

# Mathematical Modeling of Field Cancerization through the Lens of Cancer Behavioral Ecology

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## Abstract

Field cancerization is a process in which a normal tissue is replaced with pre-cancerous but histologically normal tissue. This transformed field can give rise to malignancy and contribute to tumor relapse. In this paper, we create a mathematical model of field cancerization from the perspective of cancer behavioral ecology. In our model, field cancerization arises from a breakdown in signaling integrity and control, and investigate implications for acute wounding, chronic wounding, aging, and therapeutic interventions. We find that restoration of communication networks can lead to cancer regression in the context of acute injury. Conversely, long term loss of controls, such as through chronic wounding or aging, can promote oncogenesis. These results are paralleled in therapeutic interventions: those that simply target cells in cancerous states may be less effective than those that reestablish signaling integrity. Viewing cancer as a corruption of communication systems rather than as a corruption of individual cells may lead to novel approaches for understanding and treating this disease.

## 1 Introduction

The notion of field cancerization was introduced by Slaughter in 1953 as an explanation for the multitude of oral squamous cell carcinomas, their local recurrences, and the molecular abnormalities observed in histologically benign tissue surrounding these cancers [46]. Since then, tumor fields have been discovered in many more organs [6, 12]: head and neck [24, 53], lung [21, 39, 40], vulva and cervix [11, 43], ovaries [9, 38], esophagus [22, 41], skin [15, 18, 30], breast [2, 17, 19], colon [23, 29, 56], stomach [31, 32, 33], gallbladder [51], prostate [14, 52, 57], pancreas [28], and bladder [50].

Also known as field effects or field defects, field cancerization describes carcinogen-induced genetic or epigenetic changes in the epithelium that can give rise to independent malignant lesions, often leading to multifocal tumors [44]. This process occurs in three main steps: First, a carcinogenic insult such as UVA exposure [25], smoke, or alcohol [36] induces genetic or epigenetic aberrations in a cell or population of cells. If these alterations confer a fitness advantage in the existing microenvironment, clonal expansion of the precancerous cells will occur, forming a field. Further alterations transform these cells into malignant, histologically abnormal ones, commonly recognized as cancer. In this environment, removal of cancer cells (e.g., by surgery) does not remove the underlying tumor field, so recurrence is likely.

29

30 The field cancerization theory shares many similarities with the multistage model of carcinogenesis [4, 20].  
 31 Namely, tumor initiation occurs when the initial cell or cells are transformed, tumor promotion occurs due to  
 32 the selective expansion of precancerous cells, malignant conversion occurs upon subsequent mutations or epimu-  
 33 tations, and tumor progression occurs as malignant cells acquire more aggressive characteristics, promoting re-  
 34 gional invasion and eventual distant metastasis. Although the field cancerization theory posits that “cancer does  
 35 not arise as an isolated cellular phenomenon, but rather as an anaplastic tendency involving many cells at once”  
 36 [45], field cancerization still puts the focus of cancer at the cellular level.

37

38 Here, we adopt a different view. Building on our cancer behavioral ecology work [7], we conceptualize cancer  
 39 not as an identity problem but as a relational one [47]. Namely, we view cancer as a corruption of communica-  
 40 tion systems and the potential subsequent selection of “cancerous cells” as a byproduct of this process. Under  
 41 this framework, cancerous cells are constantly being generated by normal cells, but are quickly eliminated due  
 42 to controls in the signaling system. When there is a breakdown in communication (e.g., due to a carcinogen,  
 43 wounding, or aging), these controls are weakened. This selects for cancer cells that clonally expand and create  
 44 a tumor field from which more aggressive malignancies can develop. In this paper, we create a mathematical  
 45 model to capture this process and investigate how acute wounding, chronic wounding, aging, and therapy impact  
 46 tumorigenesis.

## 47 2 Methodology

### 48 2.1 ODE Model of Normal, Precancerous, and Malignant Cells

49 To create a mathematical model of field cancerization, we construct a set of ordinary differential equations (ODEs)  
 50 to capture the dynamics of three cell populations: normal cells ( $N$ ), precancerous cells ( $P$ ), and malignant cells  
 51 ( $M$ ). We then simulate the model using a modified Gillespie algorithm, including rare, unidirectional mutations  
 52 towards malignancy [8]. The ODE model is as follows:

$$\begin{aligned}
 \frac{dN}{dt} &= \underbrace{r_N N \left( \frac{K_1 - N - P}{K_1} \right)}_{\text{Logistic Growth}} \underbrace{-d_N N}_{\text{Background Death}} \underbrace{-s(t)N}_{\text{Exogenous Death}} \\
 \frac{dP}{dt} &= \underbrace{r_P P \left( \frac{K_1 - N - P}{K_1} \right)}_{\text{Logistic Growth}} \underbrace{-d_N P}_{\text{Background Death}} \underbrace{-c_P(N, P, M)P}_{\text{Control-Induced Death}} \underbrace{-s(t)P}_{\text{Exogenous Death}} \\
 \frac{dM}{dt} &= \underbrace{r_M M \left( \frac{K_2 - M}{K_2} \right)}_{\text{Logistic Growth}} \underbrace{-d_N M}_{\text{Background Death}} \underbrace{-c_M(N, P, M)M}_{\text{Control-Induced Death}} \underbrace{-s(t)M}_{\text{Exogenous Death}}
 \end{aligned} \tag{1}$$

