# Non-monotonicity Examples

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The goal of this document is to design an example, such that vaccinated guys have moral hazard behaviors and the number of survivals is a non-monotonic function of $\alpha$ and $p$, where $\alpha$ is the number of people who get vaccinated and $p$ is vaccination success probability.

## 1 A line example

In this example, the underlying contact graph is a line. And moral hazard is defined as follows. If a person get vaccinated, with probability $\frac{\log n}{n}$ he connects to everyone else, and with probability $1 - \frac{\log n}{n}$ he does nothing. For those who are not vaccinated, they don't moral hazard.

If $\alpha = 0$, which means no one gets vaccinated, since everyone is connected, no one will survive in the end. If $\alpha = n$, which means everyone gets vaccinated, the expected number of people died in the end is $(1-p)^2 n$. The reason is as follows. Let $X \sim \text{Binomial}(\frac{\log n}{n}, n)$, then the expectation is $\mathrm{E}[X] = \log n$, and the standard deviation is $\sigma_X = \sqrt{n \frac{\log n}{n}(1 - \frac{\log n}{n})} \to \sqrt{\log n}$. $X$ value is within 2 or 3 standard deviation centered by expectation with high probability. So the number of moral hazard people is $O(\log n)$. And the probability that all of them have successful vaccines is $p^{O(\log n)} \to 0$. This means with arbitrary high probability, one moral hazard person with failed vaccine will connect to everyone. If nature picks a non-vaccinated guy or someone with failed vaccine, everyone will die except those with successful vaccines. So the expected number of people died in the end is $(1-p)^2 n$.

Now our goal is to find an $\alpha$ such that the number of people died in the end is smaller than $(1-p)^2 n$. Let $\alpha = n^{1-\epsilon}$, and $X \sim \text{Binomial}(\frac{\log n}{n}, \alpha)$. Then $X$'s expectation is $\mathrm{E}[X] = \frac{\log n}{n} n^{1-\epsilon} = \frac{\log n}{n^\epsilon} \to 0$, and standard deviation is $\sqrt{n^{1-\epsilon} \frac{\log n}{n}(1 - \frac{\log n}{n})} = \sqrt{\frac{\log n}{n^\epsilon}(1 - \frac{\log n}{n})} \to 0$. So with arbitrary high probability, the contact graph is unchanged, still a line. Among $\alpha$ vaccinated people, $p\alpha$ will have successful vaccines. If vaccination strategy is uniformly picking people from the population, we can view this as throwing $p\alpha$ blockers in the line (we have a collection of segments). The expectation of segment length roughly is $\frac{n}{p\alpha} = \frac{n^\epsilon}{p}$, which I will prove later. Now the expected number of people die in the end is $\frac{n^\epsilon}{p}$. In order to make $\frac{n^\epsilon}{p} < (1-p)^2 n$, we just need to make sure $\frac{1}{n^{1-\epsilon}} < p(1-p)^2$, which is always true when n is big.

In sum, the number of people survived is a non-monotonic function of $\alpha$, which means vaccinate less people will benefit more.

**Claim 1.** *Given an interval* $[0, 1]$*, throw* $n$ *points in the interval to separate it into a collection of segments. The expected length of each segment is* $\frac{1}{n+1}$*.*

*Proof.* When $n = 1$, we can calculate the expected length as follows.

$$\int_0^1 x\, dx = \frac{1}{2}x^2|_{x=0}^{x=1} = \frac{1}{2}$$

When $n = 2$, we can calculate the expected length as follows.

