A Multistage Carcinogenesis Framework to Study Cancer Recurrence





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Introduction

- Multistage carcinogenesis models, e.g., the Two-Stage Clonal Expansion model, have been widely used to study cancer mechanisms, incidence, and mortality risk. However, these models have not yet been used to study potential mechanisms of cancer recurrence
- We present a novel mechanistic modeling framework for cancer recurrence, which
- Provides insights into biological mechanisms driving cancer recurrence: therapeutic resistance and cancer dormancy
- Allows for parameter estimations using cancer survivor cohorts
- Adaptable to various cancer sites
- Has the potential to include time-varying covariates









- by remnant malignant stem cells, whereas later increase in recurrence rate may be driven by remnant premalignant stem cells
- Estimated treatment failure rate was higher among malignant stem cells $(S_M vs. S_P)$
- The rate of breaking from cancer dormancy was similar between these two types of cells (ρ_M vs. ρ_P) • This modeling framework shows the potential to inform mechanisms of cancer recurrence with mechanistic models and incidence/recurrence data • Future steps:
 - Fit the multistage incidence model using using localized/regional prostate cancer incidence data
 - Test the robustness of model parameters
 - Validate model in other datasets and incorporate clinical experts' feedbacks

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