bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Inferring restrictions in the temporal order of mutations during tumor progression: effects of passenger mutations, evolutionary models, and sampling

Ramon Diaz-Uriarte
Dept. Biochemistry, Universidad Autónoma de Madrid
Instituto de Investigaciones Biomédicas "Alberto Sols" (UAM-CSIC)
Madrid, Spain
ramon.diaz@iib.uam.es
rdiaz02@gmail.com
http://ligarto.org/rdiaz

2014-5-27

Abstract

In cancer progression, fixation of some driver mutations (those causally involved in the disease) can depend on the presence of other drivers. The majority of mutations present in cancer cells, however, are not drivers but passenger mutations that are not involved in disease progression.

Several methods have been developed to discover the restrictions in the temporal order of accumulation of driver mutations from cross-sectional data, but the few available comparisons of their performance assume that drivers are known, and have not examined the effects of sampling.

Here I conduct a comprehensive comparison of the performance of all available methods. In contrast to previous work, I embed order restrictions within evolutionary models of tumor progression that include passengers and drivers. This allows me to asses the effects of having to filter out passengers, of sampling schemes, and of deviations from order restrictions.

No combination of method, filtering, and sampling excels in all metrics: rankings depend on how performance is measured. However, poor choices can lead to large errors in all metrics, and when drivers are not known, performance of all methods degrades. One filtering method emerges as the best overall. In most scenarios, Oncogenetic Trees are superior to Conjunctive Bayesian Networks and Progression Networks. Single cell sampling provides no major advantage, but sampling in the final stages of the disease vs. sampling at different stages can have severe effects depending on the evolutionary model. Evolutionary model and deviations from order restrictions can have major, and counterintuitive, interactions with other factors that affect performance.

This paper provides practical recommendations for using these methods with experimental data, and shows that it is both possible and necessary to embed assumptions about order restrictions and the nature of driver status within evolutionary models of cancer progression to evaluate the performance of inferential approaches.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

1 Introduction

Cancer progression is caused by the sequential accumulation of somatic mutations, including changes in copy number (structural variants), single nucleotides (SNP variants) and DNA methylation patterns (Hanahan and Weinberg, 2011) during the life of an individual. Among the mutations causally responsible for the development of cancer (drivers) not all possible orders of accumulation seem equally likely, since the fixation of some mutations can depend on the presence of other mutations. Understanding the restrictions in the temporal order of accumulation of driver mutations could be very relevant for cancer prevention and treatment as it would allow identifying critical events (Cheng *et al.*, 2012; Gerstung *et al.*, 2011; Longerich *et al.*, 2012; Sprouffske *et al.*, 2011), but these restrictions remain poorly known (Gerstung *et al.*, 2011; Raphael and Vandin, 2014).

In this context, a variety of methods have been developed to try to infer the possible restrictions in the order of accumulation of these driver mutations from cross-sectional data; a brief review is provided next, including some recent developments, but see more extensive reviews in Hainke *et al.* (2012); Radmacher *et al.* (2001). Desper *et al.* (1999) introduced the oncogenetic tree (OT) as an extension of the linear path model (e.g. Vogelstein *et al.*, 1988): in OTs progression starts from a common (non-altered) root, and branches out, so that there are several mutational pathways that can be observed simultaneously. OTs, by virtue of being trees, can only model order restrictions where an event depends on its single parent. Another early model are distance-based trees, from Desper *et al.* (2000) (see also von Heydebreck *et al.*, 2004); these are also trees, but their meaning is rather different, since the observed mutations are only placed in the leaves or terminal nodes of the tree, and the internal nodes are unobserved and unknown events, which precludes an interpretation in terms of order restrictions like "mutation A is required for mutation B". Youn and Simon (2012) developed a method to identify the order of mutations allowing for the sequence of alterations to differ between subjects; their model, however, does not explicitly return order restrictions of events. Models that do not try to infer order restrictions will not be considered further in this paper.

Beerenwinkel *et al.* (2007a) proposed Conjunctive Bayesian Networks (CBNs) as a generalization of oncogenetic trees: these are graphs where the occurrence of a mutation can depend on the occurrence of two or more parents (i.e., a *conjunction*). The disease progression models of OTs and CBNs assume that a mutation can only occur if the preceding parent mutation(s) in the graph have occurred, what Farahani and Lagergren (2013) call monotonicity. Thus, for driver genes, under the strict OT and CBN models it would be impossible to observe a genotype that is not compatible with the relations specified in the graph. Less restrictive models for tumor progression have been proposed. A very general Markov model was proposed in Simon *et al.* (2000), and was referred to as directed acyclic graphs by Radmacher *et al.* (2001); Simon *et al.* (2000). Bulashevska *et al.* (2004) used general Bayesian Network approaches. The model in Hjelm *et al.* (2006) also allows for mutations to occur even if no other aberrations have occurred. The model in Raphael and Vandin (2014), like the one of Hjelm *et al.* (2006), simultaneously tries to find modules or pathways and their order restrictions (but note that CBNs, OTs, and similar methods can be directly applied to module/pathway data, provided those data are partitioned into predefined pathways before the analysis; e.g., Cheng *et al.*, 2012; Gerstung *et al.*, 2011).

Having a single graph means having a single set of restrictions that is common to all individuals, but that does not mean that all cells follow the same path (so the actual genotypes and their paths can be quite diverse under one graph). Mixtures of OTs (Beerenwinkel *et al.*, 2005) are one further generalization of OTs where disease progression is modeled allowing for different order restrictions in different subsets of individuals, each one modeled as an OT. By using a star as one of the trees in the mixture, these models can also account for any mutation occurring without its parent(s) having occurred. Later, Tofigh *et al.* (2011) developed the HOT and mixture of HOTs as a generalization of OTs and their mixtures. In this paper I restrict attention to finding a single graph, the approach most widely used in the literature, and one which seems to work even when there are mild departures from the single-graph assumption (Sweeney *et al.*, 2009, but see Sprouffske *et al.*, 2012). Recently, Cheng *et al.* (2012) developed a method that attempts to find

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

the order of events taking into account the evolutionary dynamics of mutation accumulation. And Farahani and Lagergren (2013) have proposed a general method, DiProg, for learning what they call Progression Networks, which include OTs, CBNs, as well as several other special types of Bayesian Networks, and that can incorporate deviations from monotonicity.

Most of the above are general methods, and can be applied to different kinds of data including cytogenetic (e.g., the first description of OTs by Desper *et al.*, 1999), gene mutation, and pathway alteration data (e.g., Gerstung *et al.*, 2011). This versatility, coupled with the increasing wealth of cross-sectional data available, provides an excellent opportunity to try to understand the still largely unknown details of the order of mutations. However, in spite of the relevance of the problem, there are very few systematic comparisons of method performance, and they do not provide a clear and robust answer to the question of method choice.

Applied usage of the above methods faces at least three major additional problems. First, most of the mutations present in cancer cells are not *driver* mutations, but *passenger* mutations not responsible for the development of cancer (e.g., Greenman *et al.*, 2007; Tomasetti *et al.*, 2013; Vogelstein *et al.*, 2013; Wood *et al.*, 2007). Passenger mutations can show a non-negligible frequency because they "hitchhike" on drivers (Greaves and Maley, 2012; Merlo *et al.*, 2006). Unless we know what mutations are drivers, the presence of passengers in our data sets requires forces us to use some filtering procedure to select which mutations (or, generally, alterations) to use with (or to pass on to) the methods to infer order restrictions. However, the simulations in the only comparison of methods (Hainke *et al.*, 2012), as well as in the original descriptions of new methods (e.g., Farahani and Lagergren, 2013; Gerstung *et al.*, 2009; Szabo and Boucher, 2008), have all been conducted assuming that the identity of the driver mutations is known. Virtually all papers that try to infer order restrictions, including methodological papers, rely on simple frequency-based selection or filtering procedures (e.g., Desper *et al.*, 1999; Diep *et al.*, 2006; Gerstung *et al.*, 2011; Gunawan *et al.*, 2007; Hjelm *et al.*, 2006; Rieker *et al.*, 2005; Sakoparnig and Beerenwinkel, 2012; Szabo and Boucher, 2008; von Heydebreck *et al.*, 2004) to select which genes to use, but the effects of these filtering approaches on the performance of the methods to infer order restrictions are completely unknown.

Second, attention to sampling decisions is largely missing from the literature: simulations that examine method performance (e.g., Farahani and Lagergren, 2013; Gerstung *et al.*, 2009; Hainke *et al.*, 2012; Szabo and Boucher, 2008) obtain genotypes directly from the generative models of the graphs but, except when we use single cell sampling, our experimental data are from samples that aggregate over many cells and the joint and marginal frequencies of mutations of those aggregates can depend not only on the aggregation *per se* but also on when we sample (due, for example, to the clonal expansion episodes).

Finally, development and evaluation of methods of reconstruction of order restrictions are conducted without consideration for the evolutionary model of tumor progression (but see Cheng *et al.*, 2012 and Discussion). This problem is highlighted by Sprouffske *et al.* (2011): referring to oncogenetic tree models they say (p. 1136) " This is not an evolutionary model because the oncogenetic tree does not represent ancestral relationships within a neoplasm but rather a summary of the observed co-occurrences of mutations across independent neoplasms". This lack of consideration for the evolutionary model is also unfortunate since it does not provide a clear mechanistic interpretation of deviations from the restrictions encoded in the graph. Of particular interest is the monotonicity restriction (a mutation in a driver gene can only be observed if the preceding parent mutations in the graph have occurred), because deviations from it can easily arise when a mutation behaves as a driver or as a passenger depending on the genetic context —i.e., depending on which other genes are mutated (Greaves and Maley, 2012; Yap *et al.*, 2012).

Direct simulation of data from the generative models of OTs, CBNs, and Progression Networks cannot be used to address any of those three problems (passengers, sampling, deviations from monotonicity). However, it is possible to incorporate the order restrictions encoded in CBNs, OTs, and other models, into plausible evolutionary models of tumor progression (in fact, Reiter *et al.*, 2013 have developed a simulation tool that incorporates simple order restrictions among four drivers; see Discussion). If we model together drivers (with possible restrictions) and passengers we can address the consequences of having to filter drivers from passengers. Incorporating order

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Factor	Description	Values
Model	Model of cancer progression	exp, Bozic, McF_4, McF_6
sh	Penalization of deviations from monotonicity	0, Inf (for ∞)
True Graph	The true graph. All possible combinations of Number of nodes and Conjunction	11-A, 11-B, 9-A, 9-B, 7-A, 7-B
Number of nodes (NumNodes)	Number of genes or alterations	11, 9, 7
Conjunction	Whether or not the graph has conjunctions	Yes, No
Sample size (S.Size)	Number of samples used for reconstructing the graph	100, 200, 1000
Sampling time (S.Time)	When the sample is taken	Last, unif (for uniform)
Sampling type (S.Type)	How tissue is collected	singleC (for single cell), wholeT_0.5 (whole tumor, detection threshold=0.5), wholeT_0.01 (whole tumor, detection threshold=0.1)
Filtering	Method for selecting drivers, of filtering passengers, when the true drivers are not known	S1, S5, J1, J5 (for frequency of Single event and Joint frequency of events, with thresholds 1% and 5% respectively)
Method	Method for reconstructing the oncogenetic tree/CBN model	CBN, CBN-A, DiP, DiP-A, OT, OT-A

Table 1: Factors considered and their levels or possible values, together with the acronyms used through the text. The within-data set factors, Filtering and Method (see text), are shown in italics. All other factors are among-data set factors. Sampling scheme, used through the text, refers to when (S.Time) and how (S.Type) we sample.

restrictions within evolutionary models would also allow us to address two questions of immediate practical relevance related to data collection: should we try to use single cell sampling now that it is becoming a realistic possibility (Eberwine *et al.*, 2013) instead of whole tumor sampling? and would it be better to try to use samples collected in the final stages of the disease vs. using samples collected also at intermediate stages? Finally, using explicit evolutionary tumor growth models also allows us to examine the consequences of deviations from the monotonicity restriction and the genetic context dependence of driver status.

In this paper I incorporate the order restrictions into evolutionary models to address how the performance of all available methods for inferring order restrictions is affected by: a) passenger mutations that lead to uncertainty about the identity of the true drivers and the need to use filtering approaches; b) sampling choices (when and how and how many to sample); c) type of underlying true graph, including presence/absence of conjunctions; d) deviations from the order restrictions encoded in the graphs (monotonicity); e) evolutionary model of tumor progression.

2 Methods

2.1 Experimental design

Details of each factor examined are discussed below, but Table 1 provides an overview of the main factors, and Figure 1 a schema of all the steps. We will deal separately with two different scenarios: one where we know the true identity of the drivers, which we will call "Drivers Known", and another scenario that replicates the common situation where the data includes both passengers and drivers and we do now know with certainty which is which, a scenario we will refer to as

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

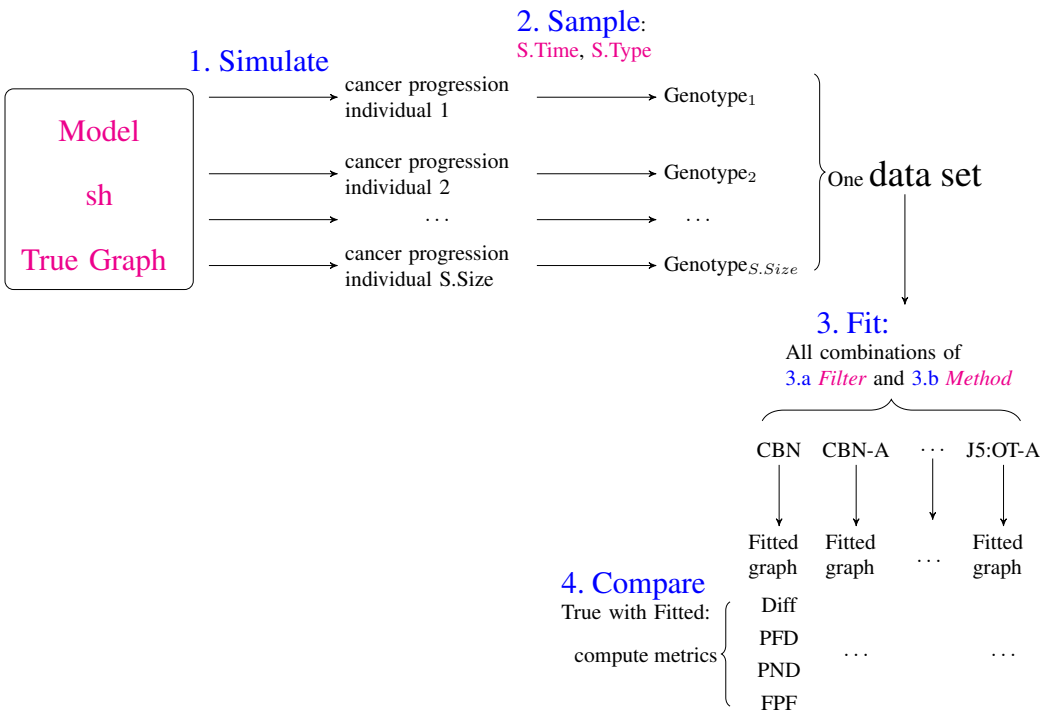

Figure 1: Schematic representation of the key steps of design and analysis, and illustration of the within- and among-data set factors. Terms in magenta are those in Table 1, and terms in italics, as in Table 1, correspond to within-data set entries. Terms in blue denote the main steps, with numbers indicating chronological order (Filter and Method are both steps and entries in the table). The process illustrated here was repeated 20 times for all possible compbinations of Model, sh, True Graph, S.Time, S.Type, S.Size.

