

Emerging Topics in Cancer Evolution

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Cancer results from an evolutionary process that yields a heterogeneous tumor with distinct subpopulations and varying sets of somatic mutations. This perspective discusses computational methods to infer models of evolutionary processes in cancer that aim to improve our understanding of tumorigenesis and ultimately enhance current clinical practice.

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1. Introduction

Cancer results from an evolutionary process where somatic mutations accumulate in distinct populations of cells.¹ This theory has been corroborated by high-throughput sequencing studies of tumors in the last decade,² demonstrating that a tumor is not homogeneous but rather composed of *clones* with varying sets of somatic mutations. This phenomenon of *intra-tumor heterogeneity* is a major cause of relapse and resistance to treatment.³ Metastasis, i.e. the migration of tumor cells to anatomical locations distinct from the primary tumor, is the primary cause of death in cancer.⁴ Thus, the life history of a tumor is the end product of an evolutionary process characterized by cell division, cell mutation and cell migration. The emerging field of *cancer phylogenetics* views cancer through the lens of evolution and employs phylogenetic techniques to reconstruct, analyze and compare life histories of tumors.⁵ This perspective will discuss recent advances in (i) computational methods for reconstructing cancer phylogenies from sequencing data, (ii) the identification of common evolutionary patterns and trajec-

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ries in cancers, (iii) inference and deconvolution of mutational signatures of cancers, and (iv) adaptive therapies for treating cancer based on evolutionary models.

2. Reconstruction of cancer phylogenies from sequencing data

Not only are tumors distinct due to separate evolutionary processes, but each tumor contains multiple *subclones* that each share a common ancestor and set of somatic mutations. *Somatic mutations* are genetic and epigenetic alterations that occur during an individual's lifetime. The former range from *single-nucleotide variants* (SNVs), which alter a single nucleotide, to *copy-number aberrations* (CNAs), which duplicate or delete large genomic regions, as well as other *structural variants* (SVs), which include CNAs in addition to inversion and transposition/translocation of genomic segments. To study cancer evolution, researchers rely on computational methods that infer phylogenies from sequencing data, underpinned by an *evolutionary model* that constrains the types of allowed changes. Initially, *bulk DNA sequencing* was used, yielding short DNA sequences, or *reads*, from millions of cells with diverse genomes. Such data require deconvolution methods,^{6–10} which yield many plausible phylogenies.¹¹ On the other hand, *single-cell DNA sequencing* (scDNA-seq) yields reads from individual cells, and generally does not require deconvolution, but has elevated error rates, requiring specialized methods to simultaneously infer trees and correct errors.^{12–15} Recent methods have been proposed to infer tumor phylogenies from bulk and scDNA-seq data of the same tumor.^{16,17} Importantly, current models for cancer evolution and corresponding phylogeny inference methods focus either only on SNVs^{6–10,12–15} or on CNAs,^{18–20} but not yet both in full generality. We anticipate that future research will focus on evolutionary models and computational methods that capture the interplay and evolutionary history of genomic SNVs, CNAs, SVs, and epigenomic alterations. Moreover, we expect that techniques that have been developed for tumor phylogeny inference will be applicable to lineage tracing.²¹

3. Identification of common evolutionary patterns and trajectories in cancers

While each cancer results from a different instantiation of an evolutionary process, the complexity of all cancers can be reduced to a small number of principles, so called *hallmarks of cancer*,²² corresponding to different biological pathways. Nevertheless, there is an exponential number of combinations of mutations in which these traits can be acquired. Cancer subtypes divide primary cancers into smaller groups based on morphological and/or molecular features. There is increasing evidence that more granular cancer subtypes based on common evolutionary patterns better stratify patients in terms of survival and therapy response.²³ Recently, several methods have been introduced to infer evolutionary trajectories from cancer phylogeny cohorts.^{23–25} Briefly, REVOLVER²³ is a machine-learning method that uses transfer learning to identify hidden evolutionary patterns in cancer cohorts. CONETT²⁶ is a combinatorial optimization method to detect recurrent tumor evolution trajectories using a consensus tree approach. Similarly, RECAP²⁵ is a computational method that resolves ambiguities in cancer sequencing data and detects subtypes of evolutionary trajectories by simultaneously (i) identifying a single tree among the solution space of trees for each patient, (ii) assigning patients to clusters and (iii) inferring a consensus tree for each cluster of patients. While current

approaches use mutations in matching genes across patients as a key signal, we anticipate further developments that will enable the inference of evolutionary trajectories composed of pathways or sets of mutated genes that are mutually interchangeable.

