C-IMMSIM simulation results

July 18, 2025

Abstract

This document includes the plots relative to the simulation and the outcome of the epitope/peptide prediction used.

Produced by the C-IMMSIM Online server available at http://c-immsim.iac.rm.cnr.it (alias to http://kraken.iac.rm.cnr.it/C-IMMSIM)

CITATIONS: For publication of results, please cite the following:

Nicolas Rapin, Ole Lund, Massimo Bernaschi, Filippo Castiglione. Computational Immunology Meets Bioinformatics: The Use of Prediction Tools for Molecular Binding in the Simulation of the Immune System. PLoS ONE 5(4): e9862

tt doi:10.1371/journal.pone.0009862, 2010

A retrospective validation

In-silico evaluation of adenoviral COVID-19 vaccination protocols: Assessment of immunological memory up to 6 months after the third dose. P. Stolfi, F. Castiglione, E. Mastrostefano, I. Di Biase, S. Di Biase, G. Palmieri, A. Prisco. Frontiers in Immunology, 13 (2022) doi: 10.3389/fimmu.2022.998262

https://www.frontiersin.org/articles/10.3389/fimmu.2022.998262i

An in vivo validation

Identification and validation of viral antigens sharing sequence and structural homology with tumor associated antigens (TAAs). C. Ragone, C. Manolio, B. Cavalluzzo, A. Petrizzo, A. Mauriello, M-L. Tornesello, F. M. Buonaguro, F. Castiglione, L. Vitagliano, M. Ruvo, M. Tagliamonte, L. Buonaguro. Journal for ImmunoTherapy of Cancer. 9:e002694 (2021)

https://jitc.bmj.com/content/9/5/e002694

Original C-IMMSIM model: www.iac.cnr.it/~filippo/c-immsim

GETTING HELP:

Scientific problems: Filippo Castiglione (filippo dot castiglione at cnr dot it) Technical problems: Ilaria Gonnella (ilaria dot gonnella at cnr dot it)

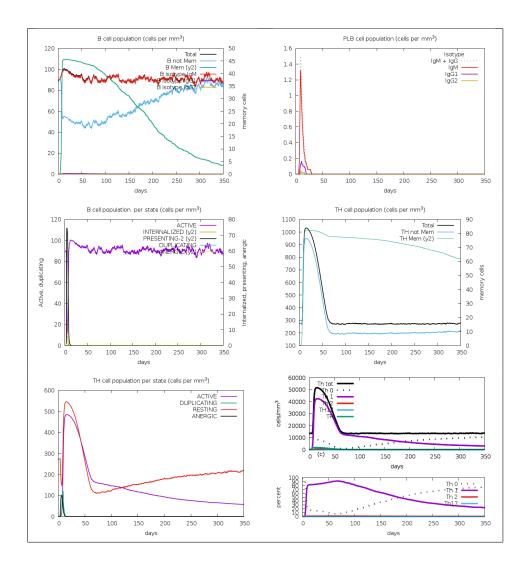


Figure 1: Cell counts shown. Legend: Act=active, Intern=internalized the Ag, Pres II = presenting on MHC II, Dup = in the mitotic cycle, Anergic = anergic, Resting = not active.

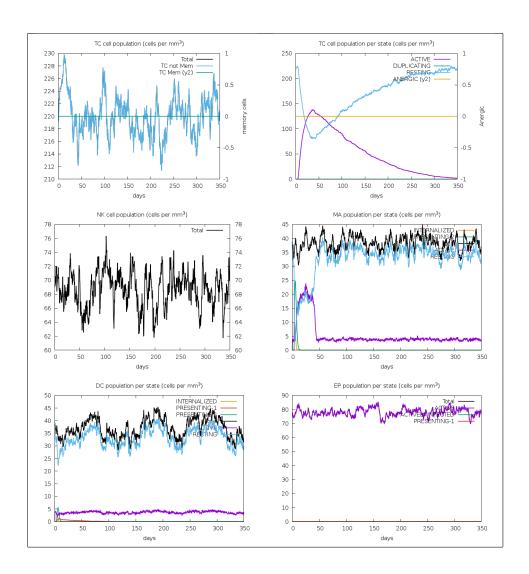


Figure 2: Legend: symbols as figure above.

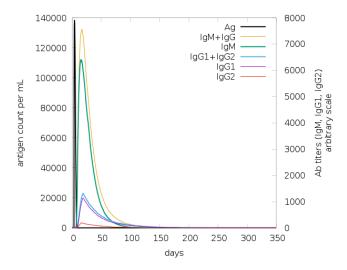


Figure 3: The virus, the immunoglobulins and the immunocomplexes.