$$\begin{aligned}
& \int_0^1 \int_0^1 |x-y|\, dxdy \\
= & \int_0^1 \int_x^1 (y-x)\, dydx + \int_0^1 \int_0^x (x-y)\, dydx \\
= & \int_0^1 (\frac{1}{2}y^2 - xy)|_{y=x}^{y=1}\, dx + \int_0^1 (xy - \frac{1}{2}y^2)|_{y=0}^{y=x}\, dx \\
= & \int_0^1 (\frac{1}{2} - x + \frac{1}{2}x^2)\, dx + \int_0^1 \frac{1}{2}x^2\, dx \\
= & \int_0^1 (\frac{1}{2} - x + x^2)\, dx \\
= & (\frac{1}{2}x - \frac{1}{2}x^2 + \frac{1}{3}x^3)|_{x=0}^{x=1} \\
= & \frac{1}{3}
\end{aligned}$$

When $n$ goes larger, this way becomes very complicated. An easier way would be the following proof. Let random variables $X_i \sim \text{Uniform}[0, 1]$ for $i = 1, 2, \ldots, n$. They represent the blockers in interval $[0, 1]$. We order them $X_{(1)} \leq X_{(2)} \leq \cdots \leq X_{(n)}$. Then the expected length of the first segment is $\text{E}[X_{(1)}]$, expected length of the second segment is $\text{E}[X_{(2)}] - \text{E}[X_1]$ ...

First we need to find the distribution of $X_{(1)}$.

$$\begin{aligned}
& \int_0^1 \Pr[x \le X_{(2)}, \ldots, x \le X_{(n)}]\, dx \\
= & \int_0^1 (1-x)^{n-1}\, dx \\
= & -\int_0^1 (1-x)^{n-1}\, d(1-x) \\
= & -\int_1^0 y^{n-1}\, dy \\
= & \int_0^1 y^{n-1}\, dy \\
= & \frac{1}{n} y^n |_{y=0}^{y=1} \\
= & \frac{1}{n}
\end{aligned}$$

In order to normalize it, we need to multiply by $n$. Based on this, we can calculate the expected value of $X_{(1)}$.

$$\begin{aligned}
\mathrm{E}[X_{(1)}] &= \int_0^1 x \cdot n\Pr[x \le X_{(2)}, \ldots, x \le X_{(n)}]\, dx \\
&= n \int_0^1 x\Pr[x \le X_{(2)}, \ldots, x \le X_{(n)}]\, dx \\
&= n \int_0^1 x(1-x)^{n-1}\, dx \\
&= n \left( \int_0^1 (1-x)^{n-1}\, dx - \int_0^1 (1-x)^n\, dx \right) \\
&= n \left( \int_0^1 y^{n-1}\, dy - \int_0^1 y_n\, dy \right) \\
&= n \left( \frac{1}{n} - \frac{1}{n+1} \right) \\
&= \frac{1}{n+1}
\end{aligned}$$

Similarly, we can calculate $\mathrm{E}[X_{(2)}] = \frac{2}{n+1}$, $\mathrm{E}[X_{(3)}] = \frac{3}{n+1}$, etc. □

## 2 Bipartite graph

In this section, we give a non-monotonicity example of bipartite graph. Consider a bipartite graph with sets $A$ and $B$ of vertices. $A$ has $\sqrt{n}$ and $B$ has $n$ vertices, organized in blocks $B_1, B_2, \ldots, B_{\sqrt{n}}$ of $\sqrt{n}$ vertices each. Vertex $i$ of $A$

is connected to blocks $B_i$ and $B_{i+1}$. Vertex $\sqrt{n}$ to $B_{\sqrt{n}}$ (can wraparound too). This bipartite graph can be viewed as Figure 1.

