doctors (if any) to B and go to Step 2a.

B. If $h \neq h'$, $f \in Ch_h(\mu(h) \cup f)$, and $m \in Ch_{h'}(\mu(h') \cup m)$, then modify matching μ by assigning f to h and m to h', having hospital h reject

$$(\mu(h) \cup f) \setminus Ch_h(\mu(h) \cup f),$$

and having hospital h' reject

$$(\mu(h') \cup m) \setminus Ch_{h'}(\mu(h') \cup m).$$

Add the rejected single doctors (if any) to B and go to Step 2a.

C. Otherwise, let hospital h and hospital h' reject the application by couple c and go to Step 2b.

(3) *Iterate through rejected single doctors*: set $B^1 = B$ and $j = 1$.

Round j:

(a) If B^j is empty, then terminate the algorithm.

(b) Otherwise, pick some single doctor s in B^j. Let $B^{j+1} = B^j \setminus s$ and increment j by one.

Iterate through the rank order lists of single doctors:

i. If single doctor s has applied to every acceptable hospital, then modify matching μ such that s is unassigned and go to Step 3a.

ii. If not, then let $\hat{h}$ be the most preferred hospital ranked by single doctor s among those which s has not yet applied to previously (either in the doctor-proposing deferred acceptance algorithm or within this algorithm.)

iii. If there is no couple member who has ever applied to hospital $\hat{h}$, then there are three cases:

A. If hospital $\hat{h}$ has a vacant position and s is acceptable to $\hat{h}$, then modify matching μ such that single doctor s is assigned to $\hat{h}$ and go to Step 3a.

B. If either hospital $\hat{h}$ prefers each of its current mates to single doctor s and there is no vacant position or s is unacceptable to $\hat{h}$, then $\hat{h}$ rejects s and go to Step 3(b)i.

C. If hospital $\hat{h}$ prefers single doctor s to one of its current mates and there is no vacant position, then modify matching μ such that s is assigned to $\hat{h}$. Hospital $\hat{h}$ rejects the least preferred doctor currently assigned there:

$$(\mu(\hat{h}) \cup s) \setminus Ch_{\hat{h}}(\mu(\hat{h}) \cup s).$$

With abuse of notation, denote this rejected doctor s and go to Step 3(b)i.

iv. If there is a couple member who has ever applied to hospital $\hat{h}$ previously within this algorithm, then terminate the algorithm.

The sequential couples algorithm terminates at Step 2(b)ii (when a couple member proposes to a hospital which has already been proposed to by another couple), Step 3a (when all couples and single doctors are assigned), or Step 3(b)iv (when a single doctor proposes to a hospital which was previously applied to by a couple member). We say that the algorithm **succeeds** if it terminates at Step 3a.

Lemma 1. *If the sequential couples algorithm succeeds, then the resulting matching is stable.*

The proof of this lemma is similar to the proof of the existence of a stable matching by Gale and Shapley (1962) in the college admissions model. The main difference is that when the sequential couples algorithm succeeds, we must verify that there are no blocking pairs including pairs which may involve members of a couple.

Proof of Lemma 1. We prove that the matching that results when the sequential couples algorithm succeeds is strongly stable (defined in Section A.2). Establishing this fact implies that the matching is stable since a strongly stable matching is a stable matching.[4]

Suppose that Algorithm 1 succeeds, producing matching μ. First, μ is individually rational since all doctors who are single or couple members have applied only to acceptable hospitals (hospital pairs for couples), and hospitals have accepted only acceptable doctors only up to their capacities in each step of Algorithms **??** and 1.

Next, to show that there is no block of matching μ, fix a hospital $h \in H$.

(1) Suppose that there exists no couple $(f, m) \in C$ such that $\{f, m\} \subseteq \mu(h)$.

(a) Assume, for contradiction, that there exists a set of doctors $D' \subseteq D$ such that hospital h and D' block μ, where there is no couple $(f, m) \in C$ such that $\{f, m\} \subseteq D'$. Since doctor d is part of a block,

$$dP_h\emptyset \quad \text{for every } d \in D'.$$

[4] Since the rest of the analysis builds on this lemma, this stronger result allows us to extend our main results when we replace stability with strong stability as the solution concept.

There are two cases to consider depending on whether D' contains any single doctors.

i. Suppose that there is a single doctor in D'. Then each single doctor $s \in D' \cap S$ is rejected by hospital h at some point of either Algorithm 1 or 2 since $hP_s\mu(s)$. The tentative assignment of hospital h at a step when single doctor s is rejected, denoted $\tilde{\mu}(h)$, satisfies

$$|\tilde{\mu}(h)| = \kappa_h \quad \text{and} \quad dP_h s \text{ for all } d \in \tilde{\mu}(h),$$

because $sP_h\emptyset$. Since, at each of later steps of both Algorithms, hospital h replaces a tentatively matched doctor only when a more preferred doctor applies, it follows that

$$|\mu(h)| = \kappa_h \quad \text{and} \quad dP_h s \text{ for all } d \in \mu(h).$$

This contradicts the assumption that hospital h and D' block matching μ.

ii. Suppose there are no single doctors in D'. Then there exists a member of some couple in D'. Without loss of generality, assume that there is some $f \in D'$ where $c = (f, m) \in C$. Since $(h, h')P_c\mu(c)$ for some $h' \in \tilde{H}$, couple c was rejected by the hospital pair (h, h') at some point of Algorithm 2. Let $\tilde{\mu}(h)$ and $\tilde{\mu}(h')$ be the tentative assignments for hospital h and hospital h' at that step, respectively. Because couple c was rejected at this step, it follows that either

$$|\tilde{\mu}(h)| = \kappa_h \quad \text{and} \quad dP_h f \text{ for all } d \in \tilde{\mu}(h),$$

or $h' \neq \emptyset$ and we have that

$$|\tilde{\mu}(h')| = \kappa_{h'} \quad \text{and} \quad dP_{h'} m \text{ for all } d \in \tilde{\mu}(h').$$

Since, at each of later steps, both hospital h and hospital h' (if $h' \neq \emptyset$) replace a tentatively matched doctor only when a more preferred doctor applies, it follows that either

$$|\mu(h)| = \kappa_h \quad \text{and} \quad dP_h f \text{ for all } d \in \mu(h),$$

or $h' \neq \emptyset$ and we have that

$$|\mu(h')| = \kappa_{h'} \text{ and } \quad dP_{h'} m \text{ for all } d \in \mu(h').$$

This contradicts the assumption that $f \in D'$ and D' block matching μ with hospital h.

(b) Consider a couple $c = (f, m)$ such that $(h, h)P_c\mu(c)$. By definition of Algorithm 2, the couple was rejected by the hospital pair (h, h) at some point in the Algorithm. Denote the matching at that point by $\tilde{\mu}$. It follows that

$$Ch_h(\tilde{\mu}(h) \cup c) = \tilde{\mu}(h) \quad \text{and} \quad f, m \notin \tilde{\mu}(h).$$

Since the sequential couples algorithm succeeds, no other doctor applies to hospital h after the step where couple c is rejected by (h, h). As a result,

$$\mu(h) = \tilde{\mu}(h).$$

Therefore,

$$f, m \notin \mu(h) \quad \text{and } \mu(h) = Ch_h(\mu(h) \cup c),$$

which contradicts the assumption that couple c and hospital h block matching μ.