"Drivers Unknown". The "Filtering" factor is only relevant for the "Drivers Unknown" scenario. When referring to the restrictions I will use the term "graphs" (e.g., following Desper *et al.*, 1999, their Figure 1). "Graph", therefore, refers to the structure that encodes the order restrictions and I will reserve the term "tree" for graphs that have no conjunctions. All the graphs were analyzed with all methods (CBN, CBN-A, OT, OT-A, DiP, DiP-A), as shown in the table and explained below in section 2.6.

Method (Drivers Known scenario) or Filtering by Method combinations (Drivers Unknown scenario) were applied to a data set: a matrix of individuals or subjects by genes (i.e., a matrix of genotypes). The same data set can be analyzed with different Methods (or different Filtering by Method combinations) but for other factors (e.g., Model) different settings of the factor (and reruns of the same settings with different seeds of the random number generator) generate different data sets. This allows us to use an experimental design with among- and within-data set factors so as to examine the effect of Method and Filtering controlling for possible among-data set variation (as explained in Sections 2.7.3 and 2.7.4), and so as to minimize computational cost. For factors Model, sh, Graph, Conjunction, S.Size, S.Type, and S.Time, the among-data set factors, I used a full factorial design (thus, $864 = 4 * 2 * 3 * 2 * 3 * 2 * 3$, among-data set factor combinations). For every combination, I used twenty independent replicate data sets. Each of the twenty replicate data sets was analyzed with every Method, or every Filtering by Method combination (the within-data set factors) to fit a graph to the data (i.e., to try to infer the order restrictions among events). Therefore, a total of $864 * 6 = 5184$ or $864 * 6 * 4 = 20736$ factor combinations for the Drivers Known and Drivers Unknown scenarios, respectively, were examined. Every data set was obtained by independently sampling different (and independently generated) simulated tumor trajectories, according to the settings of the among-data set factors. For instance, if sample size was set to 1000, I simulated 1000 tumor progression trajectories as specified by the settings of Model, sh, and True Graph, and sampled each of those trajectories as specified by the settings of S.Time and S.Type (see Figure 1). This process was repeated at every one of the 864 among-data set factors

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Model	Birth rate (b_j)	Death rate (d_j or D_N)	Mutation rate (per gene per unit time)	Cancer reached if
Bozic	1	$(1-s)^j(1+s_h)^p$	10^{-5}	$> 10^9$ cells
exp	$(1+s)^j(1-s_h)^p$ (+)	1	$b_j * 10^{-7}$	$> 10^9$ cells
McF_4	$(1+s)^j/(1+s_h)^p$	$\log(1+N/K)$	$5 * 10^{-7}$	Number of drivers ≥ 4
McF_6	$(1+s)^j/(1+s_h)^p$	$\log(1+N/K)$	$5 * 10^{-7}$	Number of drivers ≥ 6

Table 2: Main parameters for each of the tumor progression models. j is the number of drivers with their dependencies met, and p the number of drivers with dependencies not met. In all cases $s = 0.1$. s_h is set to either 0 (so it has no effect) or ∞ (so fitness of that clone is 0). N: population size. $K = 2000$. $^+$ This is really $b_j = \max(0, (1+s)^j(1-s_h)^p)$.

(and, thus the results shown here are based on 7.49 million simulated trajectories $= 4 * 2 * 3 * 2 * 3 * 2 * 20 * (1000 + 200 + 100)$).

2.2 Evolutionary models and simulation

Simulated data for the analysis were generated using different models of tumor progression. The purpose of using several models is not to compare models of tumor development, but to use a range of plausible ones so that we can examine how the true underlying model could impact the inference of restrictions, and so that we can embed the restrictions within plausible models of clonal expansion. Two of the models used, called here "Bozic" (as it is based in Bozic *et al.*, 2010) and "exp" have no density dependence and lead to exponential growth. The second set of models, called "McF_4" and "McF_6", are based in McFarland *et al.* (2013) and lead to logistic-like behavior, as death rate depends on total population size. Table 2 summarizes the main parameters used for the tumor progression models. Details about the models and choice of model parameters are provided in *Supplementary Material Section* 2.1.

To simulate data, I have used BNB, the fast stochastic algorithm of Mather *et al.* (2012). This method is closely related to the Gillespie algorithm and the next reaction method (Gibson and Bruck, 2000), but can lead to significant speed improvements. This algorithm is exact when birth, death, and mutation rates are constant between consecutive mutations, as in the "exp" and "Bozic" models. For the McFarland model (McFarland *et al.*, 2013), where death rate is density dependent, the approach in Mather *et al.* (2012) does not provide an exact simulation, but can be used to provide a very accurate approximation, as discussed by Mather *et al.* (2012). Details about the usage of BNB are provided in *Supplementary Material Section* 2.2. Examples of simulated trajectories for each model are shown in *Supplementary Figure* 3.

2.2.1 Deviations from monotonicity and genetic context dependence of driver status: sh

Genetic context dependence of driver/passenger status (Greaves and Maley, 2012; Yap *et al.*, 2012) and deviations from monotonicity (i.e., from the order of events implied by the graph of the oncogenetic model) can be closely related, and affect the performance of methods to infer order restrictions. A mutation in a driver gene for which all the preceding required mutations have occurred (i.e., a mutation in a gene that has its dependencies satisfied) will lead to an increase in fitness (through its increase of the value j, for number of drivers, as shown in Table 2). What about mutations in driver genes that do not have their dependencies satisfied? We can formulate the problem in a general context by using the terminology in Datta *et al.* (2013). Enforcing monotonicity is equivalent to considering such a mutation as a mutation in an essential housekeeping gene, which can be modeled setting s_h, in the notation of Datta *et al.* (2013), to ∞ (so fitness of such clones is zero). Deviations from monotonicity can arise, however, if such mutation is similar to a passenger mutation: it confers no fitness benefits (and if it has no deleterious effect $s_h = 0$, similar to setting $s_p = 0$ in McFarland *et al.*, 2013). Of course, in none of these cases would the value of j be increased (a driver only increases fitness if its dependencies are satisfied). In the simulations reported here I considered two extreme scenarios: a) no deviations from the graph of the oncogenetic

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

model are allowed, which I will refer to as "sh=Inf" (from ∞); b) drivers without dependencies satisfied are equivalent to passengers with no deleterious effects, which I will refer to as "sh=0". Note that the implementations I used to infer CBN and OT incorporate errors (Gerstung *et al.*, 2009, 2011; Szabo and Boucher, 2008) and the OT model explicitly allows for errors due to the occurrence of genetic events outside the model implied by the graph of the oncogenetic model (Szabo and Boucher, 2002). DiP, the method to infer Progression Networks models of Farahani and Lagergren (2013), explicitly incorporates deviations from monotonicity with the parameter ε.

2.3 True graphs, number of drivers, and number of passengers

Six different true graphs have been used, three of them with conjunctions (i.e., CBN-like) and three of them without conjunctions (i.e., OT-like), where the trees without conjunctions are derived from the graphs with conjunctions by removing conjunctions. The graphs have 7, 9, and 11 nodes. The number of nodes of the graphs targets the range of nodes commonly considered in studies that try to reconstruct graphs from real cancer data: 10, 11, and 12 in Gerstung *et al.* (2009), 7 to 11 (including gene and core pathways) in Gerstung *et al.* (2011), 7 in Desper *et al.* (1999), 11 and 12 in Sakoparnig and Beerenwinkel (2012), 8 in Sweeney *et al.* (2009), 7 (modules) in Hjelm *et al.* (2006), 9 in Jiang *et al.* (2007), 17 in Longerich *et al.* (2012) and Bulashevska *et al.* (2004), 12 in Pathare *et al.* (2009), 6 and 13 in Simon *et al.* (2000), 12 in Radmacher *et al.* (2001). The size of graphs was limited to 11 because CBN cannot deal with more than 14 events or nodes (see also Sections 2.5 and 4) and we need to allow for the possible selection of more events than 11 when Drivers are Unknown. The graphs are shown in *Supplementary Figure* 2, and we will refer to them by the number of events using post-fix A for conjunction and B no conjunction. Graph 11-A is the same as Poset 2 in Gerstung *et al.* (2009) (see their Figure 2A), and Graph 7-A is the same as the estimated graph for pancreatic cancer in Gerstung *et al.* (2011) (their Figure 2B). Graph 9 was created so as to contain an intermediate number of both nodes and conjunctions between the previous two graphs. In addition to the number of nodes and presence/absence and number of conjunctions, the six graphs used differ in other features (such as depth, total number of edges, existence or not of isolated nodes or subgraphs, existence or not of a single parental node, indegree of conjunctions, and outdegree).

Graphs with 11, nine, and seven drivers generate clones with between two and six drivers (see also *Supplementary Figure* 3), a range which is well within the range of drivers considered in the literature: although some authors, such as Datta *et al.* (2013) and Beerenwinkel *et al.* (2007b) examine scenarios with 20 drivers, most papers focus on much smaller numbers of drivers (Bozic *et al.*, 2010; McFarland *et al.*, 2013; Sprouffske *et al.*, 2011) and recent reviews suggest that the number of drivers in the cells of most tumors lies between two and six (McFarland *et al.*, 2013; Vogelstein *et al.*, 2013). Regarding number of passengers, it is now widely accepted that most mutations in cancer cells are passengers (Bozic *et al.*, 2010; Greenman *et al.*, 2007; Sjoblom *et al.*, 2006; Tomasetti *et al.*, 2013; Vogelstein *et al.*, 2013; Wood *et al.*, 2007). When considering the scenario where drivers are not known, I set the proportion of passengers to drivers constant, so that there are four passengers for every driver, a range within that considered in the literature. Our scenario is also relevant if the actual number or fraction of passengers is much larger, but many of those passengers can be excluded *a priori* based on other information, so that they are never considered as candidates for the process of filtering data and inferring graphs.

2.4 Sample size and sampling type and time

Sample size (S.Size) was set to three possible values: 100, 200, 1000. The values considered in other studies, both empirical and methodological, vary widely (e.g., 100, 400, and 800 in Sakoparnig and Beerenwinkel (2012); 83 to 95, plus a pool of 268 in Gerstung *et al.* (2011); 50, 100, 200, 500, and 1000 in Hainke *et al.* (2012); 971 in Sweeney *et al.* (2009); 887 in Longerich *et al.* (2012)). The set of 100, 200, and 1000 cover a likely range of sample sizes and will allow us to compare the magnitude of the effects of sample size with those of other factors. **Sampling time (S.Time)** refers to when sampling occurs. S.Time = last means that samples were collected at the

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

end of the simulation (at the end of cancer progression). S.Time=unif (for uniform) means that sampling time was uniformly distributed between the start and end of the simulation (so t_{tot} *sensu* Desper *et al.*, 1999 or T_s in Gerstung *et al.*, 2009, have this uniform distribution). Uniform sampling is a very simple model for obtaining cross-sectional samples of patients at different stages. Sampling uniformly between time zero and the final stages of the disease is, of course, unrealistic, but I used this type of sampling because it provides a stark contrast with sampling at the end of the disease. **Sampling type (S.Type)** refers to whether single cell or whole tumor tissue is used, and three values have been used for this factor. When S.Type = singleC (single cell), a simulation provides the genotype of one single cell (or, equivalently, one single clone), where the probability of selecting a clone is proportional to its abundance. When using whole tumor sampling, and as in Sprouffske *et al.* (2011), a biopsy is the entire tumor, but whether a gene is considered mutated or not can depend on the detection threshold, and here I used two levels: 0.5 (like Sprouffske *et al.*, 2011) and 0.01, meaning that a gene is considered mutated if it is mutated in 50% or 1%, respectively, of the cells. Of course, it is unlikely that any study using single cell would take a single sample from a patient; however, in this study we focus on cross-sectional data, and single cell sampling is the type of sampling that leads to data most similar to the type of data obtained when we simulate using the generative model of the underlying graph (as done, for instance, in Gerstung *et al.*, 2009; Hainke *et al.*, 2012; Szabo and Boucher, 2008). Moreover, single cell sampling and whole tumor sampling, as used here, can be considered two extremes in the range of sampling possibilities. Likewise, a detection threshold of 0.01 is probably unrealistically low but that setting is used because it combines the capacity of detecting very low frequency co-occurring events (as in single cell sampling) with summing over distinct cells (which could lead to problems similar to the ecological fallacy). The sampling type schemes used here ignore any possible spatial structure and tissue architecture (e.g. Vermeulen *et al.*, 2013), not because they are considered irrelevant, but because none of the evolutionary models considered here incorporate it (but note that the uniform sampling scheme can sometimes be equivalent to incorporating spatial structure, if that spatial structure is correlated with time).

2.5 Filtering

When the identity of the driver genes is not known, it is often necessary to select genes before fitting the data to the graph (i.e., before trying to infer the order restrictions). Some studies that deal with chromosomal abnormalities have used the methods of Brodeur and collaborators or Taetle and collaborators, to try to locate non-random breakpoints (see discussion in Radmacher *et al.*, 2001; Simon *et al.*, 2000) but these methods are not directly applicable to other types of data nor to our simulations. Other authors that deal with chromosomal abnormalities, or that use mutation data, have used one of the following general approaches to decide which alterations to analyze: a) selecting the most frequent mutations, either by setting a minimal number as in Szabo and Boucher (2008), Gunawan *et al.* (2007), and Hjelm *et al.* (2006), where the seven, 13, or 25, respectively, most frequent alterations are used, or setting a minimal frequency such as in Gerstung *et al.* (2011), Diep *et al.* (2006), Rieker *et al.* (2005), von Heydebreck *et al.* (2004) where the threshold is set at 5%, 5%, 10%, 10%, respectively; b) selecting the largest set of events so that every pair of events is observed at least k times, as in Szabo and Boucher (2002), Desper *et al.* (1999) where the threshold is five times, out of 124 and 117 cases, respectively (this method can be implemented searching for the largest weighted clique, as in Desper *et al.*, 1999).