53 We make the simplifying assumption that all cells grow in a logistic manner, with normal and precancerous cells  
 54 competing within the epithelium and malignant cells competing only with each other and subject to a larger carry-  
 55 ing capacity due to tumor geometry ( $K_2 > K_1$ ). We let all cells have the same background death rate ( $d_N$ ) and  
 56 include a death rate for precancerous and malignant cells ( $c_M > c_P$ ) that captures their death due to controls in  
 57 the signaling system (e.g., immune surveillance). We let

$$\begin{aligned} c_P(N, P, M) &= 0.3 + 0.3 \tanh \left( N + P + M - K_1 \left( 1 - \frac{d_N}{r_N} \right) \right) \\ c_M(N, P, M) &= 0.6 + 0.6 \tanh \left( N + P + M - K_1 \left( 1 - \frac{d_N}{r_N} \right) \right) \end{aligned} \quad (2)$$

58 where  $K_1 \left( 1 - \frac{d_N}{r_N} \right)$  is the number of cells in the tissue at healthy equilibrium. This formulation assumes that  
59 immune surveillance, for example, is dampened when the tissue is injured because the need to proliferate and  
60 repair the damage outweighs the need to eliminate potential cancer cells. When the tissue returns to homeosta-  
61 sis, the immune system adopts a more discerning phenotype and again removes cancerous cells more effectively.  
62 Control-induced death thus varies with the effects of exogenous influences like wounding, aging, or therapy.  
63 Death caused directly by these exogenous factors is captured by  $s(t)$ . We assume that the intrinsic growth rate is  
64 higher for cells with a more cancerous phenotype:  $r_M > r_P > r_N$ . The baseline parameter values used in our  
65 simulations are given in Table 1.

66

Parameter	Interpretation	Value
$K_1$	Carrying capacity of normal and precancerous cells	$10^4$ cells
$K_2$	Carrying capacity of malignant cells	$10^5$ cells
$r_N$	Intrinsic growth rate of normal cells	0.3/day
$r_P$	Intrinsic growth rate of precancerous cells	0.6/day
$r_M$	Intrinsic growth rate of malignant cells	0.8/day
$d_N$	Natural death rate	0.1/day
$c_P$	Control-induced death at homeostasis: pre-cancerous cells	0.3/day
$c_M$	Control-induced death at homeostasis: malignant cells	0.6/day
$s(t)$	Environment-induced death	0/day
$\mu_N$	Mutation rate: normal to precancerous	$10^{-3}$
$\mu_P$	Mutation rate: precancerous to malignant	$10^{-5}$

Table 1: Model parameters and values used in simulations.

## 67 2.2 Stochastic Simulation: Birth-Death-Mutation Process

68 For simulation, we use a modified Gillespie algorithm, similar to [8]. We first compute birth and death rates at  
69 each time step for each cell type from Equation 1. We then compute the total event rate by summing the birth  
70 and death rates across cell types. The time to next event is sampled from an exponential probability distribution  
71 with a mean of the total event rate. The event type is probabilistically chosen based on the relative contributions  
72 of each rate to the total event rate. This event is implemented and the procedure is repeated until a final time is  
73 reached and the simulation is stopped. If the event is death, one cell from the respective cell type compartment is  
74 eliminated. If the event is birth, we must account for the possibility of mutation. For simplicity, we allow muta-  
75 tions only from normal to precancerous cells (at rate  $\mu_N$ ) and from precancerous to malignant cells (at rate  $\mu_P$ ).  
76 If no mutation occurs, one cell is added to the relevant compartment. If a mutation occurs in a normal cell, one  
77 cell is added to the precancerous compartment. If a mutation occurs in a precancerous cell, one cell is added to  
78 the malignant compartment. This procedure is summarized in Figure 1.

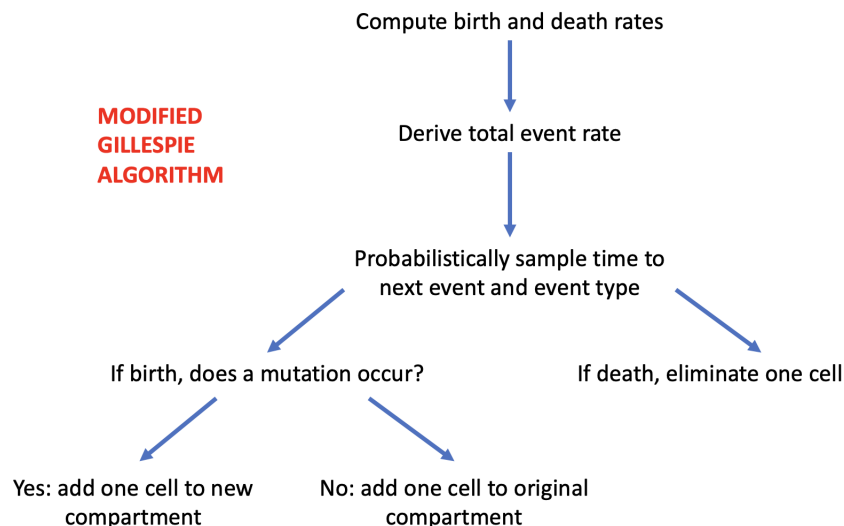


Figure 1: Flowchart depicting the modified Gillespie algorithm used for simulation.