(2) Suppose that there exists a couple $(f, m) \in C$ such that $\{f, m\} \subseteq \mu(h)$ and there is a block of matching μ involving hospital h. The assumption that the sequential couples algorithm succeeds implies that there is no couple $c \neq (f, m)$ and $h' \in \tilde{H}$ such that $(h, h')P_c\mu(c)$ or $(h', h)P_c\mu(c)$. This is because the algorithm terminates in Step 3 if two or more distinct couple members apply to the same hospital during the algorithm. Thus, the set of doctors D' that blocks matching μ with hospital h is composed solely of single doctors. This means that

$$sP_h\emptyset \quad \text{for every } s \in D', \tag{1}$$

$$hP_s\mu(s) \quad \text{for every } s \in D', \tag{2}$$

for otherwise a single doctor s is not part of a block. Let $\tilde{\mu}$ be the matching that is the result of the doctor-proposing deferred acceptance algorithm in the sub-market excluding couples. Then

$$hR_s\tilde{\mu}(s) \quad \text{for every } s \in D', \tag{3}$$

because otherwise, in light of (2), single doctor s will have applied to hospital h in Step 3 of the sequential couples algorithm, causing the algorithm to fail. Moreover,

$$\mu(h) \succ_h \tilde{\mu}(h), \tag{4}$$

because otherwise hospital h would not have accepted new applicants in Step 2 of the sequential couples algorithm, resulting in matching with $\mu(h)$. Furthermore,

$$dP_hs \quad \text{for every } d \in \tilde{\mu}(h) \cap \mu(h) \text{ and } s \in D', \tag{5}$$

because

(a) for any $s \in D' \cap \tilde{\mu}(h)$, single doctor s was rejected in Step 2 of the sequential couples algorithm at the instance when the couple (f, m) applied to hospital h. We now show dP_hs. Suppose, to the contrary, that sR_hd for some $d \in \tilde{\mu}(h) \cap \mu(h)$. Then sP_hd because $s \neq d$ and preferences are strict. This relation and responsiveness of $\succeq_h$ imply

$$\mu(h) \cup s \setminus d \;\; \succ_h \;\; \mu(h).$$

Moreover,

$$\mu(h) \cup s \setminus d \;\; \in \mathcal{A}(\tilde{\mu}(h) \cup (f, m)).$$

These facts contradict

$$\mu(h) = Ch_h(\tilde{\mu}(h) \cup (f, m)),$$

which follows from the definition of the sequential couples algorithm. Hence,

$$dP_h s \quad \text{for all } d \in \tilde{\mu}(h) \cap \mu(h).$$

(b) for any $s \in D' \setminus \tilde{\mu}(h)$, relation (3) implies $hP_s\tilde{\mu}(s)$, so stability of matching $\tilde{\mu}$ in the sub-market without couples (which coincides with both our stability definition in Section **??** and strong stability definition in Appendix A.2) implies

$$dP_h s \quad \text{for all } d \in \tilde{\mu}(h).$$

Let $\mu'(h)$ be the assignment for hospital h when D' and hospital h block matching μ. That is,

$$\mu'(h) = Ch_h(\mu(h) \cup D'). \tag{6}$$

Relation (6) and the definition of $Ch_h(\cdot)$ imply

$$\mu'(h) \succ_h \mu(h). \tag{7}$$

Relations (1) and (2) imply that

$$|\mu(h)| = \kappa_h.$$

Therefore, to block matching μ with D', hospital h should reject some doctors in $\mu(h)$. If any doctor $d \in \tilde{\mu}(h) \cap \mu(h)$ is rejected while some $s \in D'$ is accepted to produce $\mu'(h)$, then

$$\mu'(h) \cup d \setminus s \;\; \succ_h \;\; \mu'(h)$$

by responsiveness of $\succeq_h$ and relation (5), but this contradicts (6). Hence, relation (5) implies that it should be exactly couple (f, m) that is rejected by hospital h when hospital h and D' block $\mu(h)$. Since (f, m) is the only couple in $\mu(h)$ and it is not in $\mu'(h)$,

$$\mu'(h) \subseteq \tilde{\mu}(h) \cup D' \subseteq S.$$

Since $hR_s\tilde{\mu}(s)$ for every single doctor $s \in \mu'(h)$ by relation (3) and $\mu'(h) \subseteq S$, it follows that

$$\tilde{\mu}(h) \succeq_h \mu'(h), \tag{8}$$

because otherwise matching $\tilde{\mu}$ would be unstable in the sub-market without couples. Applying relations (4), (8), and then (7), we obtain

$$\mu(h) \succ_h \tilde{\mu}(h) \succeq_h \mu'(h) \succ_h \mu(h),$$

a contradiction.

□

The rest of our argument uses Lemma 1 to compute how often Algorithm 1 succeeds when singles and couples draw their preferences according to the processes described in Section **??**.

In the next two steps of the proof, we define versions of the deferred acceptance algorithm and the sequential couples algorithm in which single doctors draw their preferences iteratively within the steps of the algorithms. This representation of the two algorithms proves useful for our analysis.

Step 3: Define Stochastic Deferred Acceptance Algorithm

Algorithm 2. Stochastic Doctor-Proposing Deferred Acceptance Algorithm

(1) Initialization: Let $l = 1$. For every $s \in S$, let $A_s = \emptyset$ and order the single doctors in an arbitrarily fixed manner.

(2) Choosing the applicant:

 (a) If $l \leq |S|$, then let s be the l^{th} single doctor and increment l by one.

 (b) If not, then terminate the algorithm.

(3) Choosing the applied:

 (a) If $|A_s| \geq k$, then return to Step 2.

 (b) If not, select hospital h randomly from distribution $p_s(\cdot)$ until $h \notin A_s$, and add h to A_s.

(4) Acceptance and/or rejection:

 (a) If hospital h prefers each of its current mates to single doctor s and there is no vacant position, then hospital h rejects single doctor s. Go to Step 3.

 (b) If hospital h has a vacant position or it prefers single doctor s to one of its current mates, then hospital h accepts single doctor s. Now if hospital h had no vacant position before accepting single doctor s, then hospital h rejects the least preferred doctor among those who were matched to hospital h. Let this doctor be s and go to Step 3. If hospital h had a vacant position, then go back to Step 2.

A_s records hospitals that single doctor s has already drawn from $p_s(\cdot)$. When $|A_s| = k$ is reached, A_s is the set of hospitals acceptable to single doctor s.

Let μ be the matching that is produced when Algorithm 3 terminates. Under the doctor proposing deferred acceptance algorithm, a single doctor's application to her t^{th} most preferred hospital is independent of her preferences after $(t+1)^{\text{th}}$ choice on. Therefore matching μ is stable for the market consisting of single doctors, any of their realized preference profiles which could follow from completing the draws for random preferences, the hospitals and their (arbitrarily fixed) preferences.

