

Final project report: A network analysis of STI transmission in two different
Tjimba/Himba communities

INTRODUCTION

Disease ecology

Infectious diseases have always been a significant cause of human mortality, across all demographic strata. The major economic and cultural transitions of human history have, in turn, caused major epidemiological transitions. Despite these sweeping pathogenic changes, sexually transmitted infection (STI), such as Gonorrhea, Chlamydia, Syphilis, Herpes and HPV, has always been an important source of morbidity and/or mortality. Gonorrhea, Herpes and Chlamydia are not fatal diseases but can cause serious reproductive complications and infertility.

Many of the ancient human STIs have become relatively less important in terms of public health research and interventions in recent years for several reasons. First, STIs of bacterial origin can be easily treated with antibiotics. Second, the HIV/AIDS epidemic has caused mortality and social destruction unparalleled by any other sexually transmitted pathogen. However, there are reasons to consider the transmission dynamics of these diseases. Due to the rapid evolution of antibiotic resistance, many previously easily treated diseases, such as Gonorrhea, are now multi-drug resistant. Furthermore, people infected with Chlamydia are five times more likely to contract HIV if they have sex with an infected partner. This is important because there are small populations of people that have long-standing STI epidemics but are not connected to the adjacent, larger sexual networks where HIV occurs at very high rates. Understanding more about the transmission dynamics of non-HIV/AIDS STI will not only help prevention of diseases that are increasingly hard to treat with antibiotics but will also help population health workers to target interventions before deadly STIs are transmitted into a new population.

A network model of Tjimba/Himba reproductive health

For this class project, I want to build a model that will act as a first step in building a dynamic transmission model for a real-world example of chronic STI infection and transmission in an isolated pastoral community. The Tjimba/Himba are semi-nomadic herders adapted to the high elevation desert of northwestern Namibia. The harsh dry climate in this region makes it difficult to grow crops and find enough water for humans, let alone the livestock on which they are entirely economically dependent. Therefore, the Tjimba/Himba, being very successfully adapted to this region, have been largely left alone by colonialist development throughout the 20th century, and consequently, they remain economically, culturally and reproductively isolated from neighboring Namibian populations. While HIV/AIDS has reached a nationwide prevalence of ~20% in Namibia, the Tjimba/Himba have no discernable HIV rates in their communities. They do however have high rates other non-HIV/AIDS STIs: levels that have probably been maintained for centuries due to little change in their way of life over time. Although marriage is common in Tjimba/Himba culture, so is divorce and extra-marital sexual interaction. With sexual introduction happening at a very young age, a Tjimba/Himba man or woman will have many sexual partners throughout his/her lifetime, allowing for increased risk for multiple STIs. In the past, this risk has meant possible chronic

discomfort, pregnancy difficulty and infertility. If HIV spreads to the Tjimba/Himba community and transmits with the ease that non-fatal diseases have, the consequences could be disastrous. I intend to investigate STI transmission dynamics in the Tjimba/Himba communities in order to understand the disease ecology of a traditional, non-western population and make some claims regarding the evolutionary history of disease burden and its affect on reproduction and behavior. In order to serve that end, I will also build a social network model of STI transmission based on the particular patterns of migration and sexual dynamics of the Tjimba/Himba community. Such a model should be useful to make predictions of how transmission will change as the economic, cultural, behavioral practices change.

THE MODELS

Basic components

This project consists of two network models based on real world census data. Both models were built in NetLogo. In both cases nodes represent members of the community and links represent sexual relationships between two individuals. A disease is spread with different parameters affecting transmission. The outcome is whether a disease will either sustain or die out, given the parameter settings.

Real world census data from two villages

In the spring of 2007 I spent 8 weeks in Namibia conducting survey and census data in several villages in the Kaoko region. I have taken the census data from two of those villages to incorporate into two different social networks. In both cases, I am starting with a network of all the adults (ages 16+) in the village and starting with links only between married couples. In a few cases where a man has more than one wife, a single node starts with more than one link. The links are differentiated by sex (males=blue, females=pink) and by age-rank (ages 16-17=6; 18-24=5; 25-34=4; 35-44=3; 45-54=2; 55+=1). I chose two particular villages—Ombivango and Otjikoyo—because they each represent geographical and spatial distinctions that I think will be important in understanding different STI transmission patterns within the entire Tjimba/Himba population.

Ombivango village

Ombivango is a very remote village, just a few miles from the Namibia-Angola border. Although it is as populated as villages in closer proximity to urban centers, it is very difficult and time consuming to travel to by foot (which is the only mode of transportation available to locals) and does not receive many guests or people passing through. If infections are sustained in Ombivango, then STI is probably endemic and this probably happens via high levels of partner recycling.