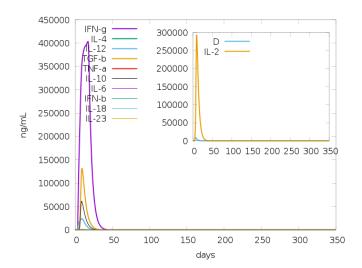


Figure 4: Concentration of cytokines and interleukins. Inset plot shows danger signal together with leukocyte growth factor IL-2.

Parker_B_scale_epitope_find Use Parker's propensity scale, takes an antigen block as input, and creates a list of residues that are possible epitopes.						
GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKTPVGRLVTVAAYFLAVGGVLLAAYVLLFLS VNVAAYFSITPSAPSYTLGPGPGFSITPSAPSKKSITPSAPSYTLKLGEKKVTIMSKDKPTIDVKMKKKMEKLQLKGTTY GVC						
000000000000000000000000001111001111111						
DoPeptideList_I: Given the antigen injected creates the list of peptides for all the NumAgProts proteins and for all i.e., 4 MHCI molecules Read class I peptide list from file? NO						
Pseudo sequence: KAAHVEQRKAQTRTV Threshold: 9.523800 Max score: 27.437000						
GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKTPVGRLVTVAAYFLAVGGVLLAAYVLLFLS VNVAAYFSITPSAPSYTLGPGPGFSITPSAPSKKSITPSAPSYTLKLGEKKVTIMSKDKPTIDVKMKKKMEKLQLKGTTY GVC						
Epitopes of protein 0 O] pos= -1 score=1.000000 unnormalised=104.8410000000 non-binding event						
Allele: A0101 Pseudo sequence: KAVHAEQRNKAQTRA Threshold: 9.456400 Max score: 29.236000						

 $Antigen\ sequence\ file:\ /opt/lampp/htdocs/C-IMMSIM/Jobs/input/38253_20250718-130113_5_UmQfQ5F1nBD3.FSA_1_001$

 ${\tt GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKTPVGRLVTVAAYFLAVGGVLLAAYVLLFLS} $$ VNVAAYFSITPSAPSYTLGPGPGFSITPSAPSKKSITPSAPSYTLKLGEKKVTIMSKDKPTIDVKMKKKMEKLQLKGTTY $$ VNCAAYFSITPSAPSYTLGPGPGFSITPSAPSKKSITPSAPSYTLKLGEKKVTIMSKDKPTIDVKMKKKMEKLQLKGTTY $$ VNCAAYFSITPSAPSYTLKLGEKKVTIMSKDKPTIDVKMKKKMEKLQLKGTTY $$ VNCAAYFSITPSAPSYTLKGEKTY $$ VNCAAYFSITPSAPSYTLKTY $$ VNCAAYFSITPSAPSYTLY $$ VNCAAYFSITPSAPSAPSYTLY $$ VNCAAYFSITPSAPSYTLY $$ VNCAAYFSITPSAPSYTLY $$ VNCAAYFSITPSAPSYTLY $$ VNCAAYFSITPSAPSYTLY $$ VNCAAYFSITPSAPSYTLY $$ VNCAAYFSITPSAPSYTLY $$ VNCAAYFSITPSAPSAPSYTLY $$ VNCAAYFSITPSAPSYTLY $$ VNCAAYFSITPSAPSYTLY $$ VNCAAYFSITPSAPSYTLY $$ VNCAAYFSITPS$

Epitopes	of	protein	0	
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0] pos= 77 score=0.005470 unnormalised=0.5766000000 FLSVNVAAY

1] pos= -1 score=0.994530 unnormalised=104.8410000000 non-binding event

Allele: B0702

Pseudo sequence: KAAREEQQIKAQTRE

Threshold: 8.702800 Max score: 28.406000

 $\textbf{Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/38253_20250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-130113_5_UmQfQ5F1nBD3.FSA_1_00123253_120250718-1200070718-1200070718-120000$

ATTEM OVVIABUBADA AU AAI DVEEDTAVAAT ADVAAD DV

 ${\tt GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKTPVGRLVTVAAYFLAVGGVLLAAYVLLFLS} \\ {\tt VNVAAYFSITPSAPSYTLGPGPGFSITPSAPSKKSITPSAPSYTLKLGEKKVTIMSKDKPTIDVKMKKKMEKLQLKGTTY} \\ {\tt GVC} \\$

Epitopes of protein 0 -----

0]	pos=	50	score=0.005479	unnormalised=0.6582000000	TPVGRLVTV
1]	pos=	89	score=0.060909	unnormalised=7.3172000000	TPSAPSYTL
2]	pos=	116	score=0.060909	unnormalised=7.3172000000	TPSAPSYTL

3] pos= -1 score=0.872703 unnormalised=104.8410000000 non-binding event

Allele: B0702

Pseudo sequence: KAAREEQQIKAQTRE

Threshold: 8.702800 Max score: 28.406000

Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/38253_20250718-130113_5_UmQfQ5F1nBD3.FSA_1_001

GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKTPVGRLVTVAAYFLAVGGVLLAAYVLLFLS VNVAAYFSITPSAPSYTLGPGPGFSITPSAPSKKSITPSAPSYTLKLGEKKVTIMSKDKPTIDVKMKKKMEKLQLKGTTY GVC

Epitopes of protein 0 -----

0]	pos=	50	score=0.005479	unnormalised=0.6582000000	TPVGRLVTV
1]	pos=	89	score=0.060909	unnormalised=7.3172000000	TPSAPSYTL
2]	pos=	116	score=0.060909	unnormalised=7.3172000000	TPSAPSYTL

3] pos= -1 score=0.872703 unnormalised=104.8410000000 non-binding event

DoPeptideList_II:

Given the antigen injected creates the list of peptides for all the ${\tt NumAgProts}$ proteins and for all i.e., 2 MHCII molecules

Read class II peptide list from file? NO

Allele: DRB1_0401

Pseudo sequence: KFAAHVEQRKAQTRV

Threshold: 2.842330 Max score: 29.818000

 ${\tt Antigen\ sequence\ file:\ /opt/lampp/htdocs/C-IMMSIM/Jobs/input/38253_20250718-130113_5_UmQfQ5F1nBD3.FSA_1_001}$

GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKTPVGRLVTVAAYFLAVGGVLLAAYVLLFLS VNVAAYFSITPSAPSYTLGPGPGFSITPSAPSKKSITPSAPSYTLKLGEKKVTIMSKDKPTIDVKMKKKMEKLQLKGTTY

Epitopes of protein 0 ------
Ol pose 52 score=0.034569 un

Epitopes	or pro	otem	1 0	-	
0]	pos=	52	score=0.034569	unnormalised=4.1646700000	VGRLVTVAA
1]	pos=	69	score=0.005019	unnormalised=0.6046700000	LLAAYVLLF
2]	pos=	73	score=0.028609	unnormalised=3.4466700000	YVLLFLSVN
3]	pos=	75	score=0.031805	unnormalised=3.8316700000	LLFLSVNVA
4]	pos=	76	score=0.045285	unnormalised=5.4556700000	LFLSVNVAA
5]	pos=	77	score=0.011410	unnormalised=1.3746700000	FLSVNVAAY
6]	pos=	85	score=0.049468	unnormalised=5.9596700000	YFSITPSAP
7]	pos=	86	score=0.122305	unnormalised=14.7346700000	FSITPSAPS
8]	pos=	103	score=0.122305	unnormalised=14.7346700000	FSITPSAPS

9] pos= -1 score=0.549226 unnormalised=66.1680000000 non-binding event

Allele: DRB1_0101

 ${\tt Pseudo \ sequence:} \ {\tt KAFAHVEQRKAQTRV}$

Threshold: 2.392440 Max score: 26.461000

Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/38253_20250718-130113_5_UmQfQ5F1nBD3.FSA_1_001

GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKTPVGRLVTVAAYFLAVGGVLLAAYVLLFLS VNVAAYFSITPSAPSYTLGPGPGFSITPSAPSKKSITPSAPSYTLKLGEKKVTIMSKDKPTIDVKMKKKMEKLQLKGTTY GVC

Epitopes of protein 0 -----

0]	pos=	9 score=0.024348 unnormalised=3.2015600000	YCRVRGGRC
1]	pos=	52 score=0.005062 unnormalised=0.6655600000	VGRLVTVAA
2]	pos=	55 score=0.065650 unnormalised=8.6325600000	LVTVAAYFL
3]	pos=	61 score=0.014530 unnormalised=1.9105600000	YFLAVGGVL
4]	pos=	62 score=0.092047 unnormalised=12.1035600000	FLAVGGVLL
5]	pos=	74 score=0.000179 unnormalised=0.0235600000	VLLFLSVNV
6]	pos=	76 score=0.013047 unnormalised=1.7155600000	LFLSVNVAA
7]	pos=	85 score=0.038318 unnormalised=5.0385600000	YFSITPSAP
8]	pos=	86 score=0.079788 unnormalised=10.4915600000	FSITPSAPS
9]	pos=	88 score=0.036721 unnormalised=4.8285600000	ITPSAPSYT
10]	pos=	95 score=0.010598 unnormalised=1.3935600000	YTLGPGPGF
11]	pos=	103 score=0.079788 unnormalised=10.4915600000	FSITPSAPS
12]	pos=	115 score=0.036721 unnormalised=4.8285600000	ITPSAPSYT
13]	nos=	-1 score=0 503204 unnormalised=66 1680000000	non-hinding

pos= -1 score=0.503204 unnormalised=66.1680000000 non-binding event 13]