The key difference between these two filtering procedures, therefore, is that the second uses the joint occurrences of pairs. To comprehensively incorporate common uses, I used four filtering procedures: two of them only consider the marginal frequency of each single event, and I use an "S" to denote "frequency of Single event", and the other two take into account joint occurrences, and a I use "J" to denote "Joint frequency of pairs of events". The procedures are S1, that selects any mutation with a frequency larger than 1%, S5 where the threshold is 5%, J1 that selects the largest set of events so that every pair of events is observed at least in 1% of the cases and J5, where the threshold is 5%. In the rare case where a filtering procedure returned more than 12 mutations, the 12 most common were selected.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

2.6 Fitting data to graphs. Methods and software for inferring order restrictions: CBN, DiP, OT

I have used three types of methods to infer order restrictions from data: methods that infer OTs, methods that infer CBNs (which should also be able to reconstruct OTs), and methods that infer Progression Networks (and, thus, should also be able to reconstruct OTs and CBNs). Each method, when applied to a data set, returns what we will refer to as a "fitted graph" (see also Figure 1). For OTs I used the R package Oncotree (Szabo and Pappas, 2013) with its default settings. Some of the analysis were rerun (see Discussion and Supplementary Material) with the implementation available in the BioConductor package Rtreemix (Bogojeska, 2014; Bogojeska *et al.*, 2008a). For CBNs as detailed in Gerstung *et al.* (2009) I used the software from Gerstung *et al.* (2011). I used the same default settings for temp (1) and steps (number of nodes^2) and started the simulated annealing search for the best poset from an initial linear poset as in Gerstung *et al.* (2011). For Progression Networks I used the DiProg program (the method we call DiP) from Farahani and Lagergren (2013) to fit monotone networks (option "MPN"), choosing the best k from 1 to 3 (and the results reported here have $\varepsilon = 0.05$). Further details about software versions and parameters used for all methods are provided in the Supplementary Material.

Other methods have been described in the literature, but I have not been able to use them here. The method in Sakoparnig and Beerenwinkel (2012) is too slow (analysis of data sets of 200 cases exceeding 4 hours) to be used in more than 100000 runs, as in this paper. The methods in Cheng *et al.* (2012) and Tofigh *et al.* (2011) have no software available. Therefore, this paper includes all currently existing approaches for which software is available.

It is important to mention here that the methods reported differed greatly in speed: the median and mean execution times, over all 172800 analysis performed by each family of methods, were 0.045 and 0.07 seconds for OT, 3.89 and 12.60 seconds for DiP, but 31 and 1127 seconds for CBN. In addition, one of the methods examined (DiProg: DiP/DiP-A) currently depends on IBM's CPLEX ILOG library, which not only is not open source but has a severely restrictive license.

2.6.1 CBN-A, OT-A, DiP-A

In some cases one or more mutations were present in all or almost all of the samples. Even if these are driver mutations on which all other events depend, events with a frequency of 1 are often removed from the graph (e.g., by the OT method) or placed as nodes that descend directly from Root and that have no descendants. This problem is particularly severe with Graphs 7A and 7B (e.g., see *Supplementary Figure* 56), but can affect all graphs (especially under the McF_6 model). To try to minimize this problem, we can augment the data by adding "pseudosamples" that have no mutations in any gene. Adding "pseudosamples" does not amount to knowing anything about the order of events, nor the truth about which genes are drivers or not (and in the Drivers Unknown scenario I always augmented after the filtering step). Data augmentation only requires being able to differentiate between presence and absence of a genetic alteration, mutation, or aberration, which is always assumed in these analyses. In this paper, "CBN-A", "DiP-A", and "OT-A", refer to using CBN, DiP, or OT on data that has been augmented by adding to it another 10% of samples filled with zeroes (0 is the code that denotes no alteration).

2.7 Analysis

There are two questions that we want to address: a) what procedures (choice of Method, Filtering, S.Time, and S.Type) are "best" (for reconstructing the underlying true graph from the data), so that we can choose a course of action when faced with new data; b) what factors have an important effect on performance, even if they are not under user control, so that future research can focus on them. The first question is most straightforwardly addressed by comparing (via statistical tests of differences) and ranking the available options (combinations of Method, Filtering, and Sampling scheme). The second question is best addressed with statistical modeling that focuses on identifying factors with relevant effects. Of course, results from each type of analysis complement each other, and should be coherent. The approaches used below reflect these two questions and are

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

based on very different procedures and assumptions. Below I detail the different analyses, after explaining how performance was measured.

2.7.1 Metrics: measuring performance

I consider here that the main goal of most studies is the reconstruction of the topology of the graph, which is what captures the order restrictions (e.g., Desper *et al.*, 1999; Farahani and Lagergren, 2013; Szabo and Boucher, 2008) . There is no single metric that can fully characterize the performance of these methods, and therefore I have used four metrics that capture their behavior along different dimensions. One is a global score of the difference between the fitted graph and the true graph, whereas the other three are measures of classification or diagnostic performance common in medical testing and machine learning (Davis and Goadrich, 2006; Pepe, 2003) that focus on the fractions or proportions across specific rows or columns of the confusion matrix (where entries in that matrix are commonly called "true positives", "false positives", "false negatives", and "true negatives"). Thus, the dimensions measured by each of these four metrics relate to concepts already familiar to researchers, and arguably capture the key features of the methods' behavior. As we will see below, using these four different metrics is also key to understanding some of the major differences between methods.

Diff is the sum of the absolute value of the entries in the matrix of the **Difference between the adjacency matrices** of the true (T) and fitted (F) graphs; this is the square of the "usual" Frobenius norm (Gentle, 2007) of that matrix difference, and is the same as the "graph edit distance" of Hainke *et al.* (2012). The **Proportion of False Discoveries (PFD)** is defined as $\frac{\text{\# of relations in } F \text{ but not in } T}{\text{\# of relations in } F}$. Following Gerstung *et al.* (2009, 2011), we define "relations" as the transitive closure of "cover relations". For instance, suppose a graph with $A \rightarrow B \rightarrow C$ (where $A \rightarrow B$ means that A needs to occur for B to occur); the cover relations are $A \rightarrow B$ and $B \rightarrow C$, but we also include $A \rightarrow C$ in the relation. As in Gerstung *et al.* (2009, 2011), we do not include the root node when finding cover relations and their transitive closure (in contrast to what is done in the computation of Diff). The numerator is, therefore, the number of false positives (FP). The **Proportion of Negative Discoveries (PND)** is defined as $\frac{\text{\# of relations in } T \text{ but not in } F}{\text{\# of relations in } T}$. The **False Positive Fraction (FPF)** is defined as $\frac{\text{\# of relations in } F \text{ but not in } T}{\text{\# of relations not in } T}$. In both PND and FPF the numerator is the number of false negatives (FN). Computation of # of relations not in T and further details for all metrics are provided in the Supplementary Material.

2.7.2 Overall ranking of Filtering, Method, and Sampling scheme

To understand what combinations of Method, Filtering, and Sampling scheme are best, I ranked them, averaging the ranks over (subsets of) the other factors (i.e., marginalizing over other factors). As "best" can depend on metric, each metric has to be dealt separately. More precisely, for each metric separately, I ranked the 36 combinations of Method by S.Time by S.Type (for the Drivers Known scenario) or the 144 combinations of Filtering by Method by S.Time by S.Type (for the Drivers Unknown scenario) in each of the 144 factor combinations defined by Graph by Model by sh by S.Size. Thus, for each metric, there were 144 separate rankings (where we ranked 36 items in the Drivers Known scenario and 144 items in the Drivers Unknown scenario). Ranking was done using the median (over the 20 replicates) of the metric. Then, for each metric, I obtained the average rank over subsets of the 144 combinations and the averaged ranks were then ranked to obtain the final rankings for each metric (e.g., Table 3 shows, on the left four columns, the ranked average ranks over the 72 combinations of Number of Nodes by Model by sh by S.Size when there are conjunctions and, on the right, the ranks over those 72 combinations when there are no conjunctions). Similar to Narendra *et al.* (2011), because the maximum and minimum ranks may differ between scenarios, the ranks were normalized before averaging.

This procedure does not take into account the repeated usage of the same data set for each of the four/sixteen methods and, thus, would not be valid if we tried to estimate standard errors of differences between, say, methods, but we are using it simply to rank alternatives. The advantage of this procedure is that it provides an overall view of the results that is equivalent to examining

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

all possible interactions of Filtering by Method by Sampling scheme, marginalizing over all other terms, and this is done with a simple procedure that does not depend on additional modeling assumptions. The disadvantage is that it does not allow us to judge the relative size of different effects.

2.7.3 Best subsets of Method and Filtering: within-data set testing

As mentioned above, for each combination of Graph, Model, sh, S. Size, S. Time and S. Type, I analyzed twenty replicate data sets, and each data set was subject to each Method or each Filtering by Method combination (section 2.1). This design allows us to use paired tests within each among-data set combination to compare each policy (where a policy is a Method in the Drivers Known scenario or a Filtering by Method combination in the Drivers Unknown scenario) with the rest of policies. Separately for each metric and for each of the 864 among-data set combinations, I declared that policy i was better (had a smaller metric) than policy j if a paired Wilcoxon test had, for the alternative hypothesis of $i < j$, a one-sided *p-value* $< 1 - (1 - 0.05)^{(1/numcomps)}$, where $numcomps$ is the number of comparisons, or the number of other policies each policy is compared against. This procedure is a simple adaptation (to a paired Wilcoxon test) of the "subset selection" procedures in the analysis of simulation experiments common in industrial settings (e.g., p. 67 and ff. in Allen, 2011 or Goldsman and Nelson, 1998). For metrics Diff, PND, and FPF, $numcomps$ is always five in the Drivers Known case and 23 in the Drivers Unknown case; for PFD sometimes fewer tests are performed if all 20 observations of a policy have missing values (due to not making any discovery). After all pairs of combinations of policies had been compared, for each policy I counted in how many cases it was significantly better than the other policies. The subset of best policies is/are the policy(es) with the largest count. If there is a single policy with that largest number of significant differences, the best subset will be composed of only one policy; otherwise, the best subset will have more than one member (meaning that we cannot tell which of those policies is better using this procedure). The best subsets for each of the 864 among-data set combinations are shown in the supplementary file "best-subsets.pdf". From these, we can then find the frequency of the different best subsets for selected combinations of factors as shown in Table 4 or 6. A detailed example of this procedure is provided in *Supplementary Material Section* 12.

2.7.4 Generalized linear modeling of performance metrics

The procedures in section 2.7.3 and 2.7.2 do not provide a direct way to compare the relative magnitude of the effects of different factors. A direct approach to this problem is to use a statistical model for each of the metrics. I used generalized linear mixed models (GLMM), where data set was a random effect and the rest of the factors in the design were regarded as fixed effects. Diff was modeled as a Poisson-distributed count, and PND, PFD, and FPF, were modeled as binomial data. Some factors, specially Number of Nodes but possibly also Model, might be regarded as random effects, but I modeled them as fixed effects since the number of different levels is too small (but see Supplementary Material). Data for the Drivers Known and Drivers Unknown scenarios were modeled separately. Models were fitted using INLA (Fong *et al.*, 2010; Rue *et al.*, 2009), with the R package R-INLA, a Bayesian approach that uses nested Laplace approximation as an alternative to Markov Chain Monte Carlo (MCMC). I run all models with two different priors and for model validation I used the cross-validated probability integral transform (PIT) (Held *et al.*, 2010), and a simple comparison of fitted vs. observed values. In addition, I also fitted the additive and two-way interaction models for Drivers Known scenario, and the additive model for the Drivers Unknown scenario, using the R package MCMCglmm (Hadfield, 2010), using three chains per model and variable; MCMCglmm differs from INLA not only on the use of MCMC (vs. Laplace approximations) but also on the priors and in the inclusion of an observation-level random effect. There were no relevant differences in results.

Models were fitted using sum-to-zero contrasts: each main effect parameter is to be interpreted as the (marginal) deviation of that level from the overall mean, and the interaction parameter as the deviation of the linear predictor of the cell mean (for that combination of levels) from the addition

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

of the corresponding main effect parameters. As explained in the Supplementary Material, we will focus on models with two-way interactions. We will refer to these analyses as the GLMM fits. Further details of the statistical modeling and interpretation of coefficients are provided in the Supplementary Material.

3 Results

We first examine the results when Drivers are Known. When the identity of drivers is not known (Drivers Unknown), we need to add the step of filtering or selecting mutations before inferring the restrictions.

3.1 Drivers Known

Figures with the median values for all metrics for all combinations of factors considered are provided in *Supplementary Material Section* 9.1, and examples of actual fitted graphs are provided in *Supplementary Material Section* 10.1. There was wide variation in performance: under some Models and with some Methods perfect results were achieved but, for those same Models and S.Sizes, there were choices of Method and Sampling scheme that led to very large errors (e.g., PFD and PND of 0.7 to 0.9). This emphasizes that even for the easiest models and largest sample sizes, careful choice of Method can be crucial. There was also a large difference in the number of relations inferred (the transitive closure of the cover relations), whether correct or incorrect: the mean values were 19.1, 18.5, 1.7, 2.6, 7.0 and 8.4 for CBN, CBN-A, DiP, DiP-A, OT, and OT-A, respectively (complete data in *Supplementary Material Section* 9.1.1).

Table 3 shows the overall ranking of Method and Sampling scheme. OT and OT-A were the best methods according to Diff and PFD. CBN and CBN-A were among the best methods according to PND (in graphs with conjunctions) and DiP and DiP-A according to FPF. This is coherent with the patterns of number of edges (number of dependency relations) inferred: CBN and CBN-A inferred more edges and thus the number of false negatives (FN) decreased, so they had larger sensitivity or recall. But this was done, however, at the cost of increasing the false positives and, thus, increasing PFD and FPF: a larger fraction of the discoveries were false (precision was smaller) and a larger fraction of the non-existing relationships were regarded as being present. DiP and DiP-A showed the opposite trend: these were the methods that inferred the smallest number of relations (in fact, in many cases no edges, beyond those from Root, were inferred), leading to a smaller number of false positives (FP), so that a smaller fraction of non-existing relations are regarded as being present, but this is done at the cost of a very large number of FN that affects not only PND, but also Diff.

Figure 2 shows the coefficients from the GLMM fits where we see that DiP and DiP-A show poor performance in all metrics except FPF, and CBN and CBN-A show poor performance in all metrics except in PND. However, the better performance of CBN/CBN-A for metric PND is concentrated in graphs with conjunction. The left column for PND in Table 3 shows that the best five methods were all CBN/CBN-A, but the right column for PND shows that OT-A occupies the first three positions. The analysis of frequencies of best subsets, in Table 4, again reveals the same patterns: OT and OT-A were clearly the best methods for metrics Diff and PFD. CBN and CBN-A were in best subsets that do not include either of the other methods in 55% of the cases for metric PND in graphs with conjunction. In the absence of conjunctions, however, the frequency of best subsets of CBN/CBN-A is the same as that of OT/OT-A, and subsets that do not include CBN/CBN-A are more prevalent than those that include CBN/CBN-A (and this association between subset and conjunction is highly significant, $p < 2.2e^{-16}$ from a chi-square test).