Otjikoyo village

In contrast to Ombivango, Otjikoyo is in (relatively) close proximity to urban centers. It takes only a few hours to get from Otjikoyo to Okanguati by foot—where there are shops to sell livestock and buy maize, medical centers, short-term jobs for young men who do not own livestock, and opportunities to meet with old friends or family members. Therefore, a lot of travel occurs between Otjikoyo and Okanguati, in both directions.

Additionally, Otjikoyo sees a lot of people passing through from more distant villages on their way to Okanguati, or the more distant Opuwo.

Modeling partner exchange

Links in the model represent sexual relationships. The imported network includes only links between married individuals. These links are yellow. To attempt to model partner-exchange dynamics in Ombivango and Otjikoyo, new links are added and removed at time intervals. These links (colored purple) represent unmarried relationships. The number of unmarried partnerships in the network can be set by the observer to either have very high rates of partner exchange or low rates. Additionally, the formation of new links will not be random but preferential based on the node's age rank. Higher age-ranks (i.e. lower ages) will be more likely to obtain partners at each time step than lower age-ranks. The same preferential partner-exchange based on age-rank is used in both village models.

Migration

Since Otjikoyo sees much more movement in and out of the village it is likely the STI infection comes from individuals who are not members of the community but who have a sexual relationship with a villager when they are passing through. Because I am assuming that Ombivango village does not experience much human traffic in and out of the village, no new nodes will be added or subtracted from this network. In order to model people moving in and out of Otjikoyo (and possibly engaging in sexual relationships as they pass through) I allowed the addition and subtraction of new nodes (called "outsider" nodes). As with the new link formations between insider nodes, links with outsider nodes will form links preferentially based on age-rank. For simplicity, all outsider nodes are not married and have an age rank of 5. The observer can choose how many outsiders of each sex to add to the network upon import.

Disease diffusion

The disease being spread in both networks is a hypothetical chronic STI. It only passes between from a male node to a female node or vice versa. The transmission probability can be varied as well as the probability of recovery. None of the STIs spreading in the Tjimba/Himba communities will go away on their own, so in reality recover probability = 0. However, some people will be able to get antibiotics if they are close enough to a clinic or if friends or traders bring pills back from their trip to the city. In the Otjikoyo network, an additional parameter for infection exists. The observer can also set the probability of outsider infection, in order to see how outsider participation in the sexual network affects STI transmission if outsider prevalence is > 0 . When a node becomes infected, it changes its shape from a filled-in circle to a target. When a node infects another node, its size increases.

The questions I want to answer with social network modeling

Applying network modeling to my research question of STI transmission has many uses. First, developing a model before going to collect field data allows one to get a better idea of which variables are likely to be the most important in explaining disease dynamics. Second, a model allows one to measure variables in a controlled way—something that can be difficult to impossible with real-world data. Although there are many variables

that I think are affecting STI transmission in the Tjimba/Himba community, I am focusing specifically on partner exchange and people movement for this project. By varying these two parameters in addition to transmission and recovery probabilities, I hope to answer the following questions:

- 1) How does sexual partner exchange affect transmission of sexually transmitted disease in a village community—with and without outsiders?
- 2) Does a skewed sex ratio of migrators affect transmission patterns?
- 3) How does partner exchange affect infection thresholds—with and without outsiders?
- 4) What are the conditions necessary for endemic versus epidemic infections?

RESULTS AND DISCUSSION

Because my questions are focused more on how social variables (partner exchange and outsider migration) affect transmission dynamics (rather than on how disease attributes affect transmission), I ran numerous preliminary simulations to determine optimal settings for the disease parameters. When analyzing affect of partner exchange, I decided to keep transmission probability set at 0.20. Above this amount, infection spread very fast throughout the whole village and varying partner exchange could make no difference. Recovery would therefore need to be kept at a lower probability (otherwise it would be very difficult to spread the disease at all unless partner exchange was set unrealistically high), so I maintained it at 0.15. Considering the fact that most people would have great difficulty accessing antibiotics, this may not be a very inaccurate assumption, but actual data would be required to know what level of recovery is most appropriate.

How does sexual partner exchange affect transmission of STI?

Not surprisingly, the greater the partner exchange (greater the number of links between nodes) the faster spread of infection and higher the rate of infection in the village. Even if the transmission probability is set low (see section below for more about transmission probability), high levels of partner exchange keep the infection spreading throughout the village. Interestingly, differences in levels of partner exchange lead to differences in the pattern and structure of spread through the village. After preliminary simulations I found that setting the partner exchange above 30 lead to such rapid and complete village infection, no important structure or pattern could be detected. Therefore, to test the importance of levels of partner exchange in the networks, I ran 50 simulations at partner-exchange level = 25 and then at level = 15 for each village (4 sets of 50 simulations altogether). After each simulation, I determined which node was the most biggest spreader based on node size. If two nodes were the same size, I counted them both as the biggest spreader for that round. I analyzed the results using linear regression in SAS—fitting a multiple covariate model with all attributes (age, sex, marriage status) as main effect variables as well as a model including an interaction between age and marriage. In every set of simulations, marriage status was a highly significant variable.

