**S1 Table. Model Parameters**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Parameter** | **Value** | **Reference** |
| T Cell Recruitment | *tdelay* | 5 days | [1] |
| *twindow* | 1 day | [1] |
| *ka* | 15 (dimensionless) | [1] |
| *ki* | 0.01 (dimensionless) | [1] |
| *r1* | 6 cells/hr | [1] |
| Diffusion | Diffusion constant | 300 mm2/sec | [2] |
| lattice size | 15 mm | [3] |
| Cancer Cells | Tumor division time | 30 hrs (20 hrs) | [1], [4-10] |
| Tumor cell lifespan | 5 days | [1] |
| Tumor cell - T cell killing time | 6 hrs | [4] |
| Macrophage activating factor secretion | 1×10-7 pg/sec | Adapted from [6] |
| T cells | T cell division time | 8 hrs | [1] |
| T cell lifespan | 41 hrs | [5] |
| T cell maximum number of kills | 5 tumor cells | [4] |
| Macrophages | Macrophage lifespan | 30 days | [11,12] |
| Macrophage recruitment rate | 1×10-8 cells/(site x sec) (2×10-8) | [6] |
| Initial number of macrophages | 2×10-3 cells/site | [6] |
| Macrophage activation threshold | 8×10-6 pg/site | [6] |
| Cytokine Secretion | Tumor cell IL-4 secretion | 10 mol/sec | [13] |
| M2 IL-4 secretion | 10 mol/sec | [13] |
| T cell IFNg secretion | 26 mol/sec | [13] |
| T cell activation | *k* | 3 (dimensionless) | model specific  |
| *s* | 0.5 (dimensionless) | model specific  |
| Other | Time step | 0.5 hrs | model specific  |
| Cell migration speed | 1 site/time step | [6] |

**References**

1. Gong C, Milberg O, Wang B, Vicini P, Narwal R, Roskos L, et al. A computational multiscale agent-based model for simulating spatio-temporal tumour immune response to PD1 and PDL1 inhibition. J R Soc Interface. 2017;14(134):20170320.
2. Wells DK, Chuang Y, Knapp LM, Brockmann D, Kath WL, Leonard JN. Spatial and functional heterogeneities shape collective behavior of tumor-immune networks. PLoS Comput Biol. 2015;11(4):e1004181.
3. Hao S-J, Wan Y, Xia Y-Q, Zou X, Zheng S-Y. Size-based separation methods of circulating tumor cells. Adv Drug Deliv Rev. 2018;125:3–20.
4. Kather JN, Poleszczuk J, Suarez-Carmona M, Krisam J, Charoentong P, Valous NA, et al. In silico modeling of immunotherapy and stroma-targeting therapies in human colorectal cancer. Cancer Res. 2017;77(22):6442–6452.
5. Kim PS, Lee PP. Modeling protective anti-tumor immunity via preventative cancer vaccines using a hybrid agent-based and delay differential equation approach. PLoS Comput Biol. 2012;8(10):e1002742.
6. Wells DK, Chuang Y, Knapp LM, Brockmann D, Kath WL, Leonard JN. Spatial and functional heterogeneities shape collective behavior of tumor-immune networks. PLoS Comput Biol. 2015;11(4):e1004181.
7. Mahlbacher G, Curtis LT, Lowengrub J, Frieboes HB. Mathematical modeling of tumor-associated macrophage interactions with the cancer microenvironment. J Immunother Cancer. 2018;6(1):1–17.
8. Knutsdottir H, Condeelis JS, Palsson E. 3-D individual cell based computational modeling of tumor cell–macrophage paracrine signaling mediated by EGF and CSF-1 gradients. Integr Biol. 2016;8(1):104–119.
9. Knútsdóttir H, Pálsson E, Edelstein-Keshet L. Mathematical model of macrophage-facilitated breast cancer cells invasion. J Theor Biol. 2014;357:184–199.
10. Norton K-A, Jin K, Popel AS. Modeling triple-negative breast cancer heterogeneity: Effects of stromal macrophages, fibroblasts and tumor vasculature. J Theor Biol. 2018;452:56–68.
11. Boissonnas A, Laviron M. Ontogeny of tumor-associated macrophages. Front Immunol. 2019;10:1799.
12. Parihar A, Eubank TD, Doseff AI. Monocytes and macrophages regulate immunity through dynamic networks of survival and cell death. J Innate Immun. 2010;2(3):204–215.
13. Han Q, Bradshaw EM, Nilsson B, Hafler DA, Love JC. Multidimensional analysis of the frequencies and rates of cytokine secretion from single cells by quantitative microengraving. Lab Chip. 2010;10(11):1391–1400.