That the best performance of OT/OT-A in graphs with conjunctions cannot be perfect should be expected, and we should only see perfect performance in these cases, if at all, with CBN/CBN-A or DiP/DiP-A. Two interesting extreme cases (which also provide an internal consistency check) are graphs "7-A" and "11-A" (both have conjunctions): perfect performance was achieved for the first with CBN-A and with DiP for the second (S.Size = 1000, McF_6, sh Inf and 0, respectively —see *Supplementary Figure* 6). However, these are extreme cases and it must be emphasized

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Method and sampling	**Conjunction**				**No conjunction**			
	Diff	PFD	PND	FPF	Diff	PFD	PND	FPF
OT-A, last, singleC	**1**	**2**	14	10	**1**	**3**	**2**	15
OT-A, last, wholeT_0.5	**2**	**1**	15	12	**2**	**4**	**3**	14
OT-A, last, wholeT_0.01	**3**	**3**	7	22	**3**	6	**1**	22
OT-A, unif, singleC	**4**	6	19	13	**4**	9	12.5	9.5
OT, unif, singleC	**5**	**5**	20	11	**5**	7	12.5	9.5
OT-A, unif, wholeT_0.01	8	11	16	24	8	11	**5**	24
OT, last, singleC	10	9	23	**1**	10	**1**	17	**2**
OT, last, wholeT_0.01	11	**4**	18	18	12	**5**	14	18
OT, last, wholeT_0.5	12	7	24	**2**	11	**2**	23	**1**
CBN-A, unif, wholeT_0.01	13	13	**1**	26	13	13	**4**	26
CBN-A, unif, singleC	14	16	**2**	28	15	15	9	29
CBN-A, unif, wholeT_0.5	15	18	**3**	34	14	16	8	31
CBN, unif, singleC	16	17	**5**	29	17	19	10	34
CBN, unif, wholeT_0.01	17	14	**4**	27	18	14	6	27
DiP-A, unif, singleC	31	28	31	**4**	31	30	31	6
DiP, last, wholeT_0.5	33	35	34	**5**	34	34	36	**5**
DiP, unif, singleC	35	31	33	**3**	35	32	33	**3**
DiP, unif, wholeT_0.5	36	36	36	6	36	36	35	**4**

Table 3: Overall ranking of all 36 combinations of method and sampling when Drivers are Known with respect to each performance metric. Methods have been ordered by their performance in the first metric. Best 5 methods are shown in bold. Only methods that are within the best 5 in at least one metric are shown (full table as well as tables split by S.Size are available from the Supplementary Material).

Best subsets	**Conjunction**				**No conjunction**			
	Diff	PFD	PND	FPF	Diff	PFD	PND	FPF
OT, OT-A	0.63	0.49	0.05	0.06	0.66	0.55	0.27	0.08
DiP, DiP-A, OT, OT-A	0.02	0.12	-	0.56	0.03	0.18	0.05	0.56
CBN, CBN-A	0.01	0.04	0.55	-	-	0.01	0.27	0.01
DiP, DiP-A	-	0.03	0.01	0.16	0.01	0.02	-	0.14
CBN, CBN-A, OT, OT-A	0.02	0.01	0.06	-	0.02	0.03	0.12	-
CBN-A	0.04	0.01	0.10	-	-	0.01	0.03	0.01
CBN	-	0.01	0.07	-	-	-	0.03	-
OT-A	0.16	0.09	0.07	-	0.15	0.03	0.14	-
OT	0.08	0.05	-	0.01	0.04	0.03	-	-
DiP, OT	-	0.04	-	0.08	0.01	0.06	-	0.07

Table 4: Frequencies of best subsets for all metrics when Drivers are Known. The table shows the frequency of the most common best subset combinations. Combinations not shown have a frequency less than 0.05 for all columns. Frequencies normalized by column total (N = 432).

that performance decreased for all methods in the presence of conjunctions because true relations were not detected (which is seen in the coefficient for PND and, thus, also Diff in Figure 2). Not all methods were affected by conjunctions in the same way, though: as seen in the interaction of Conjunction by Method, the detrimental effect of Conjunction is, in relative terms, smaller for CBN/CBN-A than for the other methods. In summary, even if what is best depends on metric, the overall ranking and the analysis of best subsets indicate that OT-A and, to a lesser extent, OT are a good overall choice; CBN and CBN-A are to be preferred over OT and OT-A only if we want to minimize PND and we suspect conjunctions are present, and DiP and DiP-A are the best choices only if we need to minimize FPF (i.e., if specificity is of paramount importance).

The effect of S.Time was marginally very small (Figure 2), but for PFD and FPF OT can substantially improve its performance when S.Time = last. DiP-A was also benefited by S.Time=last on metric PND. In contrast, CBN and CBN-A benefited slightly from sampling uniformly. That OT/OT-A performed better when S.Time=last can also be observed in the overall ranking of methods (Table 3), as well as in the change in relative frequencies of OT, OT-A and CBN in the fre-

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

quencies of best subsets as a function of S.Time (see *Supplementary Material Section* 13.1). All of these effects, however, were much smaller than the main effect of Method.

Figure 2, as well as Table 4 (full tables available in *Supplementary Material Section* 13.1) and Table 3 (full tables in *Supplementary Material Section* 11.1) show that OT-A is generally superior to OT, and similar but weaker patterns affect CBN and DiP. The magnitude of the differences between augmented and non-augmented alternatives, however, depended strongly on metric and showed interactions with other effects (e.g., S.Time). If we focus on Diff with OT and DiP there was little to loose from always using the augmented alternative, even if no mutation has a frequency of one, but this was not the case with CBN (see *Supplementary Table* 38).

Although the marginal effects of S.Type were generally small (and single cell sampling provided no benefit), overall it seems best to avoid whole tumor sampling with very small detection thresholds. However, as with many other effects, this is reverted with PND. This result is intuitively reasonable: whole tumor sampling at very low thresholds can lead to obtaining samples where we observe together two low frequency events that rarely occur together in the same individual clone (i.e., that do not correspond to a likely pattern as encoded in the graph of the oncogenetic model), leading to the observation of possible artifacts, but also allowing the detection of co-occurring events of very low frequency. The effects of S.Type were amplified by method (the interaction of Method by S.Type in Figure 2), and this effect was strongly metric-dependent.The marginal effect of S.Size was as expected: larger sample size led to better performance with all metrics. However, the effect in performance was small compared to the effects of choosing a bad method or even the effects of S.Type and S.Time for some of the metrics (or the effects of non user-controllable factors such as Model). Moreover, the effects of increases in sample size depended on method and metric: DiP/DiP-A were, comparatively, the methods that benefited the most from increasing S.Size (except for FPF).

Regarding variables that are not under user control, Model and its interactions with other factors had a strong effect on performance (see Figure 3). Overall, the McFarland models led to better performance. The differences between evolutionary models explain the interaction S.Time by Model. S.Time=uniform benefited especially McF_6 (whereas the opposite trend was observed with Bozic and exp). Due to the strong density dependence of McF_6, if we sample at the end it will not be easy to observe intermediate steps that involve only a few mutations, since the final population will be composed of clones with around five to six driver mutations.

Model also showed interactions with Method, and Model determined the effects of sh (the strength of enforcement of monotonicity) and affected its interaction with Method. Focusing on the two-way interactions depicted in Figure 3, sh showed interactions with Method: when sh=0, the performance of DiP and DiP-A was less adversely affected than that of CBN/CBN-A and OT/OT-A: all three families of procedures make allowance for deviations from monotonicity, but the model behind DiP was able to deal with them better. From that figure we also see that with Bozic and exp, sh=0 consistently led to worse performance over the four metrics, but it had the opposite effect on the McF models. This is understandable, since the McF models have very strong density dependence of fitness: if the graph specifies $A \rightarrow B$ and a clone has B without A, even if there is no explicit penalty via the birth rate (i.e., sh = 0), we will be unlikely to observe them, since they will be under a severe relative disadvantage compared to clones with A and not B, and under a much more severe disadvantage compared to clones with both A and B. Thus, even if sh = 0, the McF models by their very nature intrinsically incorporate a strong penalty for any mutation order that does not strictly conform to that encoded in the graph. In other words, genes that can act as drivers or passengers depending on genetic context are much less likely to be observed in their passenger role in the McF models. Figure 4 shows, however, that the relationship was more complex and involved interactions between Model, Method, and sh (and it also explains the counterintuitive marginal results for sh=0 for PFD and FPF). The number of FP (the numerator in PFD) was much larger with sh=0 only for CBN and CBN-A under Bozic and exp. The number of FN (the numerator in PND and FPF) was larger with sh=0 under Bozic and exp, but the difference in FN between the levels of sh depended strongly on both Method and Model. As we can see, thus, differences in evolutionary model can modify how deviations

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

from monotonicity affect the performance of different methods and these results underline the importance of explicitly considering evolutionary model and deviations from monotonicity.

Finally, Graph had an effect, which for some metrics could be large, and also presented large interactions with Model, Method and S.Time for some metrics; these effects will not be examined here further (although a specific one will be addressed in the discussion), but it is important to notice that the graphs used in this study differ in many different ways that are not simply summarized by the number of nodes (see *Supplementary Figure* 4).

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Figure 2: Drivers Known, plot of the coefficients (posterior mean and 0.025 and 0.975 quantiles) for Conjunction, Method, S.Time, S.Type and S.Size from the GLMMs for each of the metrics. X-axis labeled by the exponential of the coefficient (i.e., relative change in the odds ratio or the scale of the Poisson parameter for Diff): smaller (or lefter) is better. The vertical dashed line denotes no change relative to the overall mean (the intercept). The x-axis has been scaled to make it symmetric (e.g., a ratio of 1.25 is the same distance from the vertical line as a ratio of 1/1.25). Coefficients that correspond to a change larger than 25% (i.e., $ratio > 1.25$ or $< 1/1.25$) shown in larger red dots. The coefficients shown are only those that represent a change larger than 25% for at least one metric, or coefficients that are marginal to those shown (e.g., any main effect from an interaction that includes it).

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

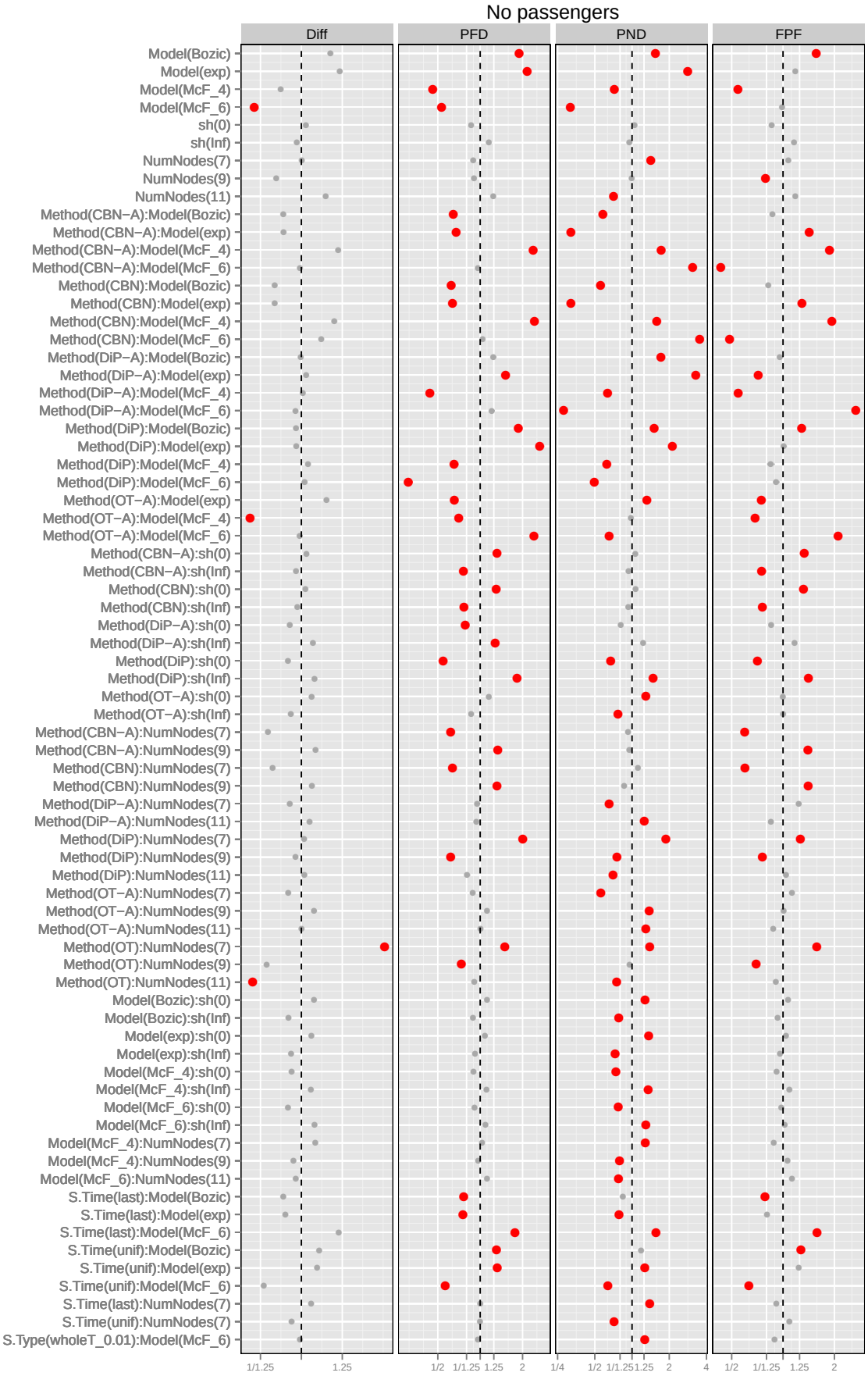

Figure 3: Drivers Known, plot of the coefficients Model, sh, Graph, and their interactions with all other terms. See legend for Figure 2.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