Step 4: Define Stochastic Sequential Couples Algorithm

Suppose that at the conclusion of Algorithm 2, we obtain matching μ. The **stochastic sequential couples algorithm** is a version of Algorithm 1 where single doctor preferences are drawn iteratively, and is defined as follows:

Algorithm 3. Stochastic Sequential Couples Algorithm

(1) Initialization:

  (a) Keep all preference lists generated in Algorithm 2. Also, for each single doctor $s \in S$, let A_s be the set generated at the end of Algorithm 2. Let the matching μ be the initial matching of the algorithm.

  (b) For each couple $c = (f, m) \in C$, construct the couples' preferences P_c according to the process defined in Section **??**.

(2) *Iterate through couples*, set $C^0 = C$, $i = 0$, and $B = \emptyset$.

  (a) If C^i is empty, then go to Step 3. Otherwise, pick some couple $c = (f, m) \in C^i$. Let $C^{i+1} = C^i \backslash c$ and increment i by one.

  (b) Let couple c apply to their most preferred pair $(h, h') \in \tilde{H} \times \tilde{H}$ that has not rejected them yet.

    i. If such a hospital (pair) does not exist, modify matching μ such that couple c is unassigned and then go to Step 2a.

    ii. If such a hospital (pair) exists, then if either hospital h or hospital h' has previously been applied to by a member (or both members) of any couple different from c, then terminate the algorithm.

    iii. Otherwise,

A. If $h = h' \neq \emptyset$ and $\{f, m\} \subseteq Ch_h(\mu(h) \cup c)$, then modify matching μ by assigning (f, m) to hospital h and having h reject

$$(\mu(h) \cup f \cup m) \setminus Ch_h(\mu(h) \cup c).$$

Add the rejected single doctors (if any) to B and go to Step 2a.

B. If $h \neq h'$, $f \in Ch_h(\mu(h) \cup f)$, and $m \in Ch_{h'}(\mu(h') \cup m)$, then modify matching μ by assigning f to h and m to h', having hospital h reject

$$(\mu(h) \cup f) \setminus Ch_h(\mu(h) \cup f),$$

and having hospital h' reject

$$(\mu(h') \cup m) \setminus Ch_{h'}(\mu(h') \cup m).$$

Add the rejected single doctors (if any) to B and go to Step 2a.

C. Otherwise, let hospital h and hospital h' reject the application by couple c and go to Step 2b.

(3) *Iterate through rejected single doctors*, set $B^1 = B$ and $j = 1$.

Round j:

(a) If B^j is empty, then terminate the algorithm.

(b) Otherwise, pick some single doctor s in B^j. Set $B^{j+1} = B^j \backslash s$ and increment j by one.

Iterate through the single doctor's rank order list (call this iteration "Round j")

i. If $|A_s| \geq k$, then go to Step 3a.

ii. If not, select hospital $\hat{h}$ randomly from distribution $\mathcal{P}^n$ until $\hat{h} \notin A_s$, and add $\hat{h}$ to A_s.

iii. If there is no couple member who has ever applied to hospital $\hat{h}$, then there are three cases:

A. If hospital $\hat{h}$ has a vacant position, then modify matching μ such that single doctor s is assigned to $\hat{h}$ and go to Step 3a.

B. If either hospital $\hat{h}$ prefers each of its current mates to single doctor s and there is no vacant position or s is unacceptable to $\hat{h}$, then $\hat{h}$ rejects s and go to Step 3(b)i.

C. If hospital $\hat{h}$ prefers single doctor s to one of its current mates and there is no vacant position, then modify matching μ such that s is assigned to $\hat{h}$. Hospital $\hat{h}$ rejects the least preferred doctor currently assigned there

$$(\mu(\hat{h}) \cup s) \setminus Ch_{\hat{h}}(\mu(\hat{h}) \cup s).$$

With abuse of notation, denote this rejected doctor s and iterate through her rank order list by going to Step 3(b)i.

iv. If there is a couple member who has ever applied to hospital $\hat{h}$ before, then terminate the algorithm.

The algorithm above terminates at Step 2(b)ii or Step 3a or Step 3(b)iv. Similarly to Algorithm 1, we say that Algorithm 3 **succeeds** if it terminates at Step 3a.

To establish Theorem 1, we investigate how often the algorithm succeeds, as every doctor d draws hospitals from his or her distribution $p_d(\cdot)$. First observe for any random market in a regular sequence,

$$\Pr[\text{Algorithm 1 succeeds}] = \Pr[\text{Algorithm 3 succeeds}].$$

That is, the probability of the algorithm's success is identical whether random preferences are drawn at once in the beginning or they are drawn one at a time during the execution of the algorithm.[5] The latter expression is useful since we can investigate the procedure step by step, utilizing conditional probabilities and conditional expectations. Thus we focus on the behavior of Algorithm 3 as the market size grows in the remainder of the proof.

Let Y_n be a random variable which counts the number of hospitals that are listed on no single doctor's preference list at the end of Algorithm 2.[6] The next step of the argument provides a lower bound on Y_n at the conclusion of Algorithm 2. For expositional simplicity, in the following we denote $k^n = k$.

Step 5: A large number of hospitals have vacancies

Lemma 1. *For any sufficiently large n,*

$$E[Y_n] \geq \frac{n}{2} e^{-r\lambda k}.$$

Proof. Condition (**??**) of Definition **??** implies that, for any n,

$$p_d(h) \leq r p_d(h') \quad \text{for all } d \in D^n, h, h' \in H^n.$$

Adding these inequalities across hospitals $h' \in H^n$, we have

$$n p_d(h) \leq r \sum_{h' \in H} p_d(h') = r \quad \text{for each } h.$$

[5]This property is called the principle of deferred decisions. See Motwani and Raghavan (1996).

[6]We abuse notation and denote a random variable and its realization by the same letter when there is no confusion.

As a result,

$$p_d(h) \leq \frac{r}{n}. \tag{9}$$

Fix a doctor d and denote her i^{th} most preferred hospital by $h_{(i)}$, if it has been drawn at the conclusion of Algorithm 2. For any $i \leq k$, inequality (9) implies

$$\sum_{j=1}^{i-1} p_d(h_{(j)}) \leq k \times \frac{r}{n}.$$

Thus for any $i \leq k$, the conditional probability that h is not the single doctor's i^{th} choice given the events that her first $(i-1)$ choices are $h_{(1)}, \ldots, h_{(i-1)}$, her i^{th} choice is drawn, and $h_{(j)} \neq h$ for all $j \leq i-1$, is bounded from below by

$$1 - \frac{p_d(h)}{1 - \sum_{j=1}^{i-1} p_d(h_{(j)})} \geq 1 - \frac{r/n}{1 - rk/n} = 1 - \frac{r}{n - rk}. \tag{10}$$