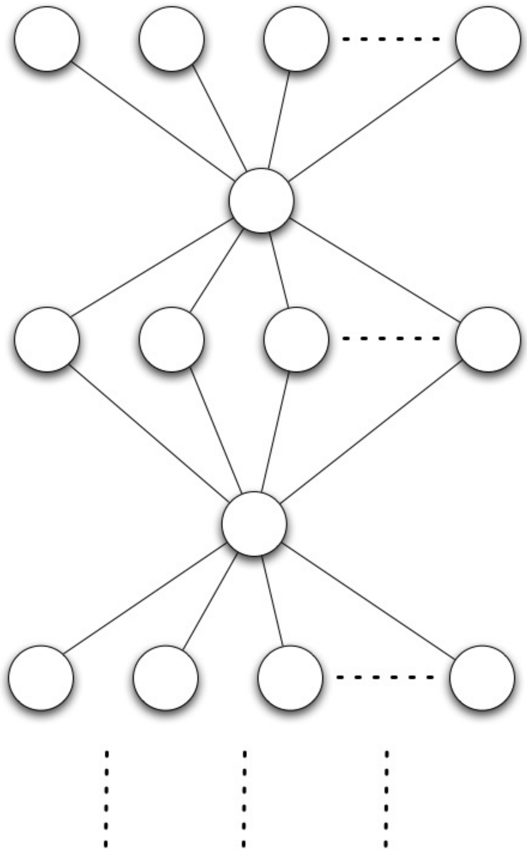

Figure 1: Bipartite example

The moral hazard model is, after vaccination, node connects with all vertices at distance 2. The good thing about this moral hazard is its behavior is local, doesn't depend on any global information.

Let $p$ be the vaccine success rate. (1) The above graph is connected. So no vaccination results in an epidemic size of $n$. (2) If all vertices are vaccinated, then every node in block $B_i$ is connected to every node in block $B_{i+1}$. The probability that all the $\sqrt{n}$ nodes in a single block $B_i$ succeed vaccination goes to 0 as $n$ goes to infinity. Once one node is infected, all the nodes that failed vaccine will die. So epidemic size is $\Omega(n)$. (3) Vaccinate all nodes in $A$. The only edges added as a result of the moral hazard make the set $A$ form a line. No new edges are added to the set in $B$. After every $1/p$ nodes along the $A$ line, we would expect one vertex to be successfully vaccinated. This would break the connected graph into components of size roughly $O(\sqrt{n}/p)$, which would be the expected epidemic size. In the worst case, there are $O(\log n)$ failed vaccination in a row along $A$ line (the probability of such case is $p^{O(\log n)} = O(1/n)$ which goes to 0). So the maximum epidemic size is $O(\sqrt{n} \log n)$ with high probability.

## 2.1 Generalization of this example

There are two ways to generalize this example. First, when a vertex is vaccinated, it connects with all vertices within distance $d$ where $d \geq 2$. For example, let $d = 4$. In such a case, if we vaccinate everyone, then the epidemic size is definitely going to be $\Omega(n)$ (worse than the case where $d = 2$). If we only vaccinate vertices in set $A$, then as long as there are two consecutive successful vaccination nodes, we can break the graph into two parts. The probability that we have two consecutive successful vaccination is $p^2$. So the expected epidemic size is $O(\sqrt{n}/p^2)$. We have non-monotonicity in this generalization.

**Open Problem 1.** *Right now if a node gets vaccinated, it connects all the neighbors at distance 2, which means it adds another $O(\sqrt{n})$ edges. If instead, we randomly connecting $O(\log n)$ nodes at distance 2, do we have non-monotonicity in this case?*

# 3 Grid example

We explore non-monotonicity example in grid.

## 3.1 Random separator

This section briefly explains why grid doesn't have this non-monotonicity under such probabilistic moral hazard behaviors. In 2 dimensional grid, if $o(n)$ nodes are faulty, then we have a component with size greater than $n/2$. In our probabilistic moral hazard model, when $\alpha = o(n)$, the underlining graph is unchanged with very high probability. As soon as $\alpha = \Theta(n)$, the grid contact graph changes to highly connected graph, which makes successfully vaccinated people the only survivals.

What we wanted to design is when $\alpha = o(n)$, the successfully vaccinated blockers will break the graph into small pieces, hence make the expected number of survivals more than the case where $\alpha = \Theta(n)$. But this is not true for grid.

## 3.2 Target separator

Although grid doesn't have $o(n)$ random separators, we can find $o(n)$ separators by targeting very easily. Now the question is can we have non-monotonicity in this case, i.e. by selectively vaccinating $o(n)$ nodes we can save more people than vaccinating everyone.