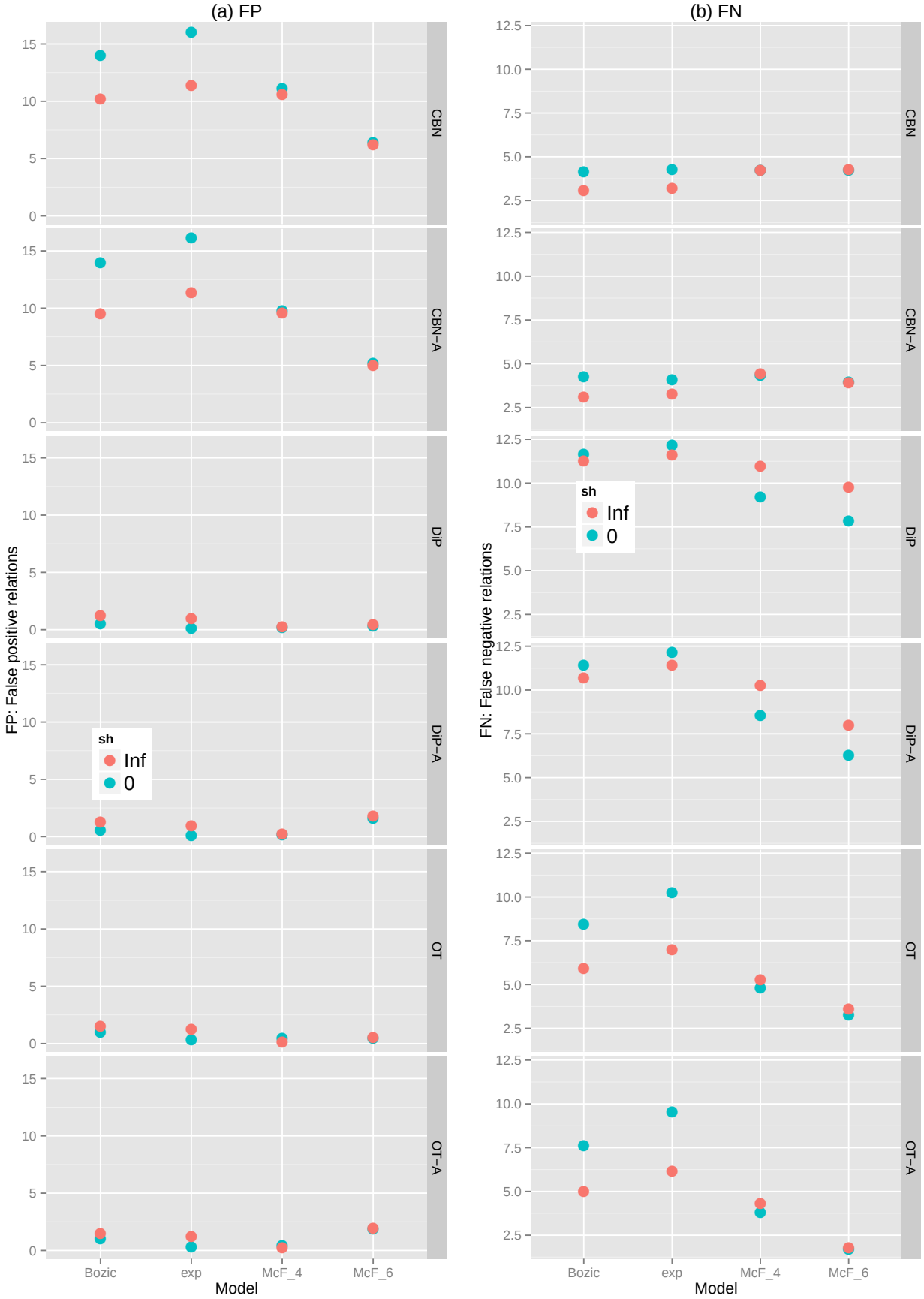

Figure 4: Mean number of (a) false positive (FP) relations and (b) false negative (FN) relations, in the Drivers Known scenario, for the different combinations of Model, Method, and sh.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

3.2 Drivers Unknown

Many results here were similar to the ones in the previous section, so we will focus on the main differences as well as the added factor of filtering. Overall, performance was worse when Drivers were Unknown (the overall mean values for Diff, PFD, PND, and PFP were 9.2, 0.30 0.53, 0.06 when Drivers were Known, but 9.4, 0.41, 0.80, and 0.002 when Drivers were Unknown —FPF is not comparable because of the way TN has to be calculated when Drivers are Unknown; see *Supplementary Material Section* 7). As those number show, the main problem was the large increase in PND, or failing to detect existing edges. However, there were cases when performance was perfect or almost perfect for all metrics (trees without conjunctions, with model McF_6, method OT-A, Dip-A, and occasionally OT, and filtering S5 and rarely S1 or J1; see *Supplementary Figure* 9.2.2).

The marginal effect of Filtering (Figure 5) was as expected: more stringent filtering (J5) decreased FP and thus led to better performance for both PFD and FPF, but less stringent filtering (S1) was better for missing fewer patterns, and thus led to better performance in PND (where J5 shows terrible performance). A reasonable overall choice is probably S5: it was the best filtering for the Diff metric, and did reasonably well for all the other metrics. However, as we have already seen repeatedly, the choice of the best filtering is metric-dependent, and if we wanted to maximize performance on each metric, S5 would only be the best choice for the Diff metric, as we can also see from the overall ranking of methods (Table 5).

One difference with the results when Drivers are Known is related to Method: here, OT/OT-A are almost always better than CBN and CBN-A. This can be seen in Figure 5 —OT and OT-A had much smaller coefficients for all metrics, except for OT under PND. The same pattern was seen in the overall ranking of methods (Table 5): CBN/CBN-A were rarely among the best performers, not even with conjunctions and with metric PND. Similar results were observed in the analysis of best subsets (Table 6): CBN/CBN-A were rarely among best subsets, and when they were it was generally in best-subsets that included also OT and OT-A, from which they could not be differentiated by the Wilcoxon tests. The results for DiP and DiP-A were similar to the Drivers Known scenario: these methods led to the smallest FPF, but did so at the cost of the other metrics. However, in this scenario DiP and DiP-A were slightly better performers than CBN and CBN-A for Diff.

Interestingly, the interactions between Filter and Method did not seem relevant for CBN/CBN-A compared to OT and DiP. Effects depended strongly on metric, but these interactions are not large enough to revert our preferences of methods. S.Type followed similar patterns as seen for the Drivers Known scenario, and its interactions with Method or Filter, even when present, had small effects that produced no change in the ordering of preferences of Filtering, Method, or S.Type. The effects of S.Size, or the interactions S.Size by Method, Model by S.Time and Method by S.Time were similar to those in the Drivers Known scenario.

Other effects and interactions, however, were different with respect to the Drivers Known scenario, illustrating that the need to filter passengers can lead to counterintuitive and much more complicated interpretation of results. The effect of S.Time for all metrics except Diff was reverted and had larger magnitude compared to the Drivers Known scenario. The cause is that S.Time affected the number of genes that were selected and thus the number of false positives (FP) and false negatives (FN). As seen in Figure 7 (which also helps see the interaction of Filtering by S.Time), under S.Time = uniform fewer genes were selected for all filtering methods (the number of genes selected is independent of Method but depends on Filtering). Under uniform sampling many of the samples have few mutations (those corresponding to the early history of the tumor), and thus fewer genes are above the filtering thresholds. As fewer genes are selected under S.Time = uniform, the number of FP goes down, and thus both PFD and FPF showed a decrease in error (and the opposite pattern was observed for PND). None of these phenomena were present when Drivers are Known, because there was no gene selection step there. For Diff, however, the marginal effect of S.Time=uniform was still slightly better than that of last-period sampling, as was when Drivers are Known.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Two other differences with the Drivers Known scenario are the poor performance of model McF_6 with metric FPF, and some of the interactions between Model and sh in several metrics, and both probably are related by the need to filter genes. The poor performance of McF_6 in FPF was not paralleled by a poor performance in PFD, which also has FN (false negatives) in the numerator. Thus, per discovery made (i.e., for each relationship found by the methods), McF_6 was actually the model that allowed achieving best results (the best PFD). But the number of errors (FN) increased disproportionately with respect to the number of edges that were not present (the denominator of FPF). Figure 8, panel (a), shows that, for all filtering methods, McF_6 was the model that resulted in the largest number of genes selected: the strong density dependence of McF_6, specially when S.Time = last, will tend to return samples where most driver mutations are present in many samples. This increase in the number of genes selected can lead to inferring a larger number of relationships and, ultimately, to an increase in FP, as shown in panel (b) (note that for each of the six Graphs, 11-A to 7-B, the total number of non-true edges is constant). This would also explain that sh=0, specially with PFD and FPF, led to a large decrease in error rates. Figure 8, panel (a) shows that, for all filtering procedures, sh=0 led to smaller number of genes being selected with models Bozic and Exp (and had no effect on the McF models), and Bozic and exp were the two models where sh=0 led to a larger relative improvement in performance in PFD and FPF. Interestingly, this effect is more pronounced in S1, and suggests that sh=Inf allows the accumulation of larger numbers of mutated genes that pass the less stringent filters, but that have too little signal for the graph inference step (in contrast, sh=0 leads to the accumulation of mutations with too low a frequency to even pass the filters). That sh should have virtually no effect on number of genes in the McF models has been explained before. These interactions, thus, highlight the complex and counterintuitive relationships between Model, sh, and Filtering, that then cascade onto the overall performance differences of the different methods.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Method and sampling	**Conjunction**				**No conjunction**			
	Diff	PFD	PND	FPF	Diff	PFD	PND	FPF
S5, OT-A, last, singleC	**1**	**7**	15	60	**1**	13	13	60
S5, OT-A, last, wholeT_0.5	**2**	**6**	23	59	**2**	**7**	23	59
J5, OT-A, last, wholeT_0.01	**3**	**1**	26	71	**4**	**2**	29	74
S5, OT-A, last, wholeT_0.01	**4**	**2**	**2**	94	**3**	**5**	**4**	94
S5, OT-A, unif, wholeT_0.01	**5**	17	33	69	**10**	17	32.5	68.5
S5, OT, unif, singleC	**6**	41	61.5	28	**9**	38	55.5	20.5
S5, OT-A, unif, singleC	**7**	50	61.5	31	**8**	49	55.5	20.5
J1, OT-A, last, singleC	**8**	15	38	80	**6**	12	37	75
J1, OT-A, last, wholeT_0.5	**9**	**10**	39	79	**7**	**6**	39	71
S5, OT-A, unif, wholeT_0.5	**10**	47	67	29.5	14	45	60.5	27.5
S5, OT, unif, wholeT_0.01	11	11	34	68	11	**10**	32.5	68.5
J1, OT-A, last, wholeT_0.01	13	21	**9**	109	15	19	**8**	108
S1, OT-A, last, wholeT_0.5	18	39	**3**	117	**5**	27	**3**	116
S1, OT-A, last, singleC	21	38	**4**	120	12	32	**2**	120
S5, OT, last, singleC	23	16	51	21	20	**8**	42	19
S5, OT, last, wholeT_0.5	24	**3**	55	16	23	**3**	49	17
J1, OT, unif, wholeT_0.01	29	**9**	36	91	30	14	36	91
S5, CBN-A, unif, wholeT_0.01	30	**4**	37	89	40	20	40	103
J5, OT, last, wholeT_0.01	31	**5**	59	32	36	**4**	62	50
S1, OT-A, last, wholeT_0.01	36	48	**1**	134	24	50	**1**	134
S5, OT, last, wholeT_0.01	38	**8**	29	83	34	**1**	24	82
J1, OT, last, wholeT_0.5	47	14	89	61	38	**9**	83	43
J5, OT, last, singleC	48	35	101	**4**	58	43	109	**4.5**
J5, DiP-A, unif, singleC	49	125	139	10.5	51	128	138	**9**
J5, OT, last, wholeT_0.5	57	20	102	**4**	75	23	112	**4.5**
J5, DiP, unif, singleC	61	131	143	**8**	60	132	144	**4.5**
J5, DiP, unif, wholeT_0.5	64	144	144	**4**	64	144	143	**4.5**
J5, DiP, last, singleC	79	115	140	**4**	81	119	140	**4.5**
J5, DiP, last, wholeT_0.5	82	137	138	**4**	83	136	139	**4.5**
S5, DiP, last, wholeT_0.5	83	134	120	**9**	87	130	110	**10**
J1, DiP, last, wholeT_0.5	91	132	134	**4**	89	134	134	**4.5**
J1, DiP, last, singleC	92	110	135	**4**	93	115	132	**4.5**
S1, OT-A, unif, wholeT_0.01	102	65	**5**	136	70	59	**5**	136
S1, OT, unif, wholeT_0.01	109	62	**6**	135	74	55	**6**	135
S1, CBN-A, unif, wholeT_0.01	137	82	**7**	143	140	81	**7**	143
S1, CBN-A, last, wholeT_0.01	142	93	**10**	137	139	94	12	137
S1, CBN, unif, wholeT_0.01	143	84	**8**	144	143	90	**9**	144

Table 5: Overall ranking of all 144 combinations of method, filtering, and sampling when Drivers are Unknown with respect to each performance metric. Methods have been ordered by their performance in the first metric. Best 10 methods are shown in bold. Only methods that are within the best 10 in at least one metric are shown (full table as well as tables split by S.Size are available from the Supplementary Material).