Let E_h be the event that $h \notin A_s$ for every $s \in S$ at the end of Algorithm 2. Since at most λnk draws are made in total by all single doctors from $p_s(\cdot)$ in Algorithm 2, inequality (10) implies that

$$\Pr(E_h) \geq \left(1 - \frac{r}{n - rk}\right)^{\lambda nk}. \tag{11}$$

We next note that for any h and any sufficiently large n,

$$\left(1 - \frac{r}{n - rk}\right)^{\lambda nk} \geq \frac{1}{2} e^{-r\lambda k},$$

which holds because

$$\begin{aligned}
\lim_{n\to\infty} \frac{\left(1 - \frac{r}{n-rk}\right)^{\lambda nk}}{\frac{1}{2}e^{-r\lambda k}} &= 2 \times \lim_{n-rk\to\infty} \frac{\left(1 - \frac{r}{n-rk}\right)^{\lambda k(n-rk)}}{e^{-r\lambda k}} \times \lim_{n\to\infty} \left(1 - \frac{r}{n - rk}\right)^{\lambda rk^2} \\
&= 2 \times 1 \times \left(\lim_{n-rk\to\infty} \left(1 - \frac{r}{n - rk}\right)^{n-rk}\right)^{\lim_{n\to\infty} \frac{\lambda rk^2}{n-rk}} \\
&= 2 > 1
\end{aligned}$$

(note that $n - rk \to \infty$ and $\frac{\lambda rk^2}{n-rk} \to 0$ as $n \to \infty$ since $k \leq \gamma \log(n)$). Thus, together with inequality (11), we conclude that

$$\Pr(E_h) \geq \frac{1}{2} e^{-r\lambda k}.$$

Using this inequality, for any sufficiently large n, we have

$$E[Y_n] = \sum_{h \in H^n} \Pr(E_h) \geq \frac{n}{2} e^{-r\lambda k},$$

completing the proof. $\square$

Step 6: Algorithm 3 succeeds with high probability.

Let $\bar{C} = bn^a$ denote the upper bound on the number of couples in the random market $\tilde{\Gamma}^n$.

Lemma 2. *For any sufficiently large n and any matching μ,*

$$\Pr\left[\textit{Algorithm 3 succeeds} \;\middle|\; Y_n > \frac{E[Y_n]}{2} \textit{ and Algorithm 2 produces } \mu\right]$$
$$\geq \left(1 - \frac{2k\bar{C}r}{n}\right)^{2k\bar{C}} \cdot \left(1 - \frac{8rk\bar{C}}{E[Y_n]}\right)^{2\bar{C}},$$

if the conditioning event has a strictly positive probability.

Proof. First, consider the event that Algorithm 3 does not terminate at Step 2(b)ii so that the algorithm reaches Step 3. For that event to happen it is enough for the following event to happen: for any two doctors $d, d' \in F \cup M$ with $d \neq d'$, there is no hospital $h \in H$ that is listed by both d and d' as an acceptable hospital. This is sufficient because our assumption on ρ implies that at most one $d \in F \cup M$ will apply to h.

Suppose $\{d_1, ..., d_{\ell-1}\} \in F \cup M$ are such that there exists no $h \in H$ listed by any pair of doctors in $\{d_1, ..., d_{\ell-1}\} \in F \cup M$. Furthermore, fix a doctor $d_\ell \in F \cup M \setminus \{d_1, ..., d_{\ell-1}\}$ and assume that her first $i-1$ choices $\{h_{(1)}, h_{(2)}, \ldots, h_{(i-1)}\}$ have no intersection with hospitals listed by the set of doctors $\{d_1, ..., d_{\ell-1}\}$. The conditional probability that her i^{th} choice $h_{(i)}$ does not have an overlap with any of the previously picked hospital is at least

$$1 - \sum_{h:h \text{ is listed by some doctor in } \{d_1,...,d_{\ell-1}\}} p_d(h) \quad - \quad \sum_{j=1}^{i-1} p_d(h_{(j)}). \tag{12}$$

Recall that by Condition (**??**) of Definition **??**, relation (9) holds:

$$p_d(h) \leq \frac{r}{n}.$$

Since there are at most $\bar{C}$ couples and each member of a couple lists at most k distinct hospitals, expression (12) is bounded from below by

$$1 - \frac{2k\bar{C}r}{n}. \tag{13}$$

Recall that there are at most $\bar{C}$ couples and each member of the couple lists at most k distinct hospitals. Expression (13) implies that the probability that for any $d, d' \in F \cup M$ with $d \neq d'$, there is no hospital $h \in H$ that is listed by both d and d' as one of their acceptable hospitals is at least

$$\left(1 - \frac{2k\bar{C}r}{n}\right)^{2k\bar{C}}, \tag{14}$$

which is positive for n sufficiently large. Expression (14) provides a lower bound of the probability that the algorithm does not terminate at Step 2(b)ii so that the algorithm reaches Step 3.

Next, we consider what happens in Step 3 assigning single doctors in the set B, conditional on the same events assumed so far and in addition that all couples are tentatively matched without the algorithm being terminated at Step 2(b)ii.

Condition (**??**) of Definition **??** implies that for any single $s \in S$,

$$p_s(h') \geq p_s(h)/r \quad \text{ for any } h, h' \in H.$$

Also observe that there are at most $2k\bar{C}$ hospitals that are listed by a couple member in $F \cup M$. Denote this set of hospitals by H_1 and note that

$$\sum_{h \in H_1} p_s(h) \leq 2k\bar{C}r \cdot \min_{h \in H}\{p_s(h)\}.$$

Moreover, there are at least $Y_n - 2k\bar{C}$ hospitals (which is positive if n is sufficiently large and $Y_n > \frac{E[Y_n]}{2}$) with vacant positions and not listed by any couple member at the beginning of Step 3 (since there are at least Y_n hospitals with vacant positions at the beginning of Step 2 and at most $2\bar{C}$ hospitals are listed by couple members). Denote this set of hospitals by H_2 and note that

$$\sum_{h \in H_2} p_s(h) \geq (Y_n - 2k\bar{C}) \cdot \min_{h \in H}\{p_s(h)\}.$$

We are interested in computing the probability that Round 1 of Step 3 ends at 3(b)iiiA as a single doctor applies to some hospital with vacant positions not listed by any couple member (rather than applying to a hospital that is listed by a couple member). This probability is bounded below by:

$$1 - \frac{\sum_{h \in H_1} p_s(h)}{\sum_{h \in H_1} p_s(h) + \sum_{h \in H_2} p_s(h)} \geq 1 - \frac{2k\bar{C}}{\frac{Y_n - 2k\bar{C}}{r} + 2k\bar{C}} > 1 - \frac{2k\bar{C}}{\frac{E[Y_n]/2 - 2k\bar{C}}{r} + 2k\bar{C}}. \tag{15}$$

Now assume that all Rounds $1, \ldots, j-1$ end at Step 3(b)iiiA. Then there are still at least $Y_n - 2k\bar{C} - (j-1)$ hospitals with a vacant position and not listed by any couple member at the end of Round $j-1$. This follows since at most $j-1$ hospitals have had their positions filled at Rounds $1, \ldots, j-1$ among those hospitals that are not listed on any single doctor's preference list at the end of Algorithm 2.