## 3 Results

We simulate the population dynamics of normal, precancerous, and malignant cells under a variety of scenarios. In each case, a set of ten simulations are performed as follows: We initialize the population at homeostatic equilibrium (6667 normal cells) and run the simulation for 750 days. We test whether the system transiently or permanently switches to a cancerous state in four scenarios: healthy tissue homeostasis, acute wounding, chronic wounding, and aging. Finally, we show how restoration of controls is more effective than removal of cancerous cells for cancer elimination.

### 3.1 Control: Healthy Case

In the healthy case, the tissue is at homeostasis. The communication network is robust. The high penalty on cells in a precancerous or malignant state should maintain a population composed primarily of normal cells. We implement this scenario in Fig. 2 by using the default parameter values given in Table 1. As expected, normal cells dominate the population at all times. Although cancerous cells occasionally arise, high control-induced death rates lead to their rapid elimination.

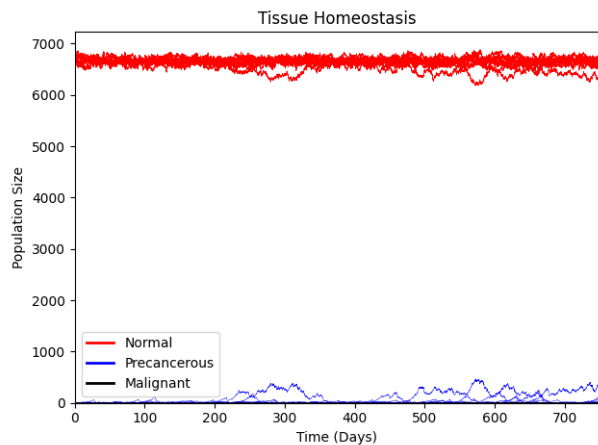


Figure 2: Healthy control. Red, blue, and black lines represent normal, precancerous, and malignant cells respectively. Each line corresponds to one, out of a total of ten, replicate simulation runs. Despite high cell division rates, precancerous and malignant cells exist at very low frequencies in the population due to high control-induced death rates. The tissue is composed of nearly all normal cells at all times.

## 92 3.2 Acute Wounding

93 With acute wounding, the tissue suffers damage due to a traumatic event which leads to the death of most its  
94 cells. In addition, cell communication networks and morphogenetic fields are disrupted and immune surveillance  
95 is dampened, leading to the transient loss of controls. As the tissue is repaired, controls are gradually reinstated.  
96 This differs from chronic wounding (Section 3.3) in two ways: the stressor only occurs once (allowing for tissue  
97 recovery and restoration of signaling integrity) and tissue damage due to the wound is severe. To simulate this,  
98 we induce the traumatic event at day 100 by setting  $s(t) = 1$  for  $t \in [100, 101]$ . This kills roughly 37% of the  
99 cells in the tissue.

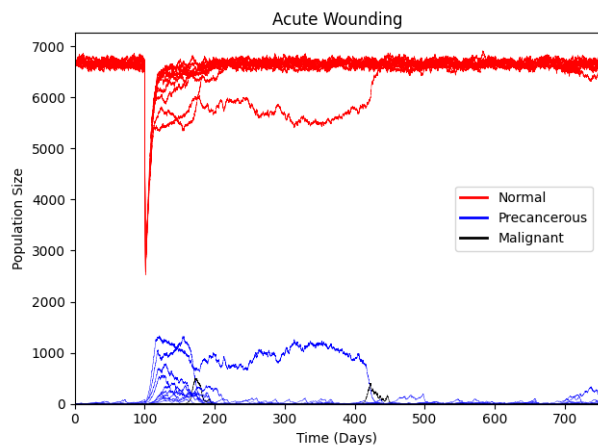


Figure 3: Acute wounding. Red, blue, and black lines represent normal, precancerous, and malignant cells respectively. Each line corresponds to one, out of a total of ten, replicate simulation runs. A traumatic event leads to rapid cell death. This leads to a loss of controls and allows for the expansion of precancerous and malignant cells. As signaling integrity is gradually restored, these cancerous cells are eliminated and the tissue returns to healthy homeostasis.

100 Before the wound, the healthy tissue is comprised almost entirely of normal cells. Once the wound occurs, the  
101 population size drops dramatically due to rapid cell death. Signaling integrity is disturbed and controls are lost,  
102 leading to the expansion of cancerous cells. However, as the communication networks are restored and controls

103 are put back in place, cells revert to their original frequencies. Restoring signaling networks is thus a potent way  
104 to promote cancer regression.

### 105 3.3 Chronic Wounding

106 Chronic wounding continually damages the tissue due to a chronic stressor such as UV radiation, tobacco, di-  
107 abetes, or ulcers. This leads to excessive inflammation and disruption of signaling integrity in the tissue, ul-  
108 timately hindering tissue repair and promoting tumorigenesis. This builds on the long-standing description of  
109 cancer as a “wound that never heals” [10, 13, 16, 26, 55]. Unlike the tightly regulated process of recovery from  
110 acute wounding, tissue injury is never resolved and controls are not reinstated. Thus, the self-limiting hyperpro-  
111 liferative behavior during epithelial regeneration is left unchecked, allowing growth of cancer [49]. To simulate  
112 this phenomenon, we assume that chronic wounding begins at day 100 and let  $s(t > 100) = 0.15$  to capture  
113 continual tissue damage (Fig. 4).