In 2D grid, a trivial separator is the cut in the middle with size $\sqrt{n}$. By applying this kind of separator recursively, we can break the grid into small square pieces, each of size $\sqrt{n}$, which means the length and height of each piece are the same, $n^{1/4}$. The total number of vertices in the separator is $O\left(\frac{\sqrt{n}}{n^{1/4}}\sqrt{n}\right) = O(n^{3/4}) = o(n)$. Now we have $O(\sqrt{n})$ these small square pieces, each of size $O(\sqrt{n})$.

Since we are considering the case that vaccination is not reliable, i.e. each vaccine fails with probability $p$, with high probability these small pieces are connected together. In order to avoid such a problem, we make the separator thick by increasing its width from 1 to $\log n$. So the total number of nodes in the separator is $O(n^{3/4}\log n) = o(n)$. Now we need to show by making the separator thicker, the probability that one small piece is connected to some other neighbor piece is really tiny.

**Claim 2.** *If the width of the separator is* $\log n$*, then the probability that there are two blocks connecting to each other goes to 0 when* $n$ *goes to infinity, with the assumption that the vaccination failure probability is no more than* $1/8$*.*

*Proof.* Let $A$ and $B$ be two neighbor blocks (i.e. they are separated by a $\log n$-width separator). For any path $L$ that connects a boundary node in $A$ with a boundary node in $B$, the probability every node on this path has failed vaccination (if it is vaccinated) is $p^{|L|}$ where $|L|$ denotes the number of nodes on path $L$. Starting from a single node, number of path with length $|L|$ on a grid is at most $4^{|L|}$. And the shortest path from $A$ to $B$ has length $\log n$. So the probability that $A$ is connected to $B$ is upper bounded by (using union bound),

$$n^{\frac{1}{4}} \sum_{i=\log n}^{\infty} 4^i p^i = n^{\frac{1}{4}} \sum_{i=\log n}^{\infty} (4p)^i = n^{\frac{1}{4}} \frac{(4p)^{\log n}}{1-4p} = n^{\frac{1}{4}} \frac{n^{\log 4p}}{1-4p}$$

From common knowledge, we can assume the vaccination failure probability $p \le 1/8$. In such assumption, $\log 4p \le -1$ (in this analysis log is the same as $\log_2$), thus, the probability that $A$ and $B$ are connected is upper bounded by $n^{1/4} n^{\log 4p}/(1-4p) \le n^{1/4}\frac{1}{(1-4p)n} \to 0$ when $n \to \infty$.

Each block only has 8 neighbor blocks with distance $\Theta(\log n)$. By union bound, the probability that this block connects any of these neighbors goes to 0 as $n$ goes to infinity (more precisely bounded by $8n^{1/4}\frac{1}{(1-4p)n}$). In the grid, we have $\sqrt{n}$ such blocks. Again by union bound, the probability that any of them connects a neighbor is upper bounded by $\sqrt{n} \cdot 8n^{1/4}\frac{1}{(1-4p)n} \to 0$ when $n \to 0$.

For those neighbors that are $\Omega(n^{1/4})$ away from a block, $A$. The probability that $A$ connects to any of them is upper bounded by

$$\sqrt{n} \sum_{i=n^{1/4}}^{\infty} 4^i p^i = \sqrt{n}\frac{(4p)^{n^{1/4}}}{1-4p} \to 0$$

In the grid, there are $\sqrt{n}$ blocks. The probability that any of them connects to a neighbor with distance $\Omega(n^{1/4})$ goes to 0 as $n$ goes to infinity.

