A QSP Model for Predicting Clinical Responses to Monotherapy, Combination and Sequential Therapy Following CTLA-4, PD-1, and PD-L1 Checkpoint Blockade

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Table S1 – Model Reactions (Start)

Table S1 – Model Reactions (End)

Table S2 – Model Reaction Rates (Start)

Table S2 – Model Reaction Rates (End)

Table S3 – Model Reaction and Rate Descriptions (Start)

Reaction Number	Reaction Description
	Distribution of Anti-CTLA-4 mAb between the central and lymph node compartments
	Distribution of Anti-CTLA-4 mAb between the central and leaky tissues
3	Distribution of Anti-CTLA-4 mAb between the central and tight tissues
	Distribution of Anti-CTLA-4 mAb between the central and tumor compartments
5	Clearance of Anti-CTLA-4 mAb from the central compartment
	The generation of Effector T cells and their migration into the blood/plasma from the designated number of lymph nodes as a
n	multiple of that from a single lymph node
	Trafficking of free Effector T cells from blood to GI vasculature
8	Trafficking of free Effector T cells from blood to Liver vasculature
9	Trafficking of free Effector T cells from blood to Spleen vasculature
10	Trafficking of free Effector T cells from blood to Lymph Node vasculature
11	The natural turnover of Effector T cells in the blood
12	Trafficking of free Effector T cells from blood to Peripheral (other tissues not directly accounted for) vasculature
13	Trafficking of free Effector T cells from blood to Tumor vasculature
14	Distribution of Anti-PD-1 mAb between the central and lymph node compartments
15	Distribution of Anti-PD-1 mAb between the central and leaky tissues
16	Distribution of Anti-PD-1 mAb between the central and tight tissues
17	Distribution of Anti-PD-1 mAb between the central and tumor compartments

Table S3 – Model Reaction and Rate Descriptions (End)

Table S4 – Definition of species in the model (Start)

Table S4 – Definition of species in the model (End)

Table S5 – Model Parameters (Start)

Table S5 – Model Parameters (End)

Table S6 – Model Algebraic Equations (Start)

Table S6 – Model Algebraic Equations (End)

Table S7 – Model Discontinuous Equation Sets (Start)

Table S7 – Model Discontinuous Equation Sets (End)

Table S8 – Model Compartment Volumes (End)

Table S9 – Parameters Varied in Virtual Clinical Trials (Start)

Table S9 – Parameters Varied in Virtual Clinical Trials (End)

Table S10 Parameters Varied in Sensitivity Analysis (End)

Table S11 – Conditions Specific to Each Clinical Scenario Simulated (End)

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Figure S1. Dose response anti-CTLA-4 mono-therapy. A) From top to bottom: Tumor response to anti-CTLA-4 therapy at doses of 0.3, 1, 3 and 10 mg/kg as represented by the colors in the bottom figure in ascending order; the blue line indicates no therapy in the top figure. Then, Effector T cell density in the tumor (second from the top), mAPC density in the lymph nodes (third from the top) and finally, the PK of anti-CTLA-4 at the given doses. **B)** Diversity of tumor response for 3 mg/kg (left) and 10 mg/kg (right). **C)** Waterfall plot of VPs at 3 mg/kg (left) and 10 mg/kg (right). **D)** Bar graph comparison parameters varied in model for each type of responder at 3 mg/kg (left) and 10 mg/kg (right). **E)** Max Effector T cell density in the tumor and average mAPC density in the lymph nodes for each responder category at 3 mg/kg (left) and 10 mg/kg (right).

Figure S2. Dose response and clinical validation of anti-CTLA-4/anti-PD-L1 combo-therapy. A) From top to bottom: Tumor response to combination therapy at doses of 0.3, 1, 3 and 10 mg/kg of anti-CTLA-4, as represented by the colors in the second from the bottom figure in ascending order and 20 mg/kg for anti-PD-L1 was used for all simulations; the blue line indicates no therapy (top figure), and orange indicates only anti-PD-L1. Then, Effector T cell density in the tumor (second from the top), mAPC density in the lymph nodes (third from the top) and finally, the PK of anti-CTLA-4 and lastly, anti-PD-L1 at the given doses. For all following figures, 20 mg/kg anti-PD-L1 and 1 mg/kg anti-CTLA-4 were used, following the same regimen. **B)** Diversity of tumor response (left), prediction of median clinical response data (right). **C)** Waterfall plot of VPs (left) and pie chart (right) with percent of virtual non-responders (NR), stable disease (SD) and partial or complete responders (PR/CR). **D)** Bar graph comparison parameters varied in model for each responder type (left) and box plots of significant differentiators (right). **E)** Max

Effector T cell density in the tumor (left) and average mAPC density in the lymph nodes (right) for each responder category.