114  
115 After establishing healthy homeostasis during the first 100 days, chronic wounding reduces the population size,  
116 thereby disrupting signaling systems and weakening controls. This allows for the expansion of precancerous and  
117 ultimately malignant cells, that eventually overtake the tissue (Fig. 4).

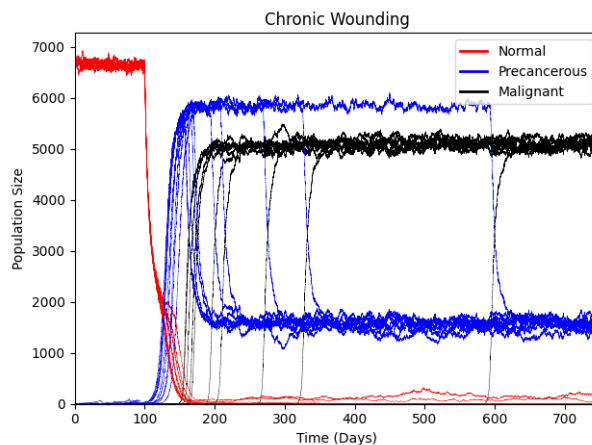


Figure 4: Chronic wounding. Red, blue, and black lines represent normal, precancerous, and malignant cells respectively. Each line corresponds to one, out of a total of ten, replicate simulation runs. Chronic wounding causes modest cell death, high cell turnover, and a corruption of communication networks. This paves the path for precancerous and malignant cells to invade the tissue.

### 118 3.4 Aging

119 Aging can be viewed as a gradual loss of controls and signaling integrity due to sarcopenia, tissue structural at-  
120 rophy, and a weakening of immunosurveillance abilities [5, 34, 35, 54]. To simulate this process, we let control-  
121 induced death be a decreasing function of time:  $c_P(N, P, M, t) := c_P(N, P, M) \exp(-0.01t)$  and  $c_M(t) :=$   
122  $c_M(N, P, M) \exp(-0.01t)$  (Fig. 5). The start of the simulation parallels that of healthy homeostasis: the com-  
123 munication system has not been disturbed and cancerous cells are unable to invade the population. Eventually,  
124 controls weaken to the extent that precancerous and malignant cells take over the population. By the end of the  
125 simulation period, no healthy cells remain. Note that the total population size far exceeds that in our other sim-  
126 ulations. This is due to the gradual decimation of controls: By the end of the simulation, control-induced death  
127 is negligible. This allows the malignant cells to grow unencumbered by the effects of the immune system, only  
128 limited in size by their carrying capacity.

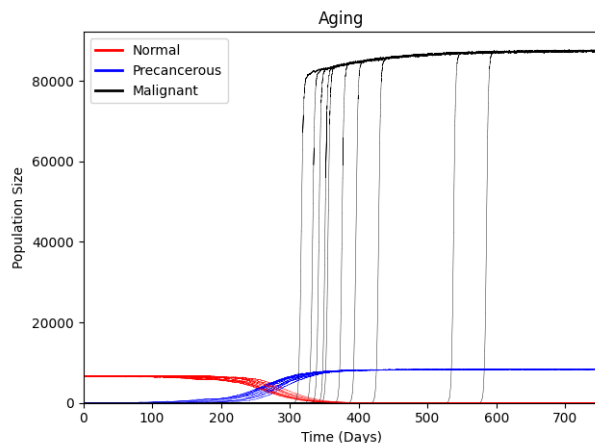


Figure 5: Aging. Red, blue, and black lines represent normal, precancerous, and malignant cells respectively. Each line corresponds to one, out of a total of ten, replicate simulation runs. As controls gradually weaken over time, precancerous and malignant cells expand to dominate the population.

### 129 3.5 Therapeutic Interventions

130 With this model of cancer initiation and progression through the lens of field cancerization and cancer behav-  
131 ioral ecology, we now consider implications for therapy. We investigate two therapeutic approaches. The first  
132 eliminates cells in the precancerous and malignant states via surgery. The second restores controls and signaling  
133 network integrity such as through immunotherapy [1, 37, 48]. In both cases, we will induce cancerization by set-  
134 ting  $c_P = c_M = 0$ . Therapeutic interventions are introduced when the cancerous population size exceeds the  
135 normal population size and the simulation is run until day 750.

136  
137 First, we consider the traditional approach of eliminating cells in the cancer state. Focusing on surgical inter-  
138 ventions, we make the extreme assumption that radical surgery removes all malignant and precancerous cells,  
139 while leaving all normal cells intact. To implement surgery, we set  $P = M = 0$  (Fig. 6). Surgery temporarily  
140 removes the cancer, but recurrence is inevitable because the lack of controls reinstates a cancer field, giving rise  
141 to malignancy.

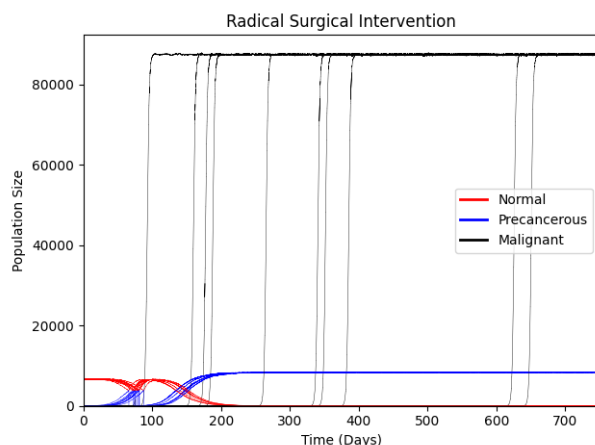


Figure 6: Impact of radical surgery. Red, blue, and black lines represent normal, precancerous, and malignant cells respectively. Each line corresponds to one, out of a total of ten, replicate simulation runs. Total elimination of precancerous and malignant cells cannot prevent tumor recurrence.