Following the steps analogous to those leading to inequality (15), we can compute that Round j, initiated by some single doctor in B^j, ends at Step 3(b)iiiA with probability of at least

$$1-\frac{2k\bar{C}}{\frac{Y_n-2k\bar{C}-(j-1)}{r}+2k\bar{C}}>1-\frac{2k\bar{C}}{\frac{E[Y_n]/2-2k\bar{C}-(j-1)}{r}+2k\bar{C}}.$$

There are at most $2\bar{C}$ rounds in Step 3 because at most $2\bar{C}$ single doctors can be displaced by couples in Step 2, so $|B|\leq 2\bar{C}$. Hence Algorithm 3 succeeds with conditional probability of at least

$$\begin{aligned}\prod_{j=1}^{2\bar{C}}\left(1-\frac{2k\bar{C}}{\frac{E[Y_n]/2-2k\bar{C}-(j-1)}{r}+2k\bar{C}}\right)&\geq\left(1-\frac{2k\bar{C}}{\frac{E[Y_n]/2-2k\bar{C}-(2\bar{C}-1)}{r}+2k\bar{C}}\right)^{2\bar{C}}\\&\geq\left(1-\frac{2k\bar{C}}{E[Y_n]/4r}\right)^{2\bar{C}},\end{aligned}\tag{16}$$

where the first inequality follows from Lemma 1, the assumption that n is sufficiently large and each $j\leq 2\bar{C}$, and the second inequality holds since $E[Y_n]/2-4k\bar{C}\geq E[Y_n]/4>0$, which follows from Lemma 1 and the assumption that n is sufficiently large.

As a result, relations (14) and (16) imply

$$\begin{aligned}&\Pr\left[\text{Algorithm 3 succeeds}\;\middle|\;Y_n>\frac{E[Y_n]}{2}\text{ and Algorithm 2 produces }\mu\right]\\&\geq\left(1-\frac{2k\bar{C}r}{n}\right)^{2k\bar{C}}\cdot\left(1-\frac{8rk\bar{C}}{E[Y_n]}\right)^{2\bar{C}}.\end{aligned}$$

□

We utilize the following mathematical result (see Lemma 4.4 of Immorlica and Mahdian (2005) for a proof).

Lemma 3. $\mathrm{Var}[Y_n]\leq E[Y_n]$ *for every* $n\in\mathbb{N}$.

Step 7: Proof of Theorem 1

Proof of Theorem 1. We obtain that

$$\begin{aligned}\Pr\left[Y_n\leq\frac{E[Y_n]}{2}\right]&\leq\Pr\left[Y_n\leq\frac{E[Y_n]}{2}\right]+\Pr\left[Y_n\geq\frac{3E[Y_n]}{2}\right]\\&=\Pr\left[|Y_n-E[Y_n]|\geq\frac{E[Y_n]}{2}\right]\leq\frac{\mathrm{Var}[Y_n]}{(E[Y_n]/2)^2}\leq\frac{4}{E[Y_n]},\end{aligned}\tag{17}$$

where the first inequality holds since any probability is nonnegative, the equality is an identity, the second inequality results from Chebyshev inequality, and the last inequality follows from Lemma 3.

By Lemma 2 we have

$$\Pr\left[\text{Algorithm 3 succeeds}\;\middle|\; Y_n > \frac{E[Y_n]}{2} \text{ and Algorithm 2 produces } \mu\right]$$
$$\geq \left(1 - \frac{2k\bar{C}r}{n}\right)^{2k\bar{C}} \cdot \left(1 - \frac{8rk\bar{C}}{E[Y_n]}\right)^{2\bar{C}}.$$

This inequality holds for any matching μ that is produced at the end of Algorithm 2. Therefore, we have the same lower bound for the probability conditional on $Y_n > E[Y_n]/2$ but not on μ. That is,

$$\Pr\left[\text{Algorithm 3 succeeds}\;\middle|\; Y_n > \frac{E[Y_n]}{2}\right] \geq \left(1 - \frac{2k\bar{C}r}{n}\right)^{2k\bar{C}} \cdot \left(1 - \frac{8rk\bar{C}}{E[Y_n]}\right)^{2\bar{C}}. \tag{18}$$

Thus we obtain

$$\begin{aligned}\Pr\left[\text{Algorithm 3 succeeds}\right] &\geq \Pr\left[Y_n > \frac{E[Y_n]}{2}\right] \cdot \left(1 - \frac{2k\bar{C}r}{n}\right)^{2k\bar{C}} \cdot \left(1 - \frac{8rk\bar{C}}{E[Y_n]}\right)^{2\bar{C}} \\ &\geq \left(1 - \frac{4}{E[Y_n]}\right) \cdot \left(1 - \frac{2k\bar{C}r}{n}\right)^{2k\bar{C}} \cdot \left(1 - \frac{8rk\bar{C}}{E[Y_n]}\right)^{2\bar{C}} \\ &\geq \left(1 - \frac{8e^{r\lambda k}}{n}\right) \cdot \left(1 - \frac{2k\bar{C}r}{n}\right)^{2k\bar{C}} \cdot \left(1 - \frac{16rk\bar{C}e^{r\lambda k}}{n}\right)^{2\bar{C}}, \end{aligned} \tag{19}$$

where the first inequality follows from the fact that probabilities are non-negative and (18), the second inequality results from (17), and the last inequality is obtained by Lemma 1.

Consider the first term of the right-hand side of inequality (19), $\left(1 - \frac{8e^{r\lambda k}}{n}\right)$. Since $k \leq \gamma \log(n)$ where $\gamma < \frac{1-2a}{r\lambda}$,

$$\frac{e^{r\lambda k}}{n} \leq \frac{e^{(1-2a)\log(n)}}{n} = \frac{n^{1-2a}}{n} = n^{-2a}.$$

Since $a > 0$, the last expression converges to 0 as n approaches infinity. Thus we conclude

$$\lim_{n\to\infty} \left(1 - \frac{8e^{r\lambda k}}{n}\right) = 1,$$

that is, the first term of the right-hand side of inequality (19) converges to one as n approaches infinity.

Next, consider the second term of the right-hand side of inequality (19), $\left(1 - \frac{2k\bar{C}r}{n}\right)^{2k\bar{C}}$. Recall that there exists $b > 0$ such that $\bar{C} < bn^a$ for any n and $k \leq \gamma \log(n)$. Thus, for any sufficiently large n,

$$\begin{aligned}
\left(1 - \frac{2k\bar{C}r}{n}\right)^{2k\bar{C}} &> \left(1 - \frac{2\gamma \log(n) bn^a r}{n}\right)^{2\gamma \log(n) bn^a} \\
&= \left(1 - \frac{2\gamma br}{n^{1-a}/\log(n)}\right)^{2\gamma(\log(n))^2 b(n^{1-a}/\log(n))n^{2a-1}} \\
&\geq \left(\frac{1}{2}e^{-2\gamma br}\right)^{2\gamma bn^{2a-1}(\log(n))^2}, \qquad (20)
\end{aligned}$$

where the last inequality follows because $\left(1 - \frac{\alpha}{x}\right)^x \geq \frac{1}{2}e^{-\alpha}$ for any $\alpha > 0$ and any sufficiently large x, and $n^{1-a}/\log(n) \to \infty$ as $n \to \infty$. Since $a < 1/2$, the term $n^{2a-1}(\log(n))^2 \to 0$ as $n \to \infty$ and hence the last expression of inequality (20) converges to one as $n \to \infty$.