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Best subsets	**Conjunction**				**No conjunction**			
	Diff	PFD	PND	FPF	Diff	PFD	PND	FPF
S1:OT-A, S5:OT-A	0.01	-	0.07	-	0.01	-	0.08	-
S1:OT, S1:OT-A	0.10	0.10	0.23	-	0.13	0.11	0.35	-
S1:OT-A	0.02	-	0.06	-	0.02	-	0.06	-
S5:OT-A	0.07	-	-	-	0.09	-	-	-
S5:OT	0.06	-	-	-	0.05	-	-	-
S5:OT, S5:OT-A	0.20	0.05	-	-	0.22	0.07	-	-
S5:DiP, S5:DiP-A, S5:OT, S5:OT-A	0.06	-	-	-	0.07	-	-	-
S1:OT, S1:OT-A, S5:OT, S5:OT-A	0.01	-	0.03	-	0.03	-	0.07	-
J5:DiP, J5:DiP-A, J5:OT, J5:OT-A	-	0.01	-	0.06	-	-	-	0.05
J5:OT, J5:OT-A, S5:OT, S5:OT-A	-	0.06	-	-	0.01	0.04	-	-
S1:CBN, S1:CBN-A, S1:OT, S1:OT-A	-	-	0.18	-	-	-	0.12	-

Table 6: Frequencies of best subsets for all metrics when Drivers are Unknown. The table shows the frequency of the most common best subset combinations. Combinations not shown have a frequency less than 0.05 for all columns or are composed of more than 10 individual best methods. Frequencies normalized by column total (N = 432). 'A:B' denotes filtering with A and using method B.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Figure 5: Drivers Unknown, plot of the coefficients for Conjunction, Filtering, Method, S.Time, S.Type and S.Size from generalized linear models. See legend for Figure 2.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

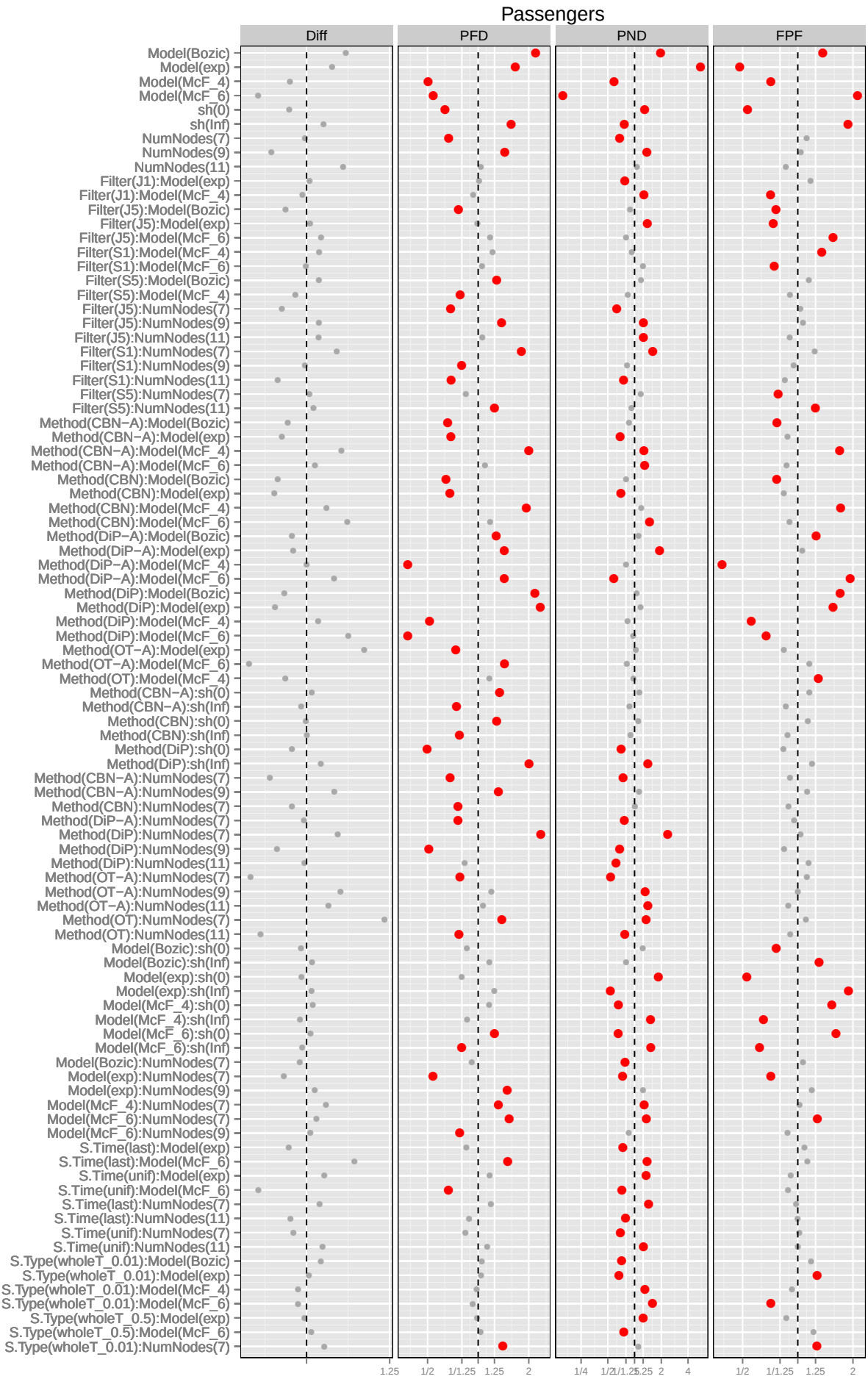

Figure 6: Drivers Unknown, plot of the coefficients Model, sh, Graph, and their interactions with all other terms. See legend for Figure 2.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

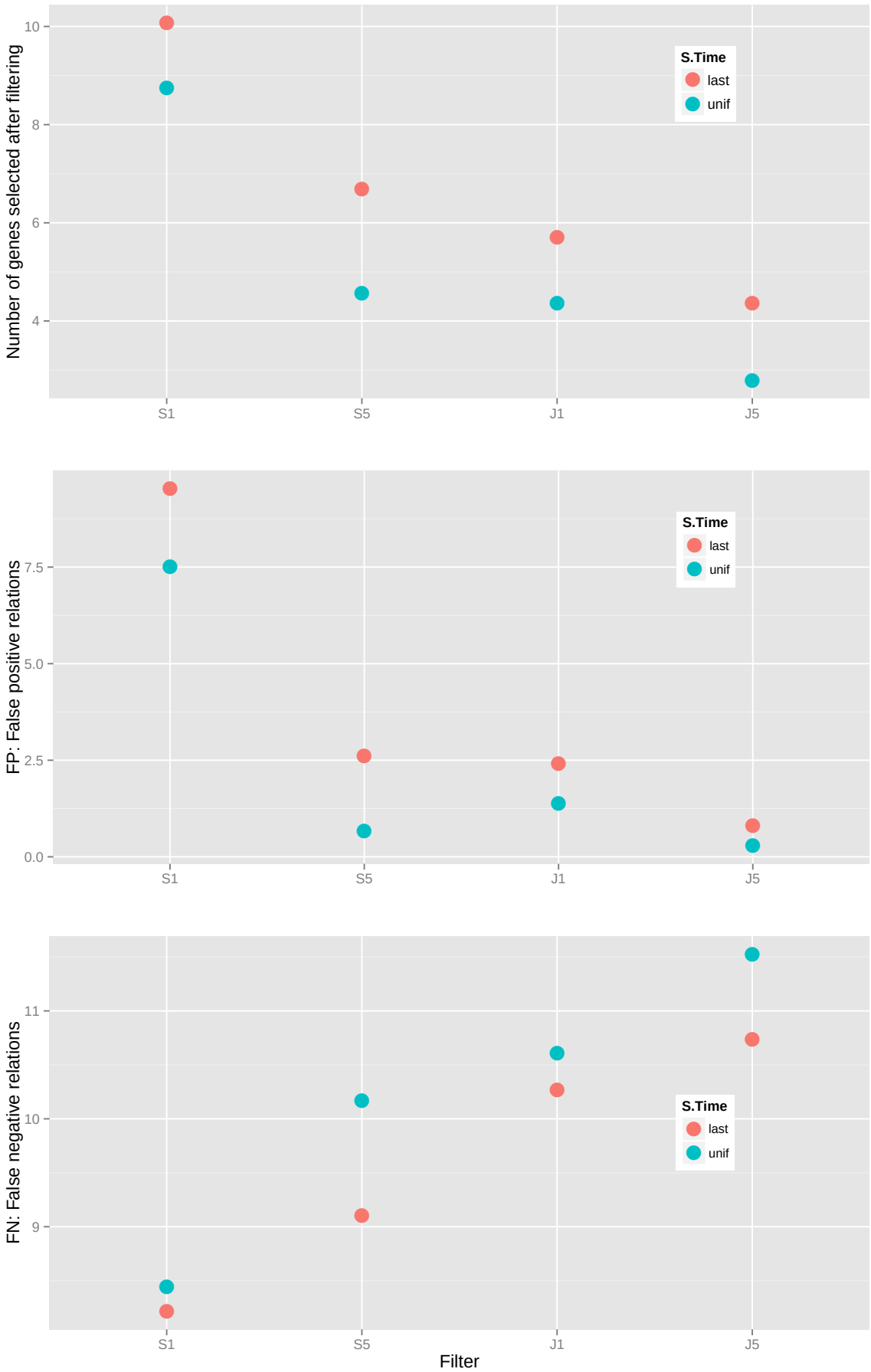

Figure 7: Mean number of genes selected, false positive (FP) relations, and false negative (FN) relations, after filtering, for each S.Time setting, when Drivers are Unknown. Note that the number of genes selected is a function of Filtering, not Method. FP and FN differ by method, so the values shown are marginal over method.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

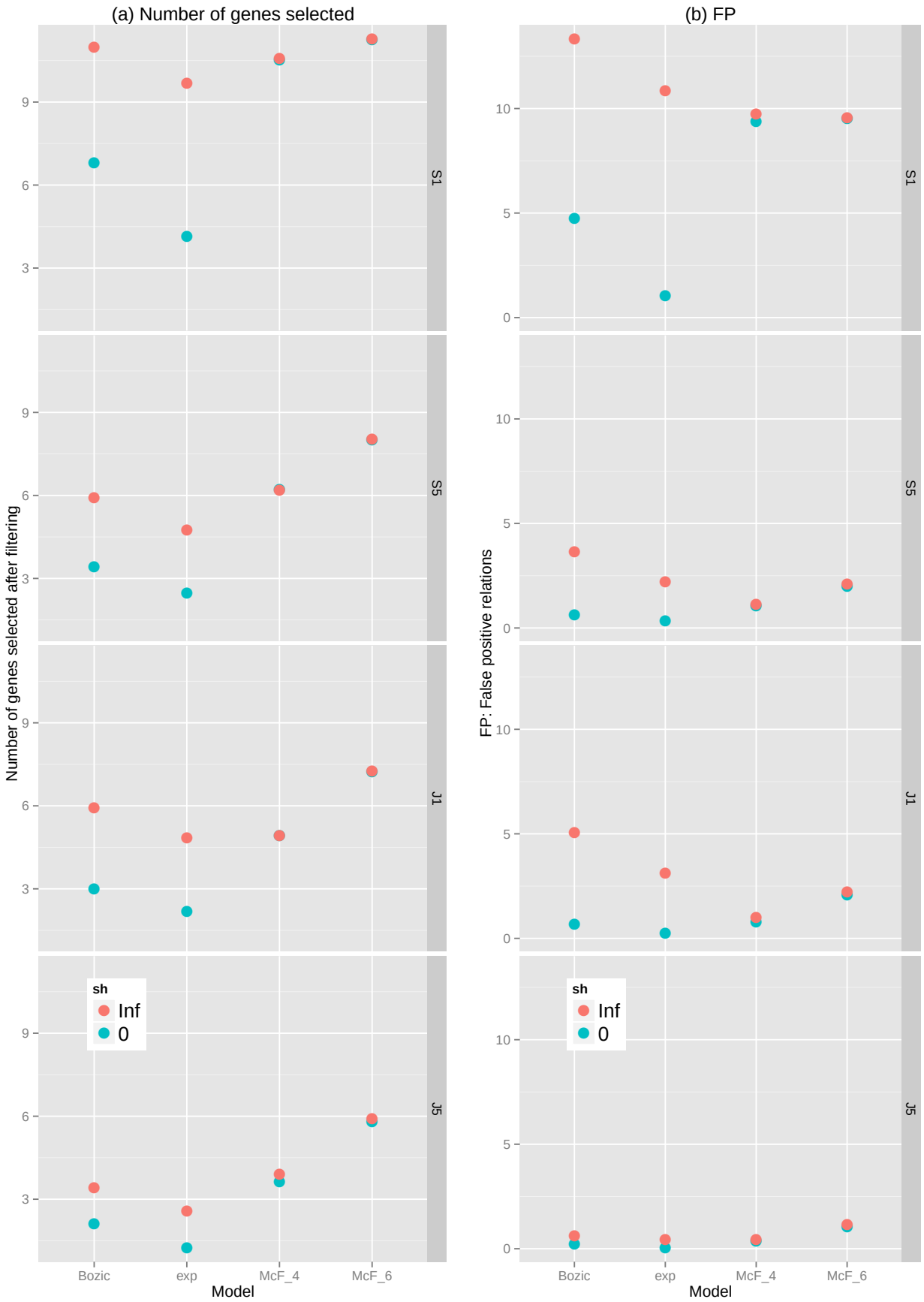

Figure 8: Mean number of (a) genes selected after filtering and (b) false positive (FP) relations for each model, filtering, and sh setting, when Drivers are Unknown. The number of genes selected is a function of Filtering, not Method. FP differs by method, so the values shown are marginal over method.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

4 Discussion

This paper presents a comprehensive study that has examined, for the first time, the effects of sampling decisions, evolutionary models, and the presence of passenger mutations in the performance of methods for the inference of restrictions in the accumulation of mutations.

From the point of view of a user of these methods with available cross-sectional data, the main results can be summarized as follows:

1. Method and sampling choice should be guided by the metric considered most important: no combination of Method, Filtering, and Sampling scheme excels in all metrics. This is not unexpected, but it is worth emphasizing that each metric is sensitive to a different kind of deviation, and the results here show that characterizing behavior with only one or two metrics could have been deceptive. Moreover, as we have seen, the relative strengths of each method are better captured using these different metrics.

2. In terms of method choice, a very simple summary is (see also figures with examples of fitted graphs in *Supplementary Material Section* 10): CBN tends to return graphs with too many edges, including too many conjunctions, DiP tends to return graphs with too few edges between non-root nodes, and OT by construction misses all conjunctions. In more detail, OT and OT-A are the best overall methods, except if we are particularly interested in minimizing PND (when we might want to consider CBN) or FPF (when we might want to consider DiProg). These conclusions hold even when we are dealing with graphs that really have conjunctions. But since it is impossible for OT to return any conjunction, further research on computationally efficient methods to recover conjunctions is sorely needed.

3. Using frequency-based statistics when we do not know which mutations are true passengers can lead to a heavy performance penalty. In addition, having to filter genes makes it much harder to intuitively understand, and reason about, what is likely to happen in any scenario, and this in turns makes interpretation of results and reconciliation of output from different methods much harder. Thus, it probably pays off to try to use other approaches that incorporate information about non-silent mutation rates, pathway information together with combinatorial properties of drivers in pathwayws, or functional consequences of mutations to differentiate drivers from passengers (e.g., Fischer *et al.*, 2011; Khurana *et al.*, 2013; Leiserson *et al.*, 2013; Vandin *et al.*, 2012; Watson *et al.*, 2013; Youn and Simon, 2011). It might not always be possible to use these other methods. If we need to rely on frequency-based approaches, selecting those mutations with a frequency larger than 5% is an overall reasonable choice (but not the single best choice for any metric other than Diff).

4. Sampling time and type, by themselves, had minor effects compared to, say, filtering or method choice (and we will rarely have control over these factors when we use data already available in databases). However, we might have information about characteristics of the tumor which indicate that it is in an exponential (the Bozic or exp models) or logistic-like growth (the McF models) phase; sampling as late as possible is to be preferred for the first cases, whereas trying to obtain samples distributed over different stages of the disease is best in the second. The best choice of sampling time, however, will depend on metric and whether or not we are certain about which are the driver genes.

5. Single cell sampling is about as good as whole tumor sampling, unless we use whole tumor sample with extremely small detection thresholds (which leads to poorer performance, except for metric PND).

6. Although with S. Size the larger the better, its effect is relatively minor for OT and CBN (not so for DiP), a result that agrees with those in Hainke *et al.* (2012), specially for some metrics; in particular, resources might be better spent trying to be certain about the identity of the true drivers than increasing sample size from 100 to 1000.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

7. Data augmentation (Section 2.6.1) is not always the right choice, although with OT and DiP there is little to loose from always using data augmentation but potentially a lot to loose from not using the augmentation approach (see *Supplementary Material Section* 16). Unfortunately, simple rules of thumb like "always use data augmentation when at least one gene has a frequency of 1, and never otherwise" do not work well, especially across all methods, and appropriate choice warrants further study.