142 We hypothesize that therapeutic interventions that focus on reestablishing signaling integrity (e.g., via CAR-

143 T therapy [48], macrophage polarization [3], tumor microenvironment modification [42], or reinstating self-  
144 regulatory feedback loops on growth factor and cytokine production [13, 27, 49]) rather than directly killing  
145 cells in a cancerous state will be more effective for tumor elimination. To implement this strategy, we restore  
146 our controls to  $c_P = 0.3$  and  $c_M = 0.6$  when the cancerous population size surpasses the normal population size  
147 (Fig. 7). As expected, restoration of controls leads to high control-induced death rates in cancerous cells, leading  
148 to their elimination and preventing tumor recurrence.

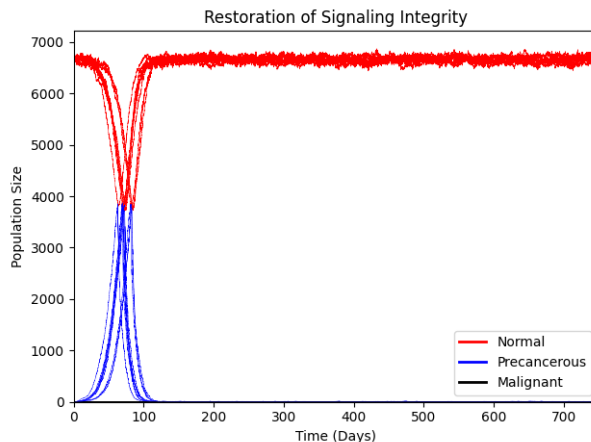


Figure 7: Impact of restoring signaling integrity. Red, blue, and black lines represent normal, precancerous, and malignant cells respectively. Each line corresponds to one, out of a total of ten, replicate simulation runs. Fortification of communication networks leads to rapid tumor regression.

## 149 4 Conclusion

150 Current cancer therapeutic efforts focus on effective ways of killing cells in a cancerous state. Although this ap-  
151 proach may be effective for elimination in the short term, it often allows recurrence. Here, we approached onco-  
152 genesis through a field cancerization lens and view oncogenesis as a three-step process: initial transformation  
153 via genetic or epigenetic aberrations, clonal expansion of precancerous clones to form a cancer field, and fur-  
154 ther transformations towards malignancy. Rather than adopting the traditional view that cancer is a disease of the  
155 cells, we take a cancer behavioral ecology approach and view cancer as a corruption of signaling systems. In this  
156 view, cancerous cells are continuously being generated within a tissue, but are quickly eliminated due to robust  
157 cell communication networks. When these networks are disrupted, “cancer cells” escape control and thrive.

158  
159 In this paper, we create a mathematical model to investigate the consequences of this world view for disruptions  
160 of signaling integrity by acute wounding, chronic wounding, and aging. Long term loss of controls does indeed  
161 lead to the expansion of cancerous cells. We also examine the efficacy of two classes of therapeutic interven-  
162 tions: traditional strategies that eliminate cancer cells and strategies that fortify the signaling networks them-  
163 selves, finding that restoration of signaling integrity is the key to prevent relapse.

164  
165 Future work will expand on this model in several directions. We plan to construct an explicit consumer-resource  
166 model to allow the growth rate of normal, precancerous, and malignant cells to depend on growth factors in the  
167 microenvironment, a key mechanism in wounding and inflammation. These models will include explicit mecha-  
168 nisms for how cancer cells hijack, corrupt, and co-opt communication networks in tissues and for tumor-immune  
169 and epithelial-stroma interactions.



## 5 Data Availability

Codes associated with the plots produced in this paper can be found at <https://github.com/abukkuri/FieldCancer>.