In Ombivango, marriage status was a highly significant variable at both the higher and lower levels of partner exchange ($p < 0.0001$). There are not many marriages within the community and this is why extensive partner exchange is an important factor for disease

spread. However, low marriage rates are probably also why married nodes are important spreaders. Married links do not die in this model and so links between two nodes (or more than two for polygynous marriages) are always intact. If a member of a married set gets infected it will always have the opportunity to be passed to the spouse. Therefore, over time, these nodes become big spreaders. Polygynous marriages contribute even more to the spreading of STI because if one member of the marriage gets infected they have the opportunity to transmit it to two other people rather quickly, in addition to whomever they are linked to in an unmarried sexual relationship at that time. Interestingly, when partner exchange was decreased from 25 to 15, sex became an important, but not quite significant factor toward likelihood of being a big spreader ($p = 0.0755$), with males being more likely than females to be the big spreader. I think this might be because there are two polygynous marriages in Ombivango village. The husband of these marriages has the possibility of infecting two women (at least) each time he becomes infected. These men were the most common super spreaders in the community and when partner exchange decreased, their effect as super spreaders was even stronger.

In Otjikoyo, the results are generally the same, with some differences. I kept the outsider levels set at 10 (5 males, 5 females) so as not to overwhelm the network with outsiders and keep insider dynamics from having an impact. In both sets of simulations, marriage was the most significant variable. At the higher level of partner exchange (25), marriage is the only significant variable but it is having much less of an effect in this model than in the Ombivango model ($p = 0.323$). However, when I ran a model with an interaction between marriage and age, I find that there is a significant interaction between these two variables ($p = 0.0063$). Sex ($p = 0.0747$) and age ($p = 0.0470$) also become close to significant. My interpretation of this is that when partner exchange is high, and the addition of outsiders brings more sources of disease, no individual stands out as an important spreader—except for one. A powerful chief lives in this village and has four wives. Each time he becomes infected he has at least a four-fold greater potential to infect others than anyone else in the village. On the few occasions that someone else was the super spreader that person was more likely to be a young, married male. When the partner exchange was lowered, the polygynous chief was still the most important super spreader but now the outsiders become significant spreaders as well, because they are always renewing an infection that would otherwise run the possibility of dying out with less transmission opportunities. The results in this simulation set are weird and hard to explain. In the main effects model, marriage is not significant ($p = 0.1295$) but sex is ($p = 0.0346$). Unfortunately, I do not think this is a real result but is based on an artifact of the model. No female outsider was ever a super spreader, but male outsiders frequently were. This must be due to a coding bug where male outsiders being introduced to the network are preferentially infected compared to the outsider females. Still this does demonstrate that outsiders are important sources of infection, particularly when levels of partner exchange decrease. This can be demonstrated by the real result of a significance of age in the interaction model. Outsiders were all given the age rank of 5 and age become a significant effect variable ($p = 0.0242$). Creating an interaction between age and marriage also made marriage significant ($p = 0.0204$, main effect; $p = 0.0009$, interaction) in this model in a reverse manner to how it has been significant for the other simulations. Not being married is associated with a greater likelihood of being a super

spreader, if you are also of a higher (younger) age rank, because the outsiders all fit this profile and they become the other major super spreaders, besides the chief.

Does a skewed sex ratio of outsiders affect transmission?

I chose to make two separate parameters out of male-outsiders and female-outsiders because I thought it would be interesting to see if having many males migrating into the village would have an effect on super spreader characteristics. For example, my hypothesis was that, as the number of male outsider increases, the number of sexual partners for young females will increase and so individual females will become more important spreaders. However, this hypothesis was not supported. Only if the number of males is raised to an unlikely extreme can any effect be seen. I think this is because the village demographic structure is one with many more females than males, so the outside-male population would have to be very high to single out individual women as major spreaders.

How does partner exchange affect infection threshold?

Partner exchange certainly affects infection threshold, much more than married links do. If there are a lot of partners in the network at any time, the infection is likely to stay active and spread. Even with a very small number of sexual partner links, it is very hard to get an infection die-out. Keeping partner exchange at 5 (average of 5 extra-marital sexual partners in the network), I tested different transmission probabilities to see at what point I could achieve a die-out the majority of the time for each village.