So, in sum, those block are totally separated with high probability under such targeting strategy, even with vaccination failures (the failure probability $p \le 1/8$). □

### 3.2.1 Moral hazard model

The moral hazard is divided into two phases, sampling and reaching out. In the sampling step, each vaccinated person samples all the neighbors within distance $l$ where $l$ is a constant. If the percent of vaccinated people in the sample region is under his threshold (say 80%), then he does nothing (i.e. he thinks it is too dangerous to moral hazard). However, if the percent of vaccinated people is above the threshold, he feels comfortable and starts reaching out. The reaching out step is described as follows. He picks a random number $d$ according to the power law distribution (i.e. $d$ gets picked with probability proportional to $1/d^{\alpha}$). Note that $d$ is independent of $n$ where $n$ is the total number of vertices in the grid). And this person connects to everybody within distance $d$.

Consider the case that we vaccinate everybody in the grid. When a person does sampling, the percentage of vaccinated people is always going to be 100%, which will exceed the threshold. So everyone will moral hazard (i.e. reaching out). Now let's look at what happens in the reaching out step. Let $X$ be a random variable with power law distribution.

$$P(X \geq d) \geq \int_{d}^{\infty} \frac{1}{y^{\alpha}} dy = \frac{d^{1-\alpha}}{\alpha - 1}$$

So among $pn$ failed vaccinated people, the probability that one of them pick a distance greater than $\sqrt{n}$ is greater than

$$\begin{aligned}
1 - \left(1 - \frac{\sqrt{n}^{1-\alpha}}{\alpha - 1}\right)^{pn} &= 1 - \left(1 - \frac{1}{\alpha - 1} \frac{1}{n^{\frac{\alpha-1}{2}}}\right)^{pn} \\
&\to 1 - \left(e^{\frac{1}{1-\alpha}}\right)^{\frac{pn}{n^{(\alpha-1)/2}}} \\
&\to 1 \quad \text{when } \tfrac{\alpha-1}{2} < 1
\end{aligned}$$

so when $1 < \alpha < 3$, there is at least one person choosing a distance that is greater than $\sqrt{n}$, which means a vertex with failed vaccination is going to connect to all the other nodes. Then if one of the vertices with failed vaccination gets infected, all of them will be infected. So if we vaccinate everyone, the epidemic size will be $\Theta(n)$.

Now we use target vaccination (stripes with width $\log n$). In those stripes, we don't vaccinate everyone. Instead, we only vaccinate half of them, vaccinated guys alternating with non-vaccinated guys in the stripes (i.e. if you look at a row or a column, vaccinated nodes will alternate with non-vaccinated nodes). In this setting, vaccinated guys won't moral hazard, since there are at most (*approximately? may need sample distance to be large*) half of the people vaccinated in their neighborhood. And the stripes can still separate unvaccinated blocks with high probability. So using this vaccination strategy, the epidemic size is $o(n)$. Detail analysis is in the following proof.

**Claim 3.** *If we vaccinate vertices in the stripe separator in a alternating fashion, it is still going to separate all the blocks with high probability, assume that vaccination failure probability is no more than* $1/16$.

*Proof.* The proof of this claim will be similar to claim 2. Look at two blocks, $A$ and $B$. Any path, $L$, that connects them will have half vaccinated nodes and half non-vaccinated nodes. So the probability that $A$ and $B$ that are connected is upper bounded by

$$n^{1/4} \sum_{i=\frac{\lg n}{2}}^{\infty} 4^i p^i = n^{1/4} \frac{(4p)^{\frac{\lg n}{2}}}{1-4p}$$

If $p \leq 1/16$, then $(4p)^{\lg n/2} \leq (1/4)^{\lg n/2} = (1/2)^{\lg n} = 1/n$. So the probability that $A$ connects with $B$ is bounded by $n^{1/4} \frac{1}{(1-4p)n} \to 0$ when $n \to 0$. The rest of the proof will be exactly the same as claim 2. □

**Observation 1.** *If we use random vaccination within the strips, by Law of Large Number, we can use the same analysis to show there is non-monotonicity.*

**Open Problem 2.** *If the moral hazard distance d is not drawn from power law distribution, for example d is a constant, do we still have non-monotonicity? (From the simulation, this is true.)*

## 3.3 Simulation results

In this section, we present the simulation results.