Figure S3. Dose response and clinical validation of anti-PD-1/anti-PD-L1 combo-therapy. A) From top to bottom: Tumor response to combination therapy at doses of 0.3, 1, 3 and 10 mg/kg of anti-PD-1, as represented by the colors in the bottom figure in ascending order and 20 mg/kg for anti-PD-L1 was used for all simulations; the blue line indicates no therapy (top figure), and orange indicates only anti-PD-L1. Then, Effector T cell density in the tumor (second from the top), mAPC density in the lymph nodes (third from the top) and finally, the PK of anti-PD-L1 and lastly, anti-PD-1 at the given doses. For all following

figures, 20 mg/kg anti-PD-L1 and 3 mg/kg anti-PD-1 was used, following the same regimen. **B)** Diversity of tumor response (left), prediction of median clinical response data (right). **C)** Waterfall plot of VPs (left) and pie chart (right) with percent of virtual non-responders (NR), stable disease (SD) and partial or complete responders (PR/CR). **D)** Bar graph comparison parameters varied in model for each responder type (left) and box plots of significant differentiators (right). **E)** Max Effector T cell density in the tumor (left) and average mAPC density in the lymph nodes (right) for each responder category.

Figure S4. Pharmacokinetics of A) anti-CTLA-4, B) anti-PD-1 and C) anti-PD-L1 at 3 mg/kg each in the serum, tumor, leaky and tight tissues, lymph and serum. Results are based on a minimal-PBPK model, combined with tumor transport equations with diffusion across the vascular surface area.

Figure S5. Simulation of tumor volume doubling time (left) and associated number of cancer cells (middle) and tumor diameter (right). A tumor doubling time of ~66 days was used for all model simulations. Variability in tumor growth was an emergent outcome for each simulation in the model.

Anti-CTLA-4 Sensitivity Analysis p-values

Anti-PD-1 Sensitivity Analysis p-values

Figure S6. Sensitivity analysis p-values for A) anti-CTLA-4, B) anti-PD-1 and C) anti-PD-L1.

 \overline{A}

Figure S7. Minimal PBPK model of antibody distribution used in the QSP model.

Figure S8. PBPK model cell trafficking used in the QSP model. Model PBPK of Effector T cell (C) trafficking through the tissues in the model via the blood (solid black lines) and lymph (dotted black lines). Also represented is the trafficking of newly primed and activated Effector T cells from the lymph node to the blood for redistribution (solid red line) the trafficking of mature APCs (solid blue line) to the lymph nodes for priming and activation of naïve T cells to Effector T cells. Cancer Debris also enter the lymph fluid and is brought to the lymph node from the tumor. The bottom panel shows how free Effector cells (C^f_v) in the tumor vasculature are bound the vascular wall (C^b_v), arrested (C^a_v), extravasated (via rate J) into the interstitial space (C_i) to interact with the cancer cells. Regulatory cells (T_{reg}) inhibit the activity of the Effector cells in the tumor and APCs (A) pick up debris to become mAPC (mA). Effector cells can exit the interstitial space (via rate Lδ) and recirculate through the lymphatic system.

A) Interaction between cancer and Effector T cells in the tumor

 T_reg C_i C_{i} T_reg Association of regulatory and T cells $f_{\rm b}$ $\mathsf{I}_{\mathsf{reg}}$

C) Priming and activation of naïve T cells in the tumor draining lymph node

Figure S9. Abstract representation of cell-cell interactions in the model. A) Effector T cells in the interstitial space of the tumor (C_i) interact with cancer cells to form a bound complex (at a rate defined by the De Pillis-Radunskaya equation described in the methods, equation 1.3). The complex then dissociates with the regeneration of cancer cells and Effector cells relative to the fraction of active checkpoint signaling (f_a) . If checkpoint signaling is fully active at inhibiting the Effector cells, for example, then only the cancer cells are regenerated ($f_a = 1$). Alternatively, is antibodies block the signaling to full effect $(f_a = 0)$, then only the Effector cells emerge from the bound interaction; along with cancer cell debris that can promote further priming and activation of Effector cells in the lymph nodes. The value of signaling comes out to be between 0 and 1 and is dependent on the checkpoint signaling and interactions with the antibodies that block it. The emerging Effector T cells undergo a recovery delay (C_R) before engaging in interactions with other cancers cells. B) Similarly, as described above, Effector T cells in the tumor interstitial space can interact with regulatory cells (T_{reg}) to form a state variable representing a bound complex. The dissociation of the bound complex determines to what extent the Effector cells are regenerated, which is directly a function of the checkpoint signaling (f_b) . C) Mature APCs (mA) interact with naïve and primed T cells (NT and PT, respectively) during two priming stages in the lymph node. Depending on the extent of checkpoint signaling (f_c) , primed T cells either become anergic (T_{Inact}) and/or activated T cells (AT); the latter proliferate and become Effector T cells (C^f_v) that migrate out into peripheral circulation.