4. Inference and deconvolution of mutational signatures of cancers

Exposures to endogenous (e.g. DNA mismatch repair deficiency) and exogenous (e.g. tobacco smoke or UV light) factors lead to characteristic patterns of SNVs, or *mutational signatures*.²⁷ That is, the set of somatic mutations in a tumor is the result of varying exposures to distinct mutational processes that can be represented by “signatures” that delineate the types of mutations associated with a given process. While initial work has focused on identifying the additive effects of mutational signatures using non-negative matrix factorization,²⁷ later work has focused on identifying non-additive secondary effects,²⁸ including interactions between DNA damage events and deficiencies in repair mechanisms. Recognizing that exposures to mutational signatures may vary during the evolution of a tumor, one line of research has focused on identifying the interplay between mutational processes and cancer evolution. TrackSig²⁹ and TrackSigFreq³⁰ aim to construct evolutionary trajectories of signature exposures, defined by changepoints in exposure ordered by pseudotime. In a similar vein, PhySigs³¹ seeks to infer the clonal dynamics of mutational signatures in a tumor by identifying exposure shifts along the edges of a given cancer phylogeny. There are important therapeutic opportunities associated with studying mutational signatures in an evolutionary context. For example, mutational signatures can be used as a biomarker for perturbed DNA damage repair (DDR),^{32,33} for which promising cancer therapies such as PARP inhibitors exist. By taking the clonality of DDR mutation signature exposures into account, one can identify cases where only a fraction of cells have a DDR deficiency and therefore the patient is unlikely to have a complete response to a therapy targeting that deficiency.

5. Adaptive therapies for treating cancer based on evolutionary models

While many targeted cancer therapies have been introduced in the past two decades,³⁴ targeted therapies often have a response rate of less than 50% in solid tumors.³⁵ Resistance to therapy can be classified as either primary, where patients show no response to treatment, or secondary, where patients initially respond but later develop resistance. A prominent example of the latter is the treatment of melanoma with vemurafenib that targets the *BRAF* V600E mutation: despite an initial dramatic response, most patients eventually relapse with drug-resistant, fatal disease.³⁶ There is growing evidence that intra-tumor heterogeneity is a major driver of resistance to therapy.³⁷ To understand why, it is important to distinguish *clonal* somatic mutations, which are present in every tumor cell, from *subclonal* somatic mutations, which are present in only a subset of tumor cells. In chronic myeloid leukemia,³⁸ treatment that targets subclonal driver mutations has been associated to resistance and recurrence. Moreover, therapy itself is an evolutionary bottleneck and may lead to previously low-abundance, resistant clones becoming dominant. Therefore, it is important to take the clonal architecture of a tumor into account when designing treatment plans. Future research directions in this area include identifying effective combination therapies, where multiple targeted drugs are

used simultaneously, as well as adaptive containment strategies where targeted drugs are used alternately in order to constrain evolution in tumors with multiple clones.³⁴ Both directions will depend on accurate computational methods for tumor phylogeny inference, as well as high-throughput sequencing and monitoring strategies such as liquid biopsies.

6. Discussion

This perspective discussed emerging topics in cancer evolution, focusing on recent advances in tumor phylogeny inference, identification of evolutionary trajectories, mutational signatures as well as cancer therapy in light of evolution. While the field has mainly focused on reconstructing a tumor's evolutionary history in terms of genetic alterations, it is important to also take the evolution of epigenetic mutations into account. Continued interdisciplinary collaboration between cancer biologists, computational method developers and clinicians on these topics will be essential towards gaining a more thorough understanding of tumor emergence, proliferation and metastatic expansion and response to therapy. Ultimately this will be an essential step towards achieving the goal of improved clinical treatments.

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