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## References

- [1] Alaa Alnefaie, Sarah Albogami, Yousif Asiri, Tanveer Ahmad, Saqer S. Alotaibi, Mohammad M. Al-Sanea, and Hisham Althobaiti. Chimeric Antigen Receptor T-Cells: An Overview of Concepts, Applications, Limitations, and Proposed Solutions. *Frontiers in Bioengineering and Biotechnology*, 10, 6 2022.
- [2] M. Amari. Loss of Heterozygosity Analyses of Asynchronous Lesions of Ductal Carcinoma in situ and Invasive Ductal Carcinoma of the Human Breast. *Japanese Journal of Clinical Oncology*, 33(11):556–562, 11 2003.
- [3] Namrata Anand, Keng Hee Peh, and Jill M. Kolesar. Macrophage Repolarization as a Therapeutic Strategy for Osteosarcoma. *International Journal of Molecular Sciences*, 24(3):2858, 2 2023.
- [4] P Armitage. Multistage models of carcinogenesis. *Environmental Health Perspectives*, 63:195–201, 11 1985.
- [5] Lieze Berben, Giuseppe Floris, Hans Wildiers, and Sigrid Hatse. Cancer and Aging: Two Tightly Interconnected Biological Processes. *Cancers*, 13(6):1400, 3 2021.
- [6] Boudewijn J.M. Braakhuis, Maarten P. Tabor, J. Alain Kummer, C. René Leemans, and Ruud H. Brakenhoff. A genetic explanation of slaughter’s concept of field cancerization: Evidence and clinical implications. *Cancer Research*, 63(8), 2003.
- [7] Anuraag Bukkuri and Fred Adler. Viewing Cancer Through the Lens of Corruption: Using Behavioral Ecology to Understand Cancer. *Frontiers in Ecology and Evolution*, 9:442, 2021.
- [8] Anuraag Bukkuri, Kenneth J. Pienta, Robert H. Austin, Emma U. Hammarlund, Sarah R. Amend, and Joel S. Brown. Stochastic models of Mendelian and reverse transcriptional inheritance in state-structured cancer populations. *Scientific Reports*, 12(1):13079, 7 2022.
- [9] Richard E. Buller, Jeffrey S. Skilling, Anil K. Sood, Steve Plaxe, Rebecca N. Baergen, and Donna J. Lager. Field cancerization: Why late “recurrent” ovarian cancer is not recurrent. *American Journal of Obstetrics and Gynecology*, 178(4):641–649, 4 1998.
- [10] Jung S. Byun and Kevin Gardner. Wounds That Will Not Heal. *The American Journal of Pathology*, 182(4):1055–1064, 4 2013.
- [11] Tang Yuan Chu, Chen Yang Shen, Heng Seng Lee, and Hang Seng Liu. Monoclonality and surface lesion-specific microsatellite alterations in premalignant and malignant neoplasia of uterine cervix: A local field effect of genomic instability and clonal evolution. *Genes Chromosomes and Cancer*, 24(2), 1999.

- 207 [12] Gabriel D. Dakubo, John P. Jakupciak, Mark A. Birch-Machin, and Ryan L. Parr. Clinical implications and  
208 utility of field cancerization, 2007.
- 209 [13] Matthew Deyell, Christopher S. Garris, and Ashley M. Laughney. Cancer metastasis as a non-healing  
210 wound, 2021.
- 211 [14] Rajiv Dhir, Barbara Vietmeier, Julie Arlotti, Marie Acquafondata, Douglas Landsittel, Robert Masterson,  
212 and Robert H. Getzenberg. Early Identification of Individuals with Prostate Cancer in Negative Biopsies.  
213 *Journal of Urology*, 171(4):1419–1423, 4 2004.
- 214 [15] S. E. Durham, K. J. Krishnan, J. Betts, and M. A. Birch-Machin. Mitochondrial DNA damage in non-  
215 melanoma skin cancer. *British Journal of Cancer*, 88(1), 2003.
- 216 [16] Harold F. Dvorak. Tumors: Wounds That Do Not Heal—Redux. *Cancer Immunology Research*, 3(1):1–11,  
217 1 2015.
- 218 [17] Darrell L. Ellsworth, Rachel E. Ellsworth, Brad Love, Brenda Deyarmin, Susan M. Lubert, Vimal Mittal,  
219 Jeffrey A. Hooke, and Craig D. Shriver. Outer Breast Quadrants Demonstrate Increased Levels of Genomic  
220 Instability. *Annals of Surgical Oncology*, 11(9):861–868, 9 2004.
- 221 [18] Alex Eshaghian, Ruth A. Vleugels, Jeffrey A. Canter, Michel A. McDonald, Thomas Stasko, and James E.  
222 Sligh. Mitochondrial DNA Deletions Serve as Biomarkers of Aging in the Skin, but Are Typically Absent  
223 in Nonmelanoma Skin Cancers. *Journal of Investigative Dermatology*, 126(2):336–344, 2 2006.
- 224 [19] David M. Euhus, Leslie Cler, Narayan Shivapurkar, Sara Milchgrub, George N. Peters, A. Marilyn Leitch,  
225 Shashank Heda, and Adi F. Gazdar. Loss of Heterozygosity in benign breast epithelium in relation to breast  
226 cancer risk. *Journal of the National Cancer Institute*, 94(11), 2002.
- 227 [20] Steven a. Frank. *Dynamics of Cancer. Incidence, Inheritance, and Evolution*. 2007.
- 228 [21] W A Franklin, A F Gazdar, J Haney, I I Wistuba, F G La Rosa, T Kennedy, D M Ritchey, and Y E Miller.  
229 Widely dispersed p53 mutation in respiratory epithelium. A novel mechanism for field carcinogenesis.  
230 *Journal of Clinical Investigation*, 100(8):2133–2137, 10 1997.
- 231 [22] Patricia C. Galipeau, Laura J. Prevo, Carissa A. Sanchez, Gary M. Longton, and Brian J. Reid. Clonal Ex-  
232 pansion and Loss of Heterozygosity at Chromosomes 9p and 17p in Premalignant Esophageal (Barrett’s)  
233 Tissue. *JNCI: Journal of the National Cancer Institute*, 91(24):2087–2095, 12 1999.
- 234 [23] W. M. Grady. Epigenetic events in the colorectum and in colon cancer. In *Biochemical Society Transac-*  
235 *tions*, volume 33, 2005.
- 236 [24] Patrick K. Ha and Joseph A. Califano. The molecular biology of mucosal field cancerization of the head  
237 and neck. *Critical Reviews in Oral Biology and Medicine*, 14(5), 2003.
- 238 [25] Bing Hu, Einar Castillo, Louise Harewood, Paola Ostano, Alexandre Reymond, Reinhard Dummer, Was-  
239 sim Raffoul, Wolfram Hoetzenecker, Günther F.L. Hofbauer, and G. Paolo Dotto. Multifocal epithelial  
240 tumors and field cancerization from loss of mesenchymal CSL signaling. *Cell*, 149(6), 2012.
- 241 [26] Yichao Hua and Gabriele Bergers. Tumors vs. Chronic Wounds: An Immune Cell’s Perspective. *Frontiers*  
242 *in Immunology*, 10, 9 2019.
- 243 [27] Yichao Hua and Gabriele Bergers. Tumors vs. Chronic Wounds: An Immune Cell’s Perspective, 9 2019.
- 244 [28] Tsutomu Izawa, Takeshi Obara, Satoshi Tanno, Yusuke Mizukami, Nobuyuki Yanagawa, and Yutaka Ko-  
245 hgo. Clonality and field cancerization in intraductal papillary-mucinous tumors of the pancreas. *Cancer*,  
246 92(7):1807–1817, 10 2001.