In Ombivango, it is never possible to get a die-out the majority of times at any transmission probability > 0 . What does happen though is that smaller chronic infection levels can be maintained that do not affect most of the population. When transmission probability is set $< .15$, no more than 17% of the population would be infected a majority of the time ($18 / 25 = 68\%$) of the time. Only at transmission probability = 0.03 do we see a major shift in disease prevalence where a very small number of individuals (1-3) are infected and cannot pass the disease to others. Even then, the disease is walled off in this fashion only 44% of the time ($11/25$).

In Otjikoyo, outsiders carrying disease ensure that infection die-out is never a possibility, even when the number of sexual partners in the network is set very low. Therefore, in an open system, partner exchange and outsiders coming and going from the network both matter in terms of determining the infection threshold. If even only 1 outsider at a time brings an infection into the network, it is enough to sustain an infection that spreads through a majority of the village. When I set the outsider infection rate to less than one infected individual at any given time, I was able to achieve a small infection that only affected 1-3 people at a time a majority of the time ($19 / 25 = 76\%$); but outsiders coming and going meant there was always at least one infected person. Otherwise, infection spread in the Otjikoyo model, will mostly lead to high infection spread in the population, even when transmission probabilities are very low. At transmission probability = 0.05, an average of $\sim 32\%$ of the population was infected after all simulations. Even at transmission probability = 0.03 (when spread could not occur in Ombivango) an average of 22% of the population were infected in all the simulations.

What are the conditions necessary for endemic versus epidemic infections?

In the Ombivango model, without outsiders bringing new infections into the village, only endemic style infections are possible. If infection is chronic and untreated, even low transmission levels and low partner exchange will maintain the infection at small levels, allowing the opportunity for bigger spread if those conditions change. In Otjikoyo, low endemic levels of STI are possible in the absence of infected outsider sexual partners, but as we can see, if there is even a low level of infection among the outsiders, as long as they are entering the model and linking with village members, they are contributing infection to the community and allowing for bursts of epidemic, even if partner exchange is not high.

According to the model, the parameter we could change to allow more die-outs and increase the infection threshold is recovery probability. If people have more access to medication to treat chronic infections, they will spend less time being infectious and it would be harder to transmit infections—especially when transmission probability is already low and when partner exchange is not high.

CONCLUSIONS AND FUTURE WORK

Some very interesting characteristics are coming out of these two models that can be very useful to understanding the real-world parameters that are leading to current high rates of STI Tjimba/Himba villages now, and how STI rates will change as Tjimba/Himba economy and culture undergoes rapid and imminent alterations. We have found that levels of unmarried sexual partner exchange really matters for STI spread in the villages, but that, in light of high partner exchange, married individuals—and especially polygynous men—can become super spreaders, if they are engaging in out of marriage sexual relationships as well. (There is no reason to believe this is not the case, given prior knowledge of the local culture.) Furthermore, outsiders migrating in and out of the community become very important to transmission dynamics by supplying a constant source of infection, even when partner exchange and transmission probability is low.

One thing that is certainly missing from this analysis that has been covered in other social network analyses of STI contact patterns through social networks are the issues of a) duration of relationships and b) overlaps or gaps between relationships. My model assumes homogeneity for both of these factors but this is unrealistic and other studies have shown that these attributes are important determinants of STI transmission in a population. Eames and Keeling (2006) show even in populations with high levels of monogamy, different lengths of relationships can lead to high variability of strain type within the community. Variation in the microbial community sets the stage for instigation of selective pressures if any of those strains incur a greater replicative advantage over the others, which can lead to higher rates of highly virulent strains, etc (Eames and Keeling 2006). My model has two types of sexual relationships—married and unmarried—and each type assumes a different relationship length. This is a step in the right direction to modeling relationship duration and STI but does not go far enough to capture the complexities of realistic relationship variation.

Recent work has shown that partner overlap (presence, lack of) and duration of infection period can be important determinants of STI transmission (Foxman, Newman et al. 2006). My model included instances of overlap (of two to several partners) in a semi-random fashion. Ploygynously married men always have overlapping sexual partners, as is inherent in the structure of the network, but unmarried relationships overlapped (with married and unmarried relationships alike) or didn't in a random fashion. This could only be partially manipulated by the observer by changing the number of partners in the network (less partners = more likely to have gaps between partnerships; more partners = more likely to have overlaps) but it cannot be manipulated systematically. This is important because we cannot quantify this aspect of sexual relationships in the village as it is currently set up in the model but it is an issue that should not be overlooked.