Most of the above results cannot be compared to any other studies, since those factors have not been considered before. Both Desper *et al.* (1999) and Szabo and Boucher (2008) provide estimates of the sample sizes needed to have high probability of recovering the true tree (tree in their case, since they deal with oncogenetic trees); they conclude that very good reconstructions are achievable with realistic sample sizes, and we have seen that, at least under several scenarios, it is possible to obtain perfect reconstructions even with sample sizes as small as 100.

The results concerning the superiority of OT with respect to CBN contrast with those of Hainke *et al.* (2012), who find that CBN outperforms OT. A more detailed discussion is provided in *Supplementary Material Section* 17, but these differences are attributable to Hainke *et al.* (2012) basing their conclusion on a single graph with a small number of nodes for each scenario. *Supplementary Figure* 51 shows the within-data set difference in the Diff metric between CBN and OT separately for the different combinations of Model, sh, Graph, and Sampling scheme (under the Drivers Known scenario only, since Hainke *et al.*, 2012 do not consider passengers): OT systematically outperformed CBN except for Graph 7A when sampling last (under all models except McF_6), and Graph 7B when sampling last under the Bozic and exponential models. This pattern was reproduced when I fitted the OT models with the Rtreemix package (Bogojeska, 2014; see *Supplementary Figure* 52). The single tree (or graph) used by Hainke *et al.* (2012) for the non-conjunction case (their Figure A1) contains five nodes, and the single graph they use for the conjunctive case contains four nodes (their Figure A7), a very small number of nodes compared to the trees that are seen on the literature (see section "True graphs, number of drivers, and number of passengers"). Our graphs 7A and 7B, those where CBN outperformed OT in certain scenarios, are the closest in number of nodes to the graphs in Hainke *et al.* (2012).

Given that the results of Hainke *et al.* (2012) are, thus, probably not really contradictory with ours, is the recommendation that practitioners generally use OT instead of CBN still valid? Probably yes, since most graphs in the literature (including studies involving citogenetic bands and genes) contain many more than four or five nodes, and we cannot be sure if the evolutionary model is one that would favor using CBN. In addition, we have focused only on the comparison between CBN and OT, since those are the only variants used in Hainke *et al.* (2012): if we included OT-A in the comparison, CBN (or CBN-A) are then very rarely better alternatives (see, e.g., the second supplementary file with the complete list of best subsets or *Supplementary Figure* 53). However, this apparent difference in results emphasizes the need for considering at least a few different scenarios with regards to potentially key variables, and suggests that a through examination of the impact of graph characteristics (and its interaction with evolutionary model and sampling scheme) on method performance is warranted.

This paper is also one of the first to explicitly connect evolutionary models with restrictions on the order of mutations. Reiter *et al.* (2013) have recently published a simulation tool where restrictions are incorporated into the evolutionary model of Bozic *et al.* (2010) via what they call "path fitness landscape"; our approach is more general as they are restricted to one evolutionary model, only four drivers, and no passengers whereas, in addition to passengers and other evolutionary models, we can specify these landscapes using arbitrary graphs and allowing for a range of deviations from monotonicity. In fact, one of the attractive features of OTs, CBNs, and Progression Networks is their mechanistic interpretation as graphs that encode restrictions in the order in which driver mutations can accumulate (e.g., Desper *et al.*, 1999; Farahani and Lagergren, 2013; Hainke *et al.*, 2012; Szabo and Boucher, 2008). And one major result of this paper is that inferring those restrictions can be strongly affected by evolutionary model (including deviations from monotonicity) and sampling scheme, and that the relative effect of these factors depends on the metric used. Yet restrictions on the order of driver mutations and evolutionary models are virtually always examined separately.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

There is a rich literature about tumor progression models that focuses on the consequences of drivers, passengers, and variation in selection pressures (e.g., Beerenwinkel *et al.*, 2007a; Bozic *et al.*, 2010; Datta *et al.*, 2013; Durrett *et al.*, 2010, 2011; McFarland *et al.*, 2013), and a largely separate body of work (e.g., see Desper *et al.*, 1999; Gerstung *et al.*, 2009; Hainke *et al.*, 2012; Radmacher *et al.*, 2001; Simon *et al.*, 2000; Szabo and Boucher, 2002, 2008; Youn and Simon, 2012) that deals with understanding the restrictions and order of accumulation of mutations (but see Gerstung *et al.*, 2011 for a connection between the λ_i of CBNs and selection coefficients, in the context of the Fisher-Wright model of tumor progression in Beerenwinkel *et al.*, 2007a). The work of Cheng *et al.* (2012) (see also Attolini *et al.*, 2010) tries to infer the order of mutations within a explicit evolutionary model of tumor progression (a Moran model in their case); unfortunately, no software is available, and thus comparisons are not possible.

Focusing on methods with available software, the actual values (and, thus, interpretation) of the conditional probabilities inferred by OTs or the λ_i parameter for the waiting time to event i, in CBNs will be a complex interplay between the restrictions encoded in the graphs and the details of the tumor progression model as well as the sampling scheme used. In fact, our way of incorporating the restrictions of the graph models into the tumor growth models when $s_h = Inf$ (i.e., when monotonicity is strictly enforced so that we fully comply with the restrictions of the graph) leads to data that conform to timed oncogenetic trees in the sense of Desper *et al.* (1999); Szabo and Boucher (2008). But in both OTs and CBNs we should expect estimated λs and conditional probabilities to vary by node level or depth (where level or depth refers here to how many edges there are in the path to the root): deeper nodes will show smaller values and, for a given depth, λs/conditional probabilities should be larger for those nodes than "unlock" more downwards mutations. The strength of this effect will increase with the number of nodes along the largest path along the graph, especially when the evolutionary model and sampling scheme result in strong selection for clones with many drivers, and we should see competition between multiple nodes that descend from the same parent.

As an example of the impact of evolutionary model and sampling scheme on the observable consequences of the restrictions encoded in the graphs, figures in *Supplementary Material Section* 18 show fitted oncogenetic trees for each of the three trees, under several scenarios. For example, *Supplementary Figure* 60 shows fitted oncogenetic trees for 11-B with a sample size of 26000 (to minimize sampling variation; see also *Supplementary Material Section* 18 for other sample sizes and graphs). The fitted trees are perfect, or almost perfect, reconstructions of the topology of the true tree (compare with *Supplementary Figure* 2), but the estimates of the conditional probabilities show large differences. The variations are in directions we would expect both between S.Time and among models, as well as among nodes (similar patterns can be seen for Tree 11 under whole tumor sampling and for Trees 9 and 7; see *Supplementary Material Section* 18). Even if the above results are intuitively reasonable, they highlight that whereas the topologies of the graphs (the partial orders) encode constraints in the order of mutations, the conditional probabilities (or λs) we estimate and, most importantly, the patterns of co-occurrence of mutations and the sets of clones we observe, will depend crucially on the evolutionary model and sampling scheme. Since the topology reconstructions depend on the patterns observed, it follows that our inferences will be strongly impacted by evolutionary model (and sampling scheme), as we have seen in the results. Moreover, examining the consequences of sampling scheme (S.Time and S.Type) and the detrimental effects of having to separate drivers from passengers on the quality of our inferences, can only be meaningfully considered with respect to an evolutionary tumor progression model that generates the data.

As mentioned in the Introduction, the above interaction between order restrictions and evolutionary model, and the unavoidable need to interpret parameters in the context of a given evolutionary model, are coherent with the limitations pointed out by Sprouffske *et al.* (2011): that oncogenetic tree models (and related models) are not really evolutionary models and do not represent ancestral relationships, but only summarize patterns of co-occurrences of mutations across samples. Virtually all studies of methods for inferring order restrictions are susceptible to this criticism, since they simulate data directly from the generative (but non-evolutionary) OT/CBN/Progression network model. However, the design I have used here completely overcomes this limitation: I

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

have simulated the data using plausible evolutionary models that incorporate the restrictions encoded in the topology of the graphs via a straightforward effect on the fitness of clones. Moreover, deviations from monotonicity are not added to the model just as an unexplained error term, but are an integral part of the evolutionary model that can be related, for instance, to the genetic context-dependence of the driver/passenger status.

Sprouffske *et al.* (2011) conclude that cross-sectional data can be misleading if we try to infer the order of mutations. But this conclusion is based on a design where a single OT is fitted to a cross-sectional sample where mutations are not restricted to obey a pre-specified set of restrictions. Thus, it is not surprising that the OT fit does not do well. The results of Sprouffske *et al.* (2011) of course highlight that if different subjects have different sets of order restrictions, then no single OT will capture these patterns, a limitation that is already recognized in the early literature on ongenetic trees (e.g., Desper *et al.*, 1999; Radmacher *et al.*, 2001), and that has prompted the development of mixtures of oncogenetic trees (e.g. Beerenwinkel *et al.*, 2005; Bogojeska *et al.*, 2008b; Tofigh *et al.*, 2011). But, by themselves, their results do not show that OTs (or CBNs or DiPs) from cross-sectional data cannot fare well if there is a true underlying set of restrictions that can be represented as a single graph. Quite to the contrary, I have shown here, embedding the restrictions in evolutionary models, that they can do very well and even recover the exact underlying graph (at least under certain scenarios). Moreover, Sprouffske *et al.* (2011) do not show that any particular within-subject method is actually capable of recovering the true paths from their data (they sidestep that problem altogether).

The key questions to be answered regarding the usage of cross-sectional data, then, are two: 1) whether the accumulation of mutations in cancer progression can be reasonably represented by a single graph that encapsulates restrictions; 2) if 1) does not hold, whether cross-sectional methods such as mixtures of oncogenetic trees can recover the set of different restrictions. If the answer to 1) is positive, the results of this paper indicate that we have methods that can (at least partially) recover those relationships, and these results also highlight possible avenues to improve them. But question 1) is one that neither this study nor the one of Sprouffske *et al.* (2011) can answer (I simulated data assuming a Yes to that question and Sprouffske *et al.*, 2011 assuming a No). Question 2) remains to be thoroughly addressed, and neither this paper nor Sprouffske *et al.*, 2011 shed light on the matter. If the answer is negative, then we need to start focusing on within-individual data, which are much harder to obtain. Nevertheless, the approaches in this paper provide a principled and general way to address that question by simulating data under scenarios were there is no single set of restrictions in common to all subjects, and examining the consequences both for our methods of inferring trajectories and for the data patterns themselves (so as to try to infer, from them, whether or not there is a single set of restrictions).

5 Acknowledgments

C. Lazaro-Perea for comments on the ms. I. B. Diaz for rooting many graphs. R. Salomón for discussion about CBNs and OTs. H. S. Farahani, T. Graham and R. Datta, M. Gerstung, K. Hainke, C. D. McFarland, W. Mather and L. Tsimring, T. Sakoparnig, K. Sprouffske, and T. Zhu for answering questions about their papers and methods and/or providing code of the implementations of their algorithms. Partially supported by Project BIO2009-12458 from the Spanish MINECO.

References

Allen, T. (2011). *Introduction to Discrete Event Simulation and Agent-Based Modeling*. Springer.

Attolini, C., Cheng, Y., Beroukhim, R., Getz, G., Abdel-Wahab, O., Levine, R. L., Mellinghoff, I. K., and Michor, F. (2010). A mathematical framework to determine the temporal sequence of somatic genetic events in cancer. *Proceedings of the National Academy of Sciences*, **107**(41), 17604–17609.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Beerenwinkel, N., Rahnenführer, J., Däumer, M., Hoffmann, D., Kaiser, R., Selbig, J., and Lengauer, T. (2005). Learning multiple evolutionary pathways from cross-sectional data. *Journal of computational biology : a journal of computational molecular cell biology*, **12**(6), 584–598.

Beerenwinkel, N., Eriksson, N., and Sturmfels, B. (2007a). Conjunctive Bayesian networks. *Bernoulli*, **13**(4), 893–909.

Beerenwinkel, N., Antal, T., Dingli, D., Traulsen, A., Kinzler, K. W., Velculescu, V. E., Vogelstein, B., and Nowak, M. A. (2007b). Genetic progression and the waiting time to cancer. *PLoS computational biology*, **3**(11), e225.

Bogojeska, J. (2014). Rtreemix: Mutagenetic tree mixture models.

Bogojeska, J., Alexa, A., Altmann, A., Lengauer, T., and Rahnenfuhrer, J. (2008a). Rtreemix: an R package for estimating evolutionary pathways and genetic progression scores. *Bioinformatics*, **24**(20), 2391–2392.

Bogojeska, J., Lengauer, T., and Rahnenführer, J. (2008b). Stability analysis of mixtures of mutagenetic trees. *BMC bioinformatics*, **9**, 165.

Bozic, I., Antal, T., Ohtsuki, H., Carter, H., Kim, D., Chen, S., Karchin, R., Kinzler, K. W., Vogelstein, B., and Nowak, M. A. (2010). Accumulation of driver and passenger mutations during tumor progression. *Proceedings of the National Academy of Sciences of the United States of America*, **107**, 18545–18550.

Bulashevska, S., Szakacs, O., Brors, B., Eils, R., and Kovacs, G. (2004). Pathways of urothelial cancer progression suggested by Bayesian network analysis of allelotyping data. *International journal of cancer. Journal international du cancer*, **110**(6), 850–6.

Cheng, Y.-K., Beroukhim, R., Levine, R. L., Mellinghoff, I. K., Holland, E. C., and Michor, F. (2012). A mathematical methodology for determining the temporal order of pathway alterations arising during gliomagenesis. *PLoS computational biology*, **8**(1), e1002337.

Datta, R. S., Gutteridge, A., Swanton, C., Maley, C. C., and Graham, T. a. (2013). Modelling the evolution of genetic instability during tumour progression. *Evolutionary applications*, **6**(1), 20–33.

Davis, J. and Goadrich, M. (2006). The relationship between Precision-Recall and ROC curves. *Proceedings of the 23rd international conference on Machine learning - ICML '06*, pages 233–240.

Desper, R., Jiang, F., Kallioniemi, O. P., Moch, H., Papadimitriou, C. H., and Schäffer, A. A. (1999). Inferring tree models for oncogenesis from comparative genome hybridization data. *J Comput Biol*, **6**(1), 37–51.

Desper, R., Jiang, F., Kallioniemi, O. P., Moch, H., Papadimitriou, C. H., and Schäffer, a. a. (2000). Distance-based reconstruction of tree models for oncogenesis. *Journal of computational biology : a journal of computational molecular cell biology*, **7**(6), 789–803.

Diep, C. B., Kleivi, K., Ribeiro, F. R., Teixeira, M. R., Lindgjaerde, O. C., and Lothe, R. A. (2006). The order of genetic events associated with colorectal cancer progression inferred from meta-analysis of copy number changes. *Genes Chromosomes Cancer*, **45**(1), 31–41.