- 247 [29] Serge Jothy, Barbara Ślesak, Antonina Harłodzińska, Jadwiga Lapińska, Jolanta Adarniak, and Jerzy  
248 Rabczyński. Field effect of human colon carcinoma on normal mucosa: Relevance of carcinoembryonic  
249 antigen expression. *Tumor Biology*, 17(1), 1996.
- 250 [30] Sagarika Kanjilal, Sara S. Strom, Gary L. Clayman, Randal S. Weber, Adel K. El-Naggar, Vivek Kapur,  
251 Kathleen K. Cummings, Leigh Anne Hill, Margaret R. Spitz, Margaret L. Kripke, and Honnavara N. Anan-  
252 thaswamy. p53 Mutations in Nonmelanoma Skin Cancer of the Head and Neck: Molecular Evidence for  
253 Field Cancerization. *Cancer Research*, 55(16), 1995.
- 254 [31] Jun Suk Kim, Chul Won Choi, Byung Soo Kim, Sang Won Shin, Yeul Hong Kim, Yong Jae Mok, Jong Suk  
255 Kim, and Bum Hwan Koo. Amplification of c-erbB-2 proto-oncogene in cancer foci, adjacent normal,  
256 metastatic and normal tissues of human primary gastric adenocarcinomas. *Journal of Korean Medical  
257 Science*, 12(4), 1997.
- 258 [32] Jung Yeon Kim and Hye Jae Cho. DNA ploidy patterns in gastric adenocarcinoma. *Journal of Korean  
259 Medical Science*, 15(2), 2000.
- 260 [33] Seung-Kyoon Kim, Hae-Ran Jang, Jeong-Hwan Kim, Seung-Moo Noh, Kyu-Sang Song, Mi-Rang Kim,  
261 Seun-Young Kim, Young-II Yeom, Nam-Soon Kim, Hyang-Sook Yoo, and Yong Sung Kim. The epige-  
262 netic silencing of LIMS2 in gastric cancer and its inhibitory effect on cell migration. *Biochemical and  
263 Biophysical Research Communications*, 349(3):1032–1040, 10 2006.
- 264 [34] Ezio Laconi, Fabio Marongiu, and James DeGregori. Cancer as a disease of old age: changing mutational  
265 and microenvironmental landscapes. *British Journal of Cancer*, 122(7):943–952, 3 2020.
- 266 [35] Carlos López-Otín, Maria A. Blasco, Linda Partridge, Manuel Serrano, and Guido Kroemer. Hallmarks of  
267 aging: An expanding universe. *Cell*, 186(2), 2023.
- 268 [36] Meenakshi Mohan and Nithya Jagannathan. Oral field cancerization: An update on current concepts, 2014.
- 269 [37] Rimjhim Mohanty, Chitran Chowdhury, Solomon Arega, Prakriti Sen, Pooja Ganguly, and Niladri Gan-  
270 guly. CAR T cell therapy: A new era for cancer treatment (Review). *Oncology Reports*, 9 2019.
- 271 [38] B. Hannah Ortiz, Cristiano Colitti, Samuel C. Mok, Monica Ailawadi, Michael G. Muto, Ross S.  
272 Berkowitz, Michael Deavers, Elvio G. Silva, and David M. Gershenson. Second primary or recurrence?  
273 Comparative patterns of p53 and K-ras mutations suggest that serous borderline ovarian tumors and subse-  
274 quent serous carcinomas are unrelated tumors. *Cancer Research*, 61(19), 2001.
- 275 [39] Hongjie Pan, Joseph Califano, Jose F. Ponte, Andrea L. Russo, Kuang-hung Cheng, Arunthathi Thia-  
276 galingam, Pratima Nemani, David Sidransky, and Sam Thiagalingam. Loss of Heterozygosity Patterns Pro-  
277 vide Fingerprints for Genetic Heterogeneity in Multistep Cancer Progression of Tobacco Smoke–Induced  
278 Non–Small Cell Lung Cancer. *Cancer Research*, 65(5):1664–1669, 3 2005.
- 279 [40] I-W. Park, I. I. Wistuba, A. Maitra, S. Milchgrub, A. K. Virmani, J. D. Minna, and A. F. Gazdar. Multiple  
280 Clonal Abnormalities in the Bronchial Epithelium of Patients With Lung Cancer. *JNCI Journal of the  
281 National Cancer Institute*, 91(21):1863–1868, 11 1999.
- 282 [41] Laura J. Prevo, Carissa A. Sanchez, Patricia C. Galipeau, and Brian J. Reid. p53-mutant clones and field  
283 effects in Barrett’s esophagus. *Cancer Research*, 59(19), 1999.
- 284 [42] Sofia Raftopoulou, Paulina Valadez-Cosmes, Zala Nikita Mihalic, Rudolf Schicho, and Julia Kargl. Tumor-  
285 Mediated Neutrophil Polarization and Therapeutic Implications. *International Journal of Molecular Sci-  
286 ences*, 23(6):3218, 3 2022.