While developing this model has been very useful in terms of narrowing in on important factors that affect STI transmission, this exercise also highlights ways that this model is likely to be infinitely simpler than the real-world situation. The preferential attachment used in this model assumed that younger people are more likely to have a) more sexual partners than older people and b) that people will be more likely to pick sexual partners in their age group. While this is largely true, a better model would incorporate gender differences into the preferential attachment. (E.g. Older men—who own a lot of cattle—will probably have the most partners of all; women probably have less partners than men on average; older men probably commonly have sexual partnerships with younger women.) Also, it is not practical to treat outsider nodes as the same individual coming and going. In reality, the migratory population has much higher turnover and is not the same people re-appearing again and again. Having the outsiders come back and be “remembered” by the model is useful on the one hand because we can visualize the importance of individual spreaders from the outsider pool. One detriment though is that it can lead to a larger infection rate among outsiders than expected after several time steps. For future analyses I can give these nodes a different recovery parameter and set it to 100% so that each time an outsider node reappears, it is not infected. Regarding outsider nodes, another important issue to adjust is how infection is set up among the males and females. For some reason, males enter the network as being preferentially infected over the females and I am not sure why but this aspect of the model needs to be modified. Finally, this model assumes the same transmission probabilities for males and females, but actually many diseases are more easily transmitted to females than males. In this sense, a network analysis of STI transmission is not actually an undirected network but a semi-directed one. While this makes the model more complicated, semi-directedness has been shown to have an effect on epidemic thresholds (Meyers, Newman et al. 2006) and should be considered, especially when one is dealing with real demographic data that exhibits unequal distribution of sexually active males and females, like in the Tjimba/Himba community.

References

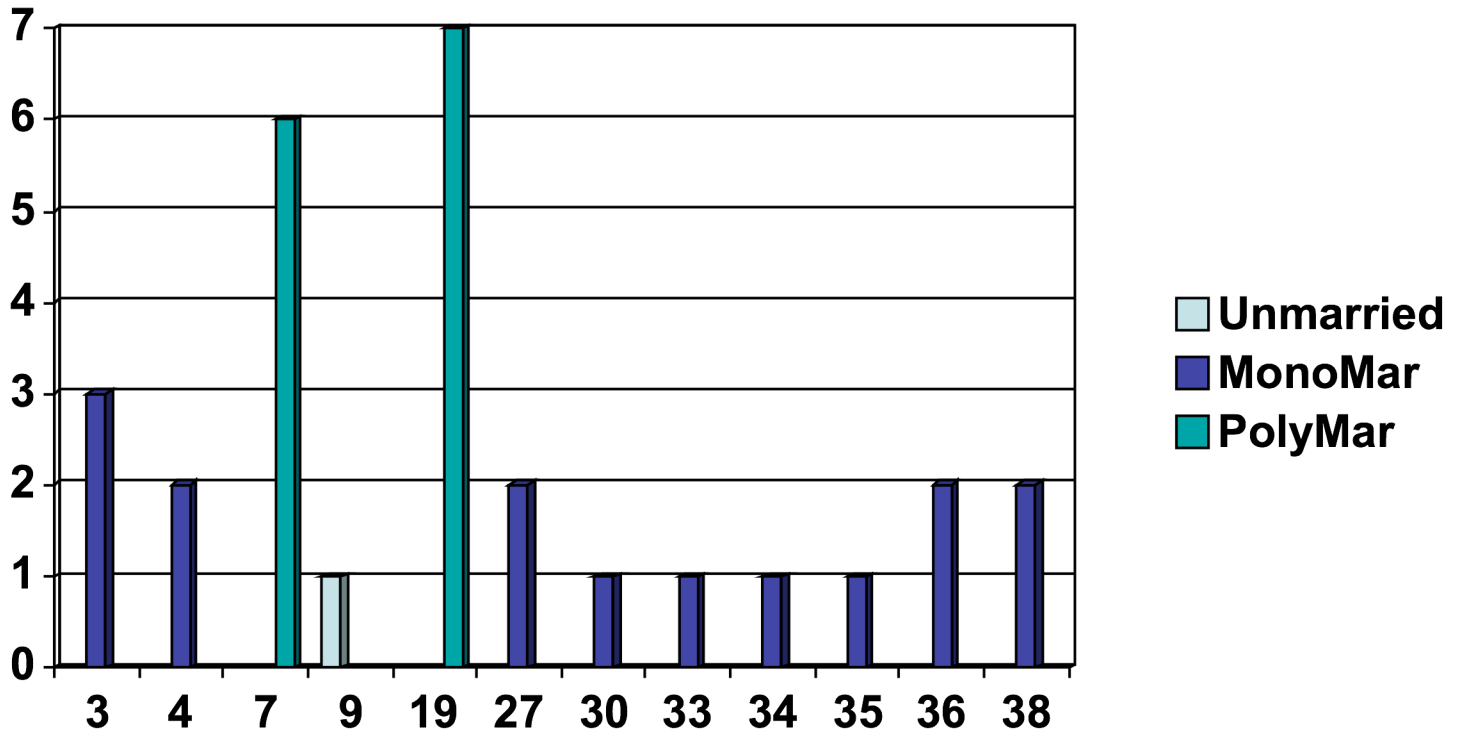
Eames, K. T. D. and M. J. Keeling (2006). "Coexistence and specialization of pathogen strains on contact networks." *American Naturalist* **168**(2): 230-241.