### 3.3.1 Moral hazard without inhibition

First we consider the case without inhibition, i.e. once a person is vaccinated, he is going to moral hazard. And our moral hazard model here is, this person will connect everyone within distance $d$, where $d$ is a constant.

The simulation result is shown in Figure 2. This simulation is running over a $500 \times 500$ grid. The $x$-axis is the fraction of population we randomly vaccinated. If the vaccination succeeds, we remove the corresponding vertex from the grid. Otherwise, this vertex moral hazard and connects every vertex within distance $d$. The $y$-axis is the largest connected component in the grid. We run 10 simulations with $d = 1, 2, \ldots, 10$ respectively, each of which is a line in Figure 2. The reason we only see 5 lines in the figure is because lines for $d = 5, 6, \ldots, 10$ overlaps completely (the straight line in the figure). From left to right, these lines the simulation with $d = 1$, $d = 2$, $d = 3$, $d = 4$ and $d = 5, \ldots, 10$. Notice that when $d = 1$ (i.e. there is no moral hazard at all), grid shatters at 50%.

**Open Problem 3.** *Is there non-monotonicity in the case without inhibition? (Note: from the simulation, there is no non-monotonicity.)*

### 3.3.2 Moral hazard with inhibition

Now we consider the case with inhibition. The model is as follows. When a person is vaccinated, he samples the neighborhood within distance $d$ where $d$ is a constant. If the fraction of vaccinated people in the neighborhood exceeds his

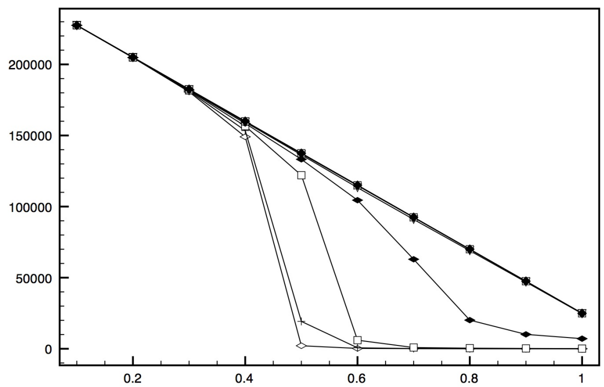


Figure 2: Moral hazard without inhibition for fixed vaccination success probability $p$ ($p = 0.9$) and various moral hazard distance $d$ values.

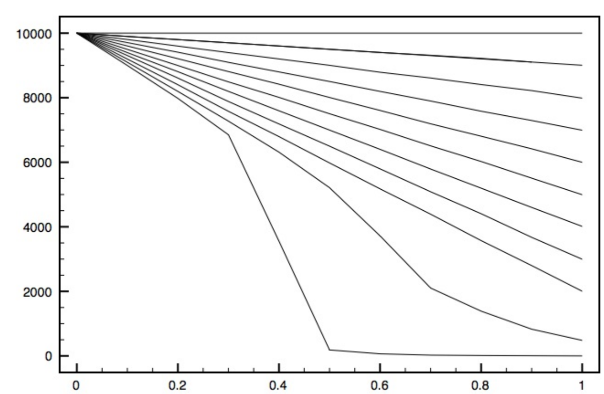


Figure 3: Moral hazard without inhibition for fixed moral hazard distance $d$ value ($d = 4$) and various vaccination success probability $p$.

threshold, he go ahead and connects everyone in this neighborhood, otherwise he does nothing.

The simulation result is shown in Figure 4 and 5. $x$-axis and $y$-axis are the same as before. And we set $d = 5$ in the simulation. Threshold for moral hazard is 100%. We can clearly see the non-monotonicity in this case.