Finally, consider the third term of the right-hand side of inequality (19), $\left(1 - \frac{16rk\bar{C}e^{r\lambda k}}{n}\right)^{2\bar{C}}$. For any sufficiently large n, this term can be bounded as

$$\begin{aligned}
\left(1 - \frac{16rk\bar{C}e^{r\lambda k}}{n}\right)^{2\bar{C}} &> \left(1 - \frac{16r\gamma \log(n) bn^a e^{r\lambda\gamma \log(n)}}{n}\right)^{2bn^a} \\
&= \left(1 - \frac{16r\gamma \log(n) bn^a n^{r\lambda\gamma}}{n}\right)^{2bn^a} \\
&= \left(1 - \frac{16r\gamma b}{n^{1-a-r\lambda\gamma}/\log(n)}\right)^{2b(n^{1-a-r\lambda\gamma}/\log(n))n^{2a-1+r\lambda\gamma}\log(n)} \\
&\geq \left(\frac{1}{2}e^{-16r\gamma b}\right)^{2b(n^{2a-1+r\lambda\gamma}\log(n))}. \qquad (21)
\end{aligned}$$

Because $\gamma < \frac{1-2a}{r\lambda}$, it follows that $2a-1+r\lambda\gamma < 2a-1+(1-2a) = 0$. This implies that $n^{2a-1+r\lambda\gamma}\log(n) \to 0$ as $n \to \infty$ and hence the last expression of inequality (21) converges to one as $n \to \infty$, which completes the proof. $\square$

A.3.1 Speed of convergence

We consider the speed of convergence. For the general model we consider, the result is as follows (whether this rate of convergence is tight is an open question).

Proposition 1. *Consider a regular sequence of random markets. The speed of convergence of the probability that there exists a stable matching is*

$$O\left(\frac{k\bar{C}^2 e^{r\lambda k}}{n}\right).$$

Proof. We invoke the following mathematical result.

Result 1 (Bernoulli's Inequality)**.** $(1+x)^y \geq 1+yx$ *for any real number* $x \geq -1$ *and nonnegative integer* y*.*

In any regular sequence of random markets, we have $2k\bar{C}r/n \leq 1$ for any large n. Thus, by Bernoulli's inequality,

$$\left(1 - \frac{2k\bar{C}r}{n}\right)^{2k\bar{C}} \geq 1 - \frac{2k\bar{C}r}{n} \times 2k\bar{C} = 1 - \frac{4k^2\bar{C}^2 r}{n}.$$

Similarly, for any large n we have

$$\left(1 - \frac{16rk\bar{C}e^{r\lambda k}}{n}\right)^{2\bar{C}} \geq 1 - \frac{16rk\bar{C}e^{r\lambda k}}{n} \times 2\bar{C} = 1 - \frac{32rk\bar{C}^2 e^{r\lambda k}}{n}.$$

These inequalities and inequality (19) imply that, for any sufficiently large n,

$$\begin{aligned}
\Pr[\text{Algorithm 3 succeeds}] &\geq \left(1 - \frac{8e^{r\lambda k}}{n}\right) \cdot \left(1 - \frac{2k\bar{C}r}{n}\right)^{2k\bar{C}} \cdot \left(1 - \frac{16rk\bar{C}e^{r\lambda k}}{n}\right)^{2\bar{C}} \\
&\geq \left(1 - \frac{8e^{r\lambda k}}{n}\right) \cdot \left(1 - \frac{4k^2\bar{C}^2 r}{n}\right) \cdot \left(1 - \frac{32rk\bar{C}^2 e^{r\lambda k}}{n}\right) \\
&\geq 1 - \frac{8e^{r\lambda k}}{n} - \frac{4k^2\bar{C}^2 r}{n} - \frac{32rk\bar{C}^2 e^{r\lambda k}}{n}.
\end{aligned}$$

Thus the speed of convergence to one is

$$O\left(\frac{8e^{r\lambda k}}{n} + \frac{4k^2\bar{C}^2 r}{n} + \frac{32rk\bar{C}^2 e^{r\lambda k}}{n}\right).$$

Note that constants generally do not matter for the rate of convergence, so the above rate of convergence can be rewritten as

$$O\left(\frac{e^{r\lambda k}}{n} + \frac{k^2\bar{C}^2}{n} + \frac{k\bar{C}^2 e^{r\lambda k}}{n}\right).$$

Further note that $e^{r\lambda k} = O(k\bar{C}^2 e^{r\lambda k}), k^2\bar{C}^2 = O(k\bar{C}^2 e^{r\lambda k})$ as $n \to \infty$ under our assumptions. This implies that the overall speed of convergence is

$$O\left(\frac{k\bar{C}^2 e^{r\lambda k}}{n}\right),$$

completing the proof. □

As a special case of interest, suppose that the number of couples and the length of doctors' preference lists are bounded along the sequence of random markets (which is equivalent to assuming that $\bar{C}$ and k are bounded by a constant). In this case, by Proposition 1, the probability that there does not exist a stable matching decreases with a rate of convergence of $O(1/n)$ as $n \to \infty$.

Number of vacancies Since the proof of Theorem 1 finds a bound of the probability by focusing on the event in which $Y_n > \frac{E[Y_n]}{2} \geq \frac{n}{4}e^{-r\lambda k} \geq \frac{n^{1-r\lambda\gamma}}{4}$, the next proposition follows from Lemma 1 and 3.

Proposition 2 (A large number of hospitals with vacancies)**.** *For any m,*

(1) *the probability that, in a sub-market without couples, the doctor-proposing deferred acceptance algorithm produces a matching in which at least m hospitals have at least one vacant position converges to one as n approaches infinity, and*

(2) *the probability that the sequential couples algorithm succeeds and at least m hospitals have at least one vacant position in the resulting matching converges to one as n approaches infinity.*

B Simulation and Computation Appendix

Figures 2 and 3 report simulations from markets with preferences drawn from a uniform distribution and from a distribution calibrated from the APPIC dataset. In this appendix, we describe the steps in our simulation and the algorithm we use to find a stable matching.

B.1 Simulating the Market's Primitives for Figures 2 and 3

The simulations reported in Figures 2 and 3 are for a one-to-one matching except for couples, who will match with pairs of positions. The number of single doctors and hospitals is denoted by n. Denote the number of couples in the market by c (with slight abuse of notation) and let the parameter which governs the length of doctors' rank order lists be $k = 10$.