- 287 [43] Adam N. Rosenthal, Andy Ryan, Deborah Hopster, and Ian J. Jacobs. Molecular evidence of a common  
288 clonal origin and subsequent divergent clonal evolution in vulval intraepithelial neoplasia, vulval squamous  
289 cell carcinoma and lymph node metastases. *International Journal of Cancer*, 99(4):549–554, 6 2002.
- 290 [44] Danely P. Slaughter, Harry W. Southwick, and Walter Smejkal. “Field cancerization” in oral stratified  
291 squamous epithelium. Clinical implications of multicentric origin. *Cancer*, 6(5), 1953.
- 292 [45] DP Slaughter. The multiplicity of origin of malignant tumors: collective review. *International Abstract of  
293 Surgery*, 79:89–98, 1944.
- 294 [46] DP Slaughter, HW Southwick, and W Smejkal. Field cancerization in oral stratified squamous epithelium.  
295 *Cancer*, 6, 1953.
- 296 [47] Ana M. Soto and Carlos Sonnenschein. The tissue organization field theory of cancer: A testable replace-  
297 ment for the somatic mutation theory. *BioEssays*, 33(5):332–340, 5 2011.
- 298 [48] Robert C. Sterner and Rosalie M. Sterner. CAR-T cell therapy: current limitations and potential strategies.  
299 *Blood Cancer Journal*, 11(4):69, 4 2021.
- 300 [49] Gopinath M. Sundaram, Shan Quah, and Prabha Sampath. Cancer: the dark side of wound healing. *FEBS  
301 Journal*, 285(24), 2018.
- 302 [50] Takeshi Takahashi, Tomonori Habuchi, Yoshiyuki Kakehi, Kenji Mitsumori, Toshiya Akao, Toshiro Ter-  
303 achi, and Osamu Yoshida. Clonal and chronological genetic analysis of multifocal cancers of the bladder  
304 and upper urinary tract. *Cancer Research*, 58(24), 1998.
- 305 [51] Moying Tang, Sergio Baez, Martha Pruyas, Alfonso Diaz, Alfonso Calvo, Erick Riquelme, and Ignacio I.  
306 Wistuba. Mitochondrial DNA Mutation at the D310 (Displacement Loop) Mononucleotide Sequence in the  
307 Pathogenesis of Gallbladder Carcinoma. *Clinical Cancer Research*, 10(3):1041–1046, 2 2004.
- 308 [52] Hirotsugu Uetsuki, Hiroyuki Tsunemori, Rikiya Taoka, Reiji Haba, Masashi Ishikawa, and Yoshiyuki  
309 Kakehi. Expression Of A Novel Biomarker, EpcA, In Adenocarcinomas And Precancerous Lesions In The  
310 Prostate. *Journal of Urology*, 174(2):514–518, 8 2005.
- 311 [53] MG Van Oijen and PJ Slootweg. Oral field cancerization: Carcinogen-induced independent events or mi-  
312 crometastatic deposits? *Cancer Epidemiology Biomarkers and Prevention*, 9(3), 2000.
- 313 [54] Manlio Vinciguerra, Antonio Musaro, and Nadia Rosenthal. Regulation of Muscle Atrophy in Aging and  
314 Disease. pages 211–233. 2010.
- 315 [55] R Virchow. Die Cellularpathologie in ihrer Begründung auf physiologische and pathologische Gewe-  
316 belehre. *Verlag von August Hirschfeld, Berlin.*, 1858.
- 317 [56] Jaw Yuan Wang, Yung Hsin Wang, Shu Wen Jao, Chien Yu Lu, Chao Hung Kuo, Huang Ming Hu,  
318 Jan Sing Hsieh, Inn Wen Chong, Tian Lu Cheng, and Shiu Ru Lin. Molecular mechanisms underlying the  
319 tumorigenesis of colorectal adenomas: Correlation to activated K-ras oncogene. *Oncology Reports*, 16(6),  
320 2006.
- 321 [57] Yan Ping Yu, Douglas Landsittel, Ling Jing, Joel Nelson, Baoguo Ren, Lijun Liu, Courtney McDonald,  
322 Ryan Thomas, Rajiv Dhir, Sydney Finkelstein, George Michalopoulos, Michael Becich, and Jian-Hua Luo.  
323 Gene Expression Alterations in Prostate Cancer Predicting Tumor Aggression and Preceding Development  
324 of Malignancy. *Journal of Clinical Oncology*, 22(14):2790–2799, 7 2004.