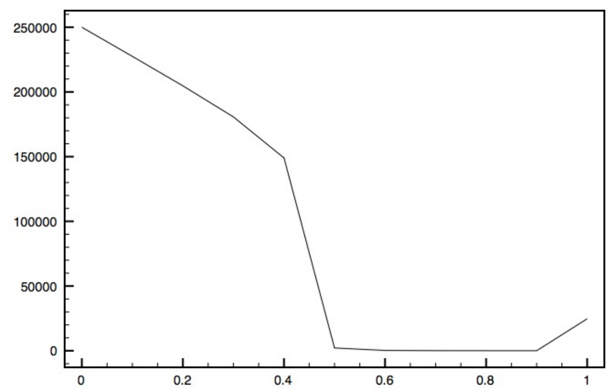


Figure 4: Moral hazard with inhibition.

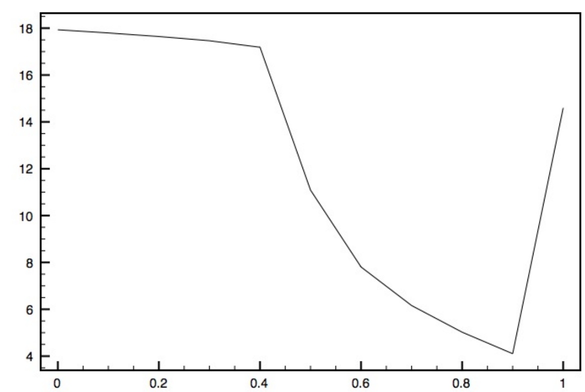


Figure 5: Moral hazard with inhibition in *log* scale.

# 4 Complete graph

Let the contact network be a complete graph, and the vaccination success probability be $p$. Instead of considering highly infectious disease, let $q_1 = c/n$ be the disease transmission probability over edges, where $n$ is the total number of vertices and $c$ is a constant greater than 1. The moral hazard model is as follows. When a vertex gets vaccinated, it increases the disease transmission probability on the edges to other vaccinated vertices. Let $q_2 = c'/(1-p)n$ be this probability, where $c'$ is a constant greater than 1.

Let $\alpha$ be the fraction of vertices we choose to vaccinate. If $\alpha = 0$, then no one is going to moral hazard. Since $q_1 n = c > 1$, we know this random graph will almost surely have a giant component of size $\Theta(n)$. If $\alpha = 1$, then everyone will moral hazard to everyone else. Since $q_2(1-p)n = c' > 1$, we know this random graph will almost surely have a giant component of size $\Theta\left((1-p)n\right) = \Theta(n)$.

Now we are going to analyze the case where $0 < \alpha < 1$. We show that there exists such $\alpha$, the largest component size in the random graph will be $o(n)$. Hence we can have non-monotonicity in this moral hazard model.

We can classify vertices into 2 categories. Let $A$ be the set of unvaccinated vertices ($|A| = (1-\alpha)n$), and $B$ be the set of vertices with failed vaccination ($|B| = \alpha(1-p)n$). The rest of vertices will be removed from this graph since they have successful vaccination. So we don't consider them at all. We just need to analyze what's the size of largest connected component in $A \cup B$. We can view this in the following way. First we do an edge percolation with probability $q_1$ on $A \cup B$. In order to make the size of largest connected component small, we need $q_1 \cdot |A \cup B| < 1$, from which we have $\alpha > \left(1 - \frac{1}{c}\right)\frac{1}{p}$. If this is satisfied, then the largest connected component size is $O\left(\lg n\right)$ under this percolation with probability $q_1$. Next we consider the percolation on vertices in $B$ only (due to moral hazard $q_2 > q_1$. Since $q_2 |B| < 1$, this leads to $O\left(\lg n\right)$ sized components restricted to $B$. Putting two steps together, we have components of size $O\left(\lg^2 n\right)$.