For the market based on the uniform distribution, we proceed as follows:

- Each of the n programs is independently assigned to one of five regions with equal probability. For each program, draw the ordering of single doctors and couple members from the uniform distribution. Each hospital finds all single doctors and couple members acceptable.
- For each of the n single doctors, draw k programs without replacement from the uniform distribution.
- For each of the $2c$ couple members, independently draw two lists of length k from the uniform distribution, and append the null program (representing being unassigned) to the end of each couple member's list. To construct the couple's joint rank order list, we proceed as follows:
  - The first couple member, chosen arbitrarily, is the primary member.
  - Compose the list of program pairs from the two independent lists from each couple member, generating $(k + 1)^2$ pairs of programs.
  - If any program pair is from two distinct regions, then it is dropped from the set of program pairs. (If a program is paired with one couple member being unassigned, it is not dropped.)

– Next, for each remaining program pair, compute the sum of the couple members' rankings for each pair, and order the program pairs in descending order according to the sum of the ranks. Pairs with the same sum of ranks are ordered in favor of the primary couple members' ranking.

We simulate 100 markets for each value of n and c reported in Figure 2.

For markets based on APPIC, we follow similar steps, except preferences are drawn from a distribution using information from the APPIC dataset. As mentioned in the text, the APPIC dataset only identifies the region of each program. Program identifiers are anonymized each year, preventing us from linking programs across years. These data limitations necessitate that we proxy for program and applicant attributes using the capacity and submitted rank order lists. The dimensions of heterogeneity in the APPIC data are:

(1) the region of the program, which is one of 10 regions based on the first digit of the program's zip code for U.S. regions plus Canada region;

(2) the size of the program (measured by the total number of applicants assigned to the program);

(3) the region of the applicant, which we proxy for using the region of the doctor's first choice;

(4) the popularity of the program, which we proxy by the number of times the program is ranked among the top 13 choices by applicants in that year;

(5) the desirability of an applicant, which we proxy by the number of times an applicant is ranked among the top 25 choices of programs in that year.

The program popularity and applicant desirability measures are based on cutoffs. For programs, we consider the top 13 choices because most applicants rank fewer than 13 choices. For example, in Table 1, at least 75 percent of single doctors and at least 75 percent of couple members rank fewer than 13 distinct programs. For applicants, we consider being ranked among the top 25 because more than 75 percent of programs rank fewer than 25 applicants as shown in Table 1. It is worth emphasizing that these measures are constructed based on submitted rankings, rather than based on criteria measured before preferences were submitted. As a result, our estimates should not be seen as revealing the underlying taste parameters of market participants.

To fit models of both applicant and program preferences, we first relate program market share, defined as the fraction of participants who rank a program as their first choice, to the variables we've constructed from our dataset. Table B1 reports estimates from two specifications which use a program's first choice market share as the dependent variable. Column (1) reports estimates including proxies for program quality, the number of programs in the same region in that year, the number of applicants in the region in that year, year effects and program region fixed effects. Column (2) includes controls for year-program region interactions together with program quality proxies. It is not surprising that we can explain a significant share of the aggregate first choice variation using our quality proxy given that it is constructed based on submitted rankings.

The last column reports estimates for single doctors from a discrete-choice rank ordered logit model estimated using STATAs `rologit` command, which estimates the rank-ordered logistic regression via maximum likelihood (using the standard normalization of the error term). The estimates here relate the dimensions of the dataset (program quality, program region, applicant region) to applicant rank order lists. We also experimented with models using program-specific fixed effects, but most estimates were too imprecise to be useful. We use the point estimates in column (3) to simulate doctor's ranking of programs.

To calibrate preferences for hospitals, we relate applicant market share, defined as the fraction of programs ranking an applicant as their top choice, to the variables in our dataset. Table B2 reports estimates following Table B1, but for program demand for applicants. In addition to proxies for applicant desirability, we also include an indicator for whether the applicant is a couple member. Column (1) reports estimates with separate year and applicant region fixed effects, while the estimates in column (2) include year-region interactions. Here, the R^2 is smaller than in the program market share regressions possibly because there are more unobserved applicant level characteristics than captured by our proxy for applicant desirability. To estimate a program's preference for applicants, we fit rank ordered logit models for the program's ranking of applicants in column (3). These point estimates form the basis of the data generating process used to construct programs' orderings of applicants.

For the calibrated market, it is necessary to replicate the attributes of our dataset as we vary the market size n. To do so, we take n draws with replacement of programs in the APPIC dataset for all years and endow each with the region and quality attribute of the program. Then we take our single doctor preference estimates to construct predicted rank order lists for the set of programs drawn. The couples preferences are constructed by taking two single doctors and forming a joint rank order list following the procedure for the uniform case described above. To scale applicants, we take n draws with replacement of applicants from the APPIC dataset and endow each with the region and desirability, and couple member indicator attribute of the applicant. Finally, we take our program preference estimates to construct predicted rank order lists for the set of applicants drawn. We simulate 100 markets for each value of n and c reported in Figure 3. When we calculate the predicted rankings for programs and applicants, we use the models reported in column (3) of Tables B1 and B2, respectively, plus an error term that has Gumbel distribution with mode 0 and scale 1.

B.2 Finding a Stable Matching

The following procedure is used to find a stable matching in Figures 2 and 3 given the hospital and doctor preferences and hospital capacities:

(1) Apply the doctor-proposing deferred acceptance algorithm in the market with only single doctors and hospitals.

(2) Place the couples into a stack and process them in an arbitrary order. The first couple proposes to their top choice they have not proposed to yet and proceeds down their list (that is, applies to their most preferred hospitals that have not yet rejected them) until one of the following possibilities:

- The couple is accepted at the hospitals they apply to and no other doctors are displaced. Remove the assigned couple from the couples stack and proceed to the next couple in the couples stack.
- A single doctor(s) are rejected due to the proposal of the couple, who is in turn accepted. Remove the assigned couple from the couples stack, add the single doctor(s) to the stack of single doctors, and proceed to the next couple in the couples stack.
- A couple member is rejected due to the proposal of the couple, who is in turn accepted. Remove the assigned couple from the couples stack, and add the rejected couple member and the other member of that couple to the couples stack. Proceed to the next couple in the couples stack.
- A single doctor and couple member are rejected due to the proposal of a couple, who is in turn accepted. Remove the assigned couple from the couples stack. Add the rejected single doctor to the stack of single doctors, and add the other member of that couple to the couples stack. Proceed to the next couple in the couples stack.
- If the couple exhausts their list without displacing either a single doctor or another couple, leave the couple unassigned and remove them from the couples stack. Proceed to the next couple in the couples stack.

(3) Process the doctors in the single doctor stack one at a time in an arbitrary given order. The first single doctor proposes to her top choice she has not proposed to yet and proceeds down her list until one of following possibilities:

- A single doctor is accepted at the hospital they apply to and no other doctors are displaced. Remove the assigned single doctor from the single doctor stack and proceed to the next single doctor in the single doctor stack.
- A single doctor is rejected due to the proposal of the single doctor, who is in turn accepted. Add the rejected single doctor to the single doctor stack.
- A couple member is rejected due to the proposal of the single doctor, who is in turn accepted. Add the rejected couple member and the other member of that rejected couple to the couples stack. Proceed to the next single doctor in the single doctor stack.
- If the single doctor exhausts their list without displacing either another single doctor or a couple, leave the single doctor unassigned and remove her from the single doctor stack. Proceed to the next single doctor in the single doctor stack.