Foxman, B., M. E. J. Newman, et al. (2006). "Measures of sexual partnerships: Lengths, gaps, overlaps and sexually transmitted infection." *Sexually Transmitted Diseases* **33**: 209-214.

Meyers, L. A., M. E. J. Newman, et al. (2006). "Predicting epidemics on directed contact networks." *Journal of Theoretical Biology* **240**: 400-418.

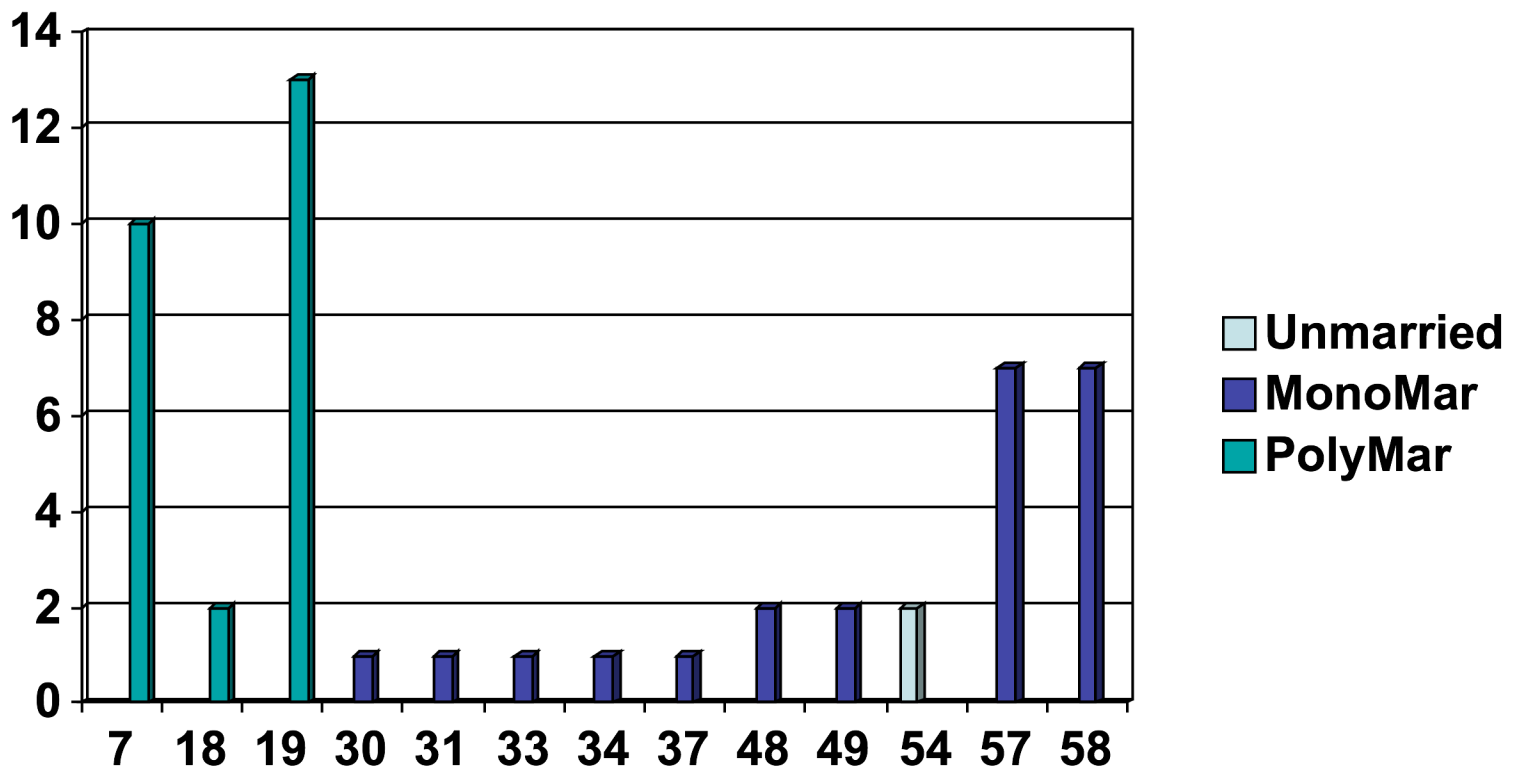