**Observation 2.** *The above moral hazard model can be applied to $G(n,p)$ graphs, and by the same argument, we have non-monotonicity there.*

## 4.1 Simulation results

In this section, we show simulation results on complete graph moral hazard model. From the analysis above, we know as long as we satisfy the following equations, we will have nonmonotonicity in complete graph.

$$
\begin{aligned}
&c > 1 \\
&c' > 1 \\
&c(1-\alpha p) < 1 \\
&c'\alpha < 1
\end{aligned}
$$

After simple calculation, we can the range of $c$ and $c'$.

$$1 < c < \frac{1}{1-p}$$
$$1 < c' < \frac{pc}{c-1}$$

The simulation runs on a complete graph with 10,000 vertices. For each vaccination success probability, we calculate the range of $c$ and $c'$ using the inequalities above. And we pick 10 values in each range to run simulation. That is for each combination of vaccination success probability $p$, $c$ and $c'$, we run simulation with 10% of people getting vaccinated, 20% of people getting vaccinated, ..., 100% of people getting vaccinated. If there is nonmonotonicity with this set of parameters, we mark a point in Figure 6, in which x-axis is $c$, y-axis is vaccination success probability $p$, and z-axis is $c'$.

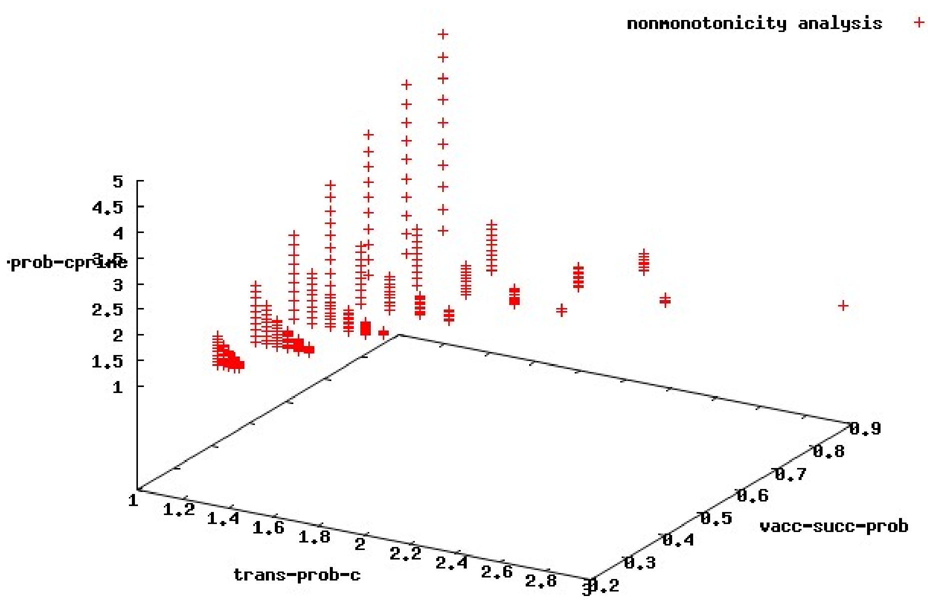


Figure 6: Moral hazard in complete graph

From Figure 6, we can see the simulation matches our analysis result very well. For almost all the simulation we run, we get nonmonotonicity result.

**ToDo 1.** *Draw 3D body formed by* $1 < c < \frac{1}{1-p}$ *and* $1 < c' < \frac{pc}{c-1}$. *(Don't know how to do it using gnuplot yet)*

**ToDo 2.** *In the simulation, when vaccination success probability is high, add more simulation points by making the step size of c and $c'$ smaller. In this way, can make FIgure 6 look better.*

# 5 Pow law graphs

Lots of real networks turn out to be power law graphs, like the Internet, social networks, human sexual networks, etc [5, 4, 1, 8, 2]. So it makes more sense to come up with some non-monotonicity on power law graphs.

**ToDo 3.** *Theoretical result on scale free graphs.*

## 5.1 Simulation results

In this section, we show simulation results on randomly generated scale free graphs with 100,000 vertices.

**ToDo 4.** *After simulation is done, add 3d plot here, similar to Figure 6.*

**ToDo 5.** *Run simulation on real world graph which is approximately a scale free graph.*

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