Durrett, R., Foo, J., Leder, K., Mayberry, J., and Michor, F. (2010). Evolutionary dynamics of tumor progression with random fitness values. *Theoretical population biology*, **78**(1), 54–66.

Durrett, R., Foo, J., Leder, K., Mayberry, J., and Michor, F. (2011). Intratumor heterogeneity in evolutionary models of tumor progression. *Genetics*, **188**(2), 461–77.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Eberwine, J., Sul, J.-Y., Bartfai, T., and Kim, J. (2013). The promise of single-cell sequencing. *Nature Methods*, **11**(1), 25–27.

Farahani, H. S. and Lagergren, J. (2013). Learning oncogenetic networks by reducing to mixed integer linear programming. *PloS one*, **8**(6), e65773.

Fischer, A., Greenman, C., and Mustonen, V. (2011). Germline fitness-based scoring of cancer mutations. *Genetics*, **188**(2), 383–93.

Fong, Y., Rue, H. v., and Wakefield, J. (2010). Bayesian inference for generalized linear mixed models. *Biostatistics (Oxford, England)*, **11**(3), 397–412.

Gentle, J. E. (2007). *Matrix Algebra*. Springer, New York.

Gerstung, M., Baudis, M., Moch, H., and Beerenwinkel, N. (2009). Quantifying cancer progression with conjunctive Bayesian networks. *Bioinformatics (Oxford, England)*, **25**(21), 2809–2815.

Gerstung, M., Eriksson, N., Lin, J., Vogelstein, B., and Beerenwinkel, N. (2011). The Temporal Order of Genetic and Pathway Alterations in Tumorigenesis. *PLoS ONE*, **6**(11), e27136.

Gibson, M. a. and Bruck, J. (2000). Efficient Exact Stochastic Simulation of Chemical Systems with Many Species and Many Channels. *The Journal of Physical Chemistry A*, **104**(9), 1876–1889.

Goldsman, D. and Nelson, B. (1998). Statistical screening, selection, and multiple comparison procedures in computer simulation. *Proceedings of the 30th conference on Winter simulation*, **1**(1994), 159–166.

Greaves, M. and Maley, C. C. (2012). Clonal evolution in cancer. *Nature*, **481**(7381), 306–13.

Greenman, C., Stephens, P., Smith, R., Dalgliesh, G. L., Hunter, C., Bignell, G., Davies, H., Teague, J., Butler, A., Stevens, C., Edkins, S., O'Meara, S., Vastrik, I., Schmidt, E. E., Avis, T., Barthorpe, S., Bhamra, G., Buck, G., Choudhury, B., Clements, J., Cole, J., Dicks, E., Forbes, S., Gray, K., Halliday, K., Harrison, R., Hills, K., Hinton, J., Jenkinson, A., Jones, D., Menzies, A., Mironenko, T., Perry, J., Raine, K., Richardson, D., Shepherd, R., Small, A., Tofts, C., Varian, J., Webb, T., West, S., Widaa, S., Yates, A., Cahill, D. P., Louis, D. N., Goldstraw, P., Nicholson, A. G., Brasseur, F., Looijenga, L., Weber, B. L., Chiew, Y.-E., DeFazio, A., Greaves, M. F., Green, A. R., Campbell, P., Birney, E., Easton, D. F., Chenevix-Trench, G., Tan, M.-H., Khoo, S. K., Teh, B. T., Yuen, S. T., Leung, S. Y., Wooster, R., Futreal, P. A., and Stratton, M. R. (2007). Patterns of somatic mutation in human cancer genomes. *Nature*, **446**(7132), 153–8.

Gunawan, B., von Heydebreck, A., Sander, B., Schulten, H. J., Haller, F., Langer, C., Armbrust, T., Bollmann, M., Gasparov, S., Kovac, D., and Füzesi, L. (2007). An oncogenetic tree model in gastrointestinal stromal tumours (GISTs) identifies different pathways of cytogenetic evolution with prognostic implications. *J Pathol*, **211**(4), 463–470.

Hadfield, J. (2010). MCMC Methods for Multi-response Generalized Linear Mixed Models: The MCMCglmm R Package. *Journal of Statistical Software*, **33**(2), 1–22.

Hainke, K., Rahnenführer, J., and Fried, R. (2012). Cumulative disease progression models for cross-sectional data: A review and comparison. *Biometrical journal. Biometrische Zeitschrift*, **54**(5), 617–40.

Hanahan, D. and Weinberg, R. (2011). Hallmarks of Cancer: The Next Generation. *Cell*, **144**(5), 646–674.

Held, L., Schrödle, B., and Rue, H. (2010). Posterior and cross-validatory predictive checks: a comparison of MCMC and INLA. In T. Kneib and G. Tutz, editors, *Statistical Modelling and Regression Structures*, chapter 6, pages 91–110. Physica-Verlag HD.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Hjelm, M., Höglund, M., and Lagergren, J. (2006). New probabilistic network models and algorithms for oncogenesis. *J Comput Biol*, **13**(4), 853–865.

Jiang, H. Y., Huang, Z. X., Zhang, X. F., Desper, R., and Zhao, T. (2007). Construction and analysis of tree models for chromosomal classification of diffuse large B-cell lymphomas. *World J Gastroenterol*, **13**(11), 1737–1742.

Khurana, E., Fu, Y., Chen, J., and Gerstein, M. (2013). Interpretation of Genomic Variants Using a Unified Biological Network Approach. *PLoS Computational Biology*, **9**(3), e1002886.

Leiserson, M. D. M., Blokh, D., Sharan, R., and Raphael, B. J. (2013). Simultaneous Identification of Multiple Driver Pathways in Cancer. *PLoS Computational Biology*, **9**(5), e1003054.

Longerich, T., Mueller, M. M., Breuhahn, K., Schirmacher, P., Benner, A., and Heiss, C. (2012). Oncogenetic tree modeling of human hepatocarcinogenesis. *International journal of cancer. Journal international du cancer*, **130**(3), 575–83.

Mather, W. H., Hasty, J., and Tsimring, L. S. (2012). Fast stochastic algorithm for simulating evolutionary population dynamics. *Bioinformatics (Oxford, England)*, **28**(9), 1230–1238.

McFarland, C. D., Korolev, K. S., Kryukov, G. V., Sunyaev, S. R., and Mirny, L. a. (2013). Impact of deleterious passenger mutations on cancer progression. *Proceedings of the National Academy of Sciences of the United States of America*, **110**(8), 2910–5.

Merlo, L. M. F., Pepper, J. W., Reid, B. J., and Maley, C. C. (2006). Cancer as an evolutionary and ecological process. *Nature Reviews Cancer*, **6**(12), 924–935.

Narendra, V., Lytkin, N. I., Aliferis, C. F., and Statnikov, A. (2011). A comprehensive assessment of methods for de-novo reverse-engineering of genome-scale regulatory networks. *Genomics*, **97**(1), 7–18.

Pathare, S., Schäffer, A. A., Beerenwinkel, N., and Mahimkar, M. (2009). Construction of oncogenetic tree models reveals multiple pathways of oral cancer progression. *International journal of cancer. Journal international du cancer*, **124**(12), 2864–2871.

Pepe, M. (2003). *The statistical evaluation of medical tests for classification and prediction*. Oxford University Press, Oxford, UK.

Radmacher, M. D., Simon, R., Desper, R., Taetle, R., Schaffer, A. A., and Nelson, M. A. (2001). Graph Models of Oncogenesis with an Application to Melanoma. *Journal of Theoretical Biology*, **212**(4), 535–548.

Raphael, B. and Vandin, F. (2014). Simultaneous Inference of Cancer Pathways and Tumor Progression from Cross-Sectional Mutation Data. In R. Sharan, editor, *Research in Computational Molecular Biology. Lecture Notes in Computer Science, v. 8394*, pages 250–264. Springer International Publishing.

Reiter, J., Bozic, I., Chatterjee, K., and Nowak, M. (2013). TTP: tool for tumor progression. In N. Sharygina and H. Veith, editors, *Computer Aided Verification, Lecture Notes in Computer Science*, pages 101–106. Springer-Verlag, Berlin, Heidelberg.

Rieker, R. J., Penzel, R., Aulmann, S., Blaeker, H., Morresi-Hauf, A., Hecker, E., Otto, H. F., Mechtersheimer, G., and von Heydebreck, A. (2005). Oncogenetic tree models based on cytogenetic data: new insights into the development of epithelial tumors of the thymus. *Cancer Genet Cytogenet*, **158**(1), 75–80.

Rue, H. v., Martino, S., and Chopin, N. (2009). Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, **71**(2), 319–392.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Sakoparnig, T. and Beerenwinkel, N. (2012). Efficient sampling for Bayesian inference of conjunctive Bayesian networks. *Bioinformatics (Oxford, England)*, **28**(18), 2318–24.

Simon, R., Desper, R., Papadimitriou, C. H., Peng, A., Alberts, D. S., Taetle, R., Trent, J. M., and Schäffer, A. A. (2000). Chromosome abnormalities in ovarian adenocarcinoma: III. Using breakpoint data to infer and test mathematical models for oncogenesis. *Genes, Chromosomes and Cancer*, **28**(1), 106–120.

Sjoblom, T., Jones, S., Wood, L. D., Parsons, D. W., Lin, J., Barber, T. D., Mandelker, D., Leary, R. J., Ptak, J., Silliman, N., Szabo, S., Buckhaults, P., Farrell, C., Meeh, P., Markowitz, S. D., Willis, J., Dawson, D., Willson, J. K. V., Gazdar, A. F., Hartigan, J., Wu, L., Liu, C., Parmigiani, G., Park, B. H., Bachman, K. E., Papadopoulos, N., Vogelstein, B., Kinzler, K. W., and Velculescu, V. E. (2006). The Consensus Coding Sequences of Human Breast and Colorectal Cancers. *Science*, **314**(5797), 268–274.

Sprouffske, K., Pepper, J. W., and Maley, C. C. (2011). Accurate reconstruction of the temporal order of mutations in neoplastic progression. *Cancer prevention research (Philadelphia, Pa.)*, **4**(7), 1135–44.

Sprouffske, K., Merlo, L. M. F., Gerrish, P. J., Maley, C. C., and Sniegowski, P. D. (2012). Cancer in light of experimental evolution. *Current biology : CB*, **22**(17), R762–71.

Sweeney, C., Boucher, K. M., Samowitz, W. S., Wolff, R. K., Albertsen, H., Curtin, K., Caan, B. J., and Slattery, M. L. (2009). Oncogenetic tree model of somatic mutations and DNA methylation in colon tumors. *Genes, chromosomes & cancer*, **48**(1), 1–9.

Szabo, A. and Boucher, K. (2002). Estimating an oncogenetic tree when false negatives and positives are present. *Mathematical Biosciences*, **176**(2), 219–236.

Szabo, A. and Boucher, K. M. (2008). Oncogenetic trees. In W.-Y. Tan and L. Hanin, editors, *Handbook of cancer models with applications*, chapter 1, pages 1–24. World Scientific.

Szabo, A. and Pappas, L. (2013). Oncotree: Estimating oncogenetic trees.

Tofigh, A., Sjolund, E., Hoglund, M., and Lagergren, J. (2011). A global structural EM algorithm for a model of cancer progression. In J. Shawe-Taylor, R. Zemel, P. Bartlett, F. Pereira, and K. Weinberger, editors, *Advances in Neural Information Processing Systems*, volume 24, pages 163–171. Curran Associates, Inc.

Tomasetti, C., Vogelstein, B., and Parmigiani, G. (2013). Half or more of the somatic mutations in cancers of self-renewing tissues originate prior to tumor initiation. *Proceedings of the National Academy of Sciences of the United States of America*, **110**(6), 1999–2004.

Vandin, F., Upfal, E., and Raphael, B. J. (2012). De novo discovery of mutated driver pathways in cancer. *Genome research*, **22**(2), 375–85.

Vermeulen, L., Morrissey, E., van der Heijden, M., Nicholson, A. M., Sottoriva, A., Buczacki, S., Kemp, R., Tavaré, S., and Winton, D. J. (2013). Defining stem cell dynamics in models of intestinal tumor initiation. *Science (New York, N.Y.)*, **342**(6161), 995–8.

Vogelstein, B., Fearon, E. R., Hamilton, S. R., Kern, S. E., Preisinger, A. C., Leppert, M., Smits, A. M. M., and Bos, J. L. (1988). Genetic Alterations during Colorectal-Tumor Development. *New England Journal of Medicine*, **319**(9), 525–532.

Vogelstein, B., Papadopoulos, N., Velculescu, V. E., Zhou, S., Diaz, L. a., and Kinzler, K. W. (2013). Cancer Genome Landscapes. *Science*, **339**(6127), 1546–1558.

von Heydebreck, A., Gunawan, B., and Füzesi, L. (2004). Maximum likelihood estimation of oncogenetic tree models. *Biostatistics*, **5**(4), 545–556.

bioRxiv preprint doi: https://doi.org/10.1101/005587; this version posted May 27, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Watson, I. R., Takahashi, K., Futreal, P. A., and Chin, L. (2013). Emerging patterns of somatic mutations in cancer. *Nature reviews. Genetics*, **14**(10), 703–718.

Wood, L. D., Parsons, D. W., Jones, S., Lin, J., Sjoblom, T., Leary, R. J., Shen, D., Boca, S. M., Barber, T., Ptak, J., Silliman, N., Szabo, S., Dezso, Z., Ustyanksky, V., Nikolskaya, T., Nikolsky, Y., Karchin, R., Wilson, P. A., Kaminker, J. S., Zhang, Z., Croshaw, R., Willis, J., Dawson, D., Shipitsin, M., Willson, J. K. V., Sukumar, S., Polyak, K., Park, B. H., Pethiyagoda, C. L., Pant, P. V. K., Ballinger, D. G., Sparks, A. B., Hartigan, J., Smith, D. R., Suh, E., Papadopoulos, N., Buckhaults, P., Markowitz, S. D., Parmigiani, G., Kinzler, K. W., Velculescu, V. E., and Vogelstein, B. (2007). The Genomic Landscapes of Human Breast and Colorectal Cancers. *Science*, **318**(5853), 1108–1113.

Yap, T. a., Gerlinger, M., Futreal, P. A., Pusztai, L., and Swanton, C. (2012). Intratumor heterogeneity: seeing the wood for the trees. *Science translational medicine*, **4**(127), 127ps10.

Youn, A. and Simon, R. (2011). Identifying cancer driver genes in tumor genome sequencing studies. *Bioinformatics (Oxford, England)*, **27**(2), 175–81.

Youn, A. and Simon, R. (2012). Estimating the order of mutations during tumorigenesis from tumor genome sequencing data. *Bioinformatics (Oxford, England)*, **28**(12), 1555–61.