Appendix of results

Ombivango—partner exchange = 25



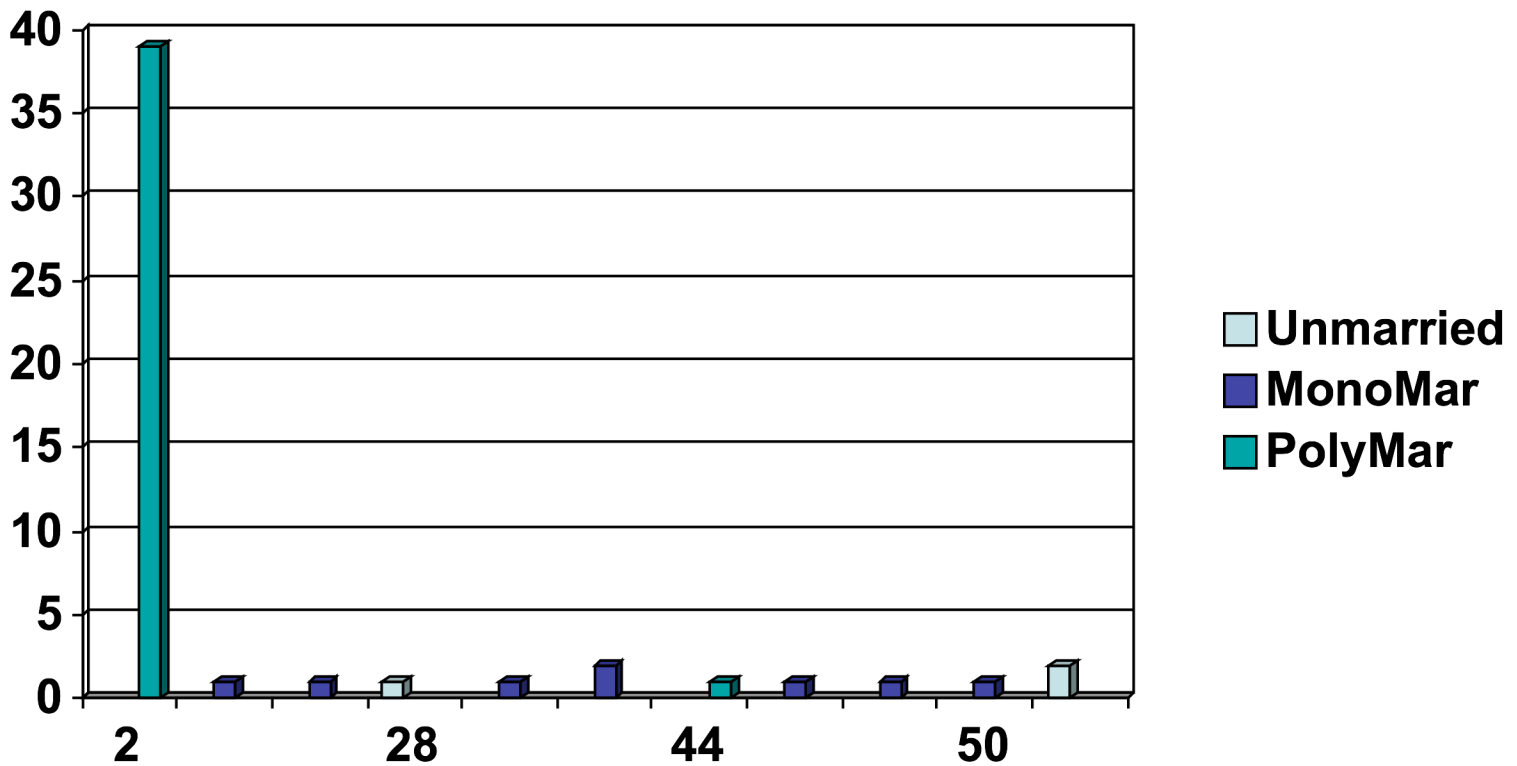
Parameter	Estimate	Chi-sq p-value
Intercept	-2.7519	0.0058
Age	0.2181	0.1645
Sex	0.4179	0.2482
Married	1.4170	<0.0001

Ombivango—partner exchange = 15



Parameter	Estimate	Chi-sq p-value
Intercept	-3.1890	0.0392
Age	0.1371	0.8724
Sex	0.9968	0.5729
Married	2.0830	<0.0001