(4) Iterate by processing the couples stack and the singles stack as in the last two steps, alternating between both stacks as long as they are not empty. Note that since doctors propose down their list, this process must eventually terminate.

(5) Check that the resulting match is stable by verifying there are no blocking pairs for the given assignment. If it is stable, output the matching and terminate the algorithm.

(6) If the match is not stable, there must be a blocking coalition.

- Place every couple in the market on the couples stack. Place every single doctor in the market on the single doctor stack. At this step, no doctor withdraws from their current assigned position.
- Start with the couples stack following step 2. Each couple in the stack starts by proposing to their top choice (and not their top choice which has not rejected them yet). Next, move to the single doctor stack following step 3. If proposing doctor(s) are more preferred than existing match partners for the hospital, the proposing doctor(s) withdraws from their current assignment. Iterate between steps 2 and 3 as above, except any time a doctor is displaced the displaced doctor begin by proposing from their top choice down.
- If an applicant (either single doctor or couple) applies to the same alternative on their rank order list 100 times, declare failure.

The APPIC dataset only includes a program's ranking over individual doctors even though it is a many-to-one market. We assume that when comparing applicants, a program prefers the higher ranked applicant. When comparing two sets of couple members at the same program, the program always prefers the couple pair based on the highest ranked couple member.

Table A1. Comparison of Stable Matchings in Markets with and without Couples

Matching Market	Applicant type	Applicants: Choice Received: 1st	2nd	3rd	4th	5th+	Unassigned
without couples	single	36.8%	16.9%	10.1%	6.1%	11.2%	18.9%
with couples	single	36.0%	16.6%	10.1%	6.2%	11.6%	19.5%
	couple	18.0%	9.9%	8.2%	5.1%	53.7%	5.2%

Notes: This table reports the choice received in the applicant-optimal stable matching in a market with single applicants and without couples versus a stable matching in the market with couples in the Association of Psychology Postdoctoral and Internship Centers match, averaged over years 1999-2007. An applicant is counted as unassigned even if being unassigned is among her top five choices.

Table A2. Difference between Stable Matchings in Markets with and without Couples

Year	Single Applicants Receiving Less Preferred Assignment in Market with Couples		Programs Receiving More Preferred Assignment in Market with Couples	
	Number	Percent	Number	Percent
1999	35	1.2%	45	4.2%
2000	78	2.7%	92	8.4%
2001	86	3.0%	95	8.6%
2002	54	1.9%	62	5.8%
2003	51	1.7%	62	5.7%
2004	65	2.2%	73	6.8%
2005	53	1.7%	63	5.7%
2006	80	2.5%	78	7.1%
2007	69	2.0%	71	6.3%

Notes: This table reports differences between the applicant-optimal in the market without couples and a stable matching in the market with couples in the Association of Psychology Postdoctoral and Internship Centers match. A program receives a more preferred assignment if there is any responsive representation of its preferences for which the assignment is more preferred. There are no single applicants who receive a more preferred assignment in the market with couples and there are no programs that receive a less preferred assignment (for any responsive representation) in the market with couples.

Table A3. Properties of the Set of Stable Matching in the Market without Couples

	Single Applicants Receiving More Preferred Assignment in Applicant-Optimal Stable Matching		Programs Receiving Less Preferred Assignment in Applicant-Optimal Stable Maching	
Year	Number	Percent	Number	Percent
1999	2	0.1%	2	0.2%
2000	7	0.2%	7	0.6%
2001	8	0.3%	8	0.7%
2002	2	0.1%	2	0.2%
2003	6	0.2%	6	0.6%
2004	7	0.2%	7	0.6%
2005	0	0.0%	0	0.0%
2006	6	0.2%	6	0.5%
2007	10	0.3%	10	0.9%

Notes: This table reports differences between the applicant-optimal and program-optimal stable matching in the Association of Psychology Postdoctoral and Internship Centers matching market without couples. A program receives a less preferred assignment if there is any responsive representation of its preferences for which the assignment is less preferred.

Table B1. Applicant Demand for Programs

Dependent variable:	Program Top Choice Market Share		Applicant's ranking of program
	(1)	(2)	(3)
Program characteristics			
quality/1000	0.03641***	0.03660***	-6.8509***
	(0.001438)	(0.001445)	(0.5350)
(quality/1000)²	0.1379***	0.1373***	36.407***
	(0.02421)	(0.02433)	(6.5114)
number of programs in program's region	-0.000003592**	.	0.0007440
	(0.000001146)		(0.0004892)
number of applicants in program's region	0.000001637***	.	-0.0002778*
	(3.269e-07)		(0.0001386)
applicant is in the same region as the program	.	.	-1.1236***
	.	.	(0.006922)
Year effects	Yes	No	.
Program region effects	Yes	No	Yes
Year × Program region effects	No	Yes	.
log likelihood	.	.	-377,944.23
R^2	0.3797	0.3816	0.04016
Number of participants	10,611	10,611	27,428

Notes: Table reports OLS estimates of program market share on program characteristics in columns (1) and (2). Program market share is defined as the fraction of applicants ranking the program first. Column (3) presents estimates from rank ordered logit using applicant's choices. Program's quality is defined as number of times the program is ranked among the top 13 choices by applicants. Program's region is defined as the first digit of program's zip code. Applicant's region is defined as the region of the applicant's first-choice program. Psuedo R2 reported in column (3).

Table B2. Program Demand for Applicants

Dependent variable:	Applicant Desirability (based on top-ranking)		Program's ranking of applicant
	(1)	(2)	(3)
Applicant characteristics			
quality/1000	0.04731***	0.04736***	-111.46***
	(0.002955)	(0.002961)	(2.3734)
$(\text{quality}/1000)^2$	1.3421***	1.3432***	3232.9***
	(0.1916)	(0.1920)	(119.31)
is couple	-0.0001049**	-0.0001063**	0.04469*
	(0.00003411)	(0.00003422)	(0.02122)
number of programs	9.419e-07	.	-0.0002380
in applicant's region	(5.545e-07)	.	(0.0004693)
number of applicants	-2.824e-08	.	-0.0002839*
in region	(1.516e-07)	.	(0.0001266)
applicant is in the same region as	.	.	-0.1563***
the program	.	.	(0.006049)
Year effects	Yes	No	.
Applicant region effects	Yes	No	Yes
Year × Applicant region effects	No	Yes	.
log likelihood	.	.	-355,645.65
R^2	0.1484	0.1501	0.007942
Number of participants	26,335	26,335	10,092

Notes: Table reports OLS estimates of applicant desirability on applicant characteristics in columns (1) and (2). Applicant desirability is defined as the fraction of programs ranking an applicant first. Column (3) presents estimates from rank ordered logit using program choices over applicants. Applicant's quality is defined as number of times the applicant is ranked among the top 25 choices by programs. Program's region is defined as the first digit of program's zip code. Applicant's region is defined as the region of the applicant's first-choice program. Psuedo R2 reported in column (3).

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