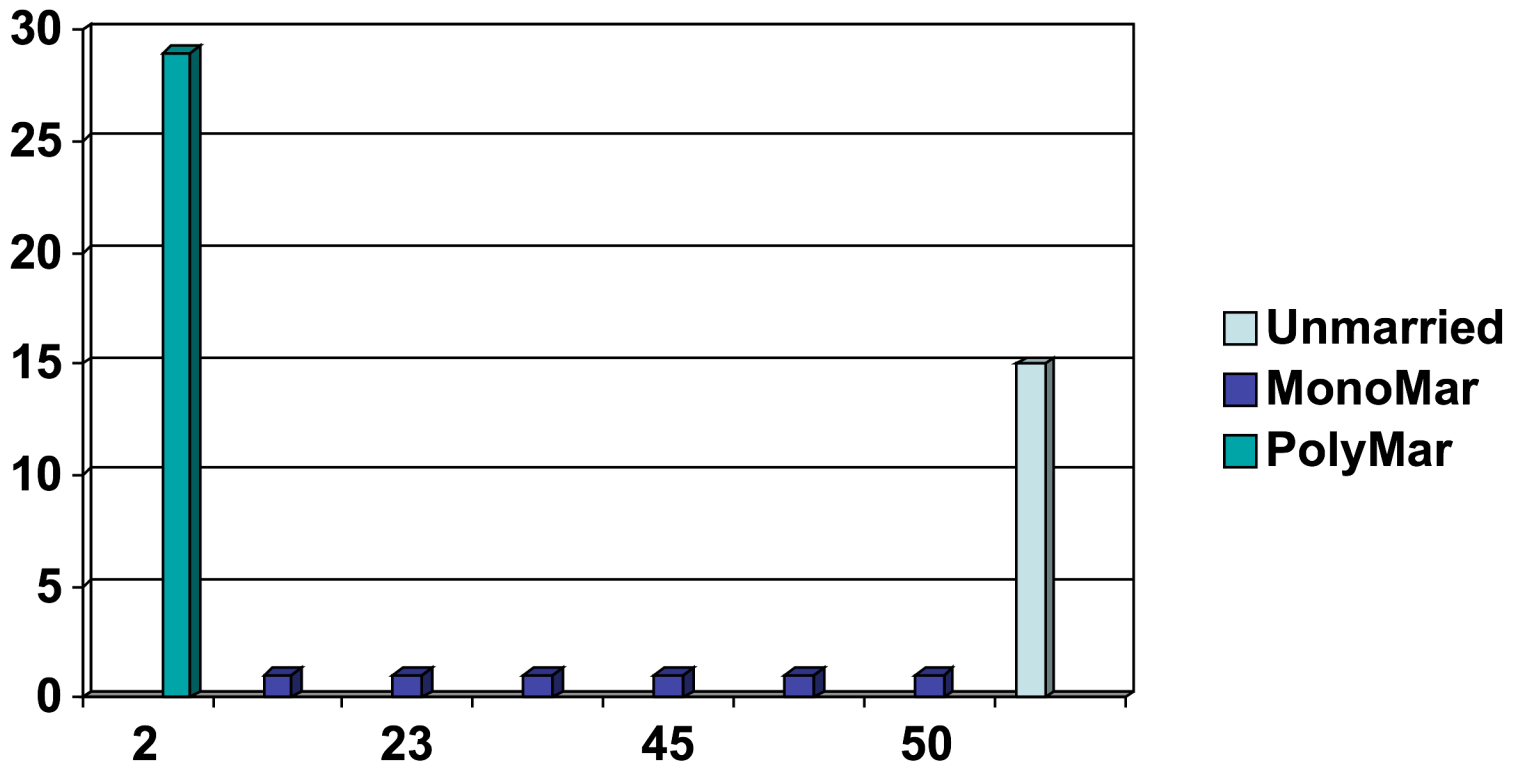
Otjikoyo—partner exchange = 25



Parameter	Estimate	Chi-sq p-value
Intercept	-0.7443	0.7588
Age	-0.5687	0.2230
Sex	2.2187	0.1037
Married	2.1625	0.0323

Parameter	Estimate	Chi-sq p-value
Intercept	-9.3614	0.0161
Age	2.1747	0.0470
Sex	2.2828	0.0747
Married	8.3067	0.0007
Age*married	-1.9319	0.0063

Otjikoyo—partner exchange = 15



Parameter	Estimate	Chi-sq p-value
Intercept	-1.0506	0.6085
Age	-0.3740	0.3437
Sex	2.4382	0.3437
Married	1.2961	0.1295

Parameter	Estimate	Chi-sq p-value
Intercept	-8.7368	0.0075
Age	2.0731	0.0242
Sex	2.4954	0.0204
Married	6.7764	0.0009
Age*married	-1.7326	0.0037