Kinetic modelling of autoimmune diseases

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Structure of the talk

1. Introduction

Motivation & biological considerations Autoimmune diseases

2. The model for autoimmunity

Cellular interactions Kinetic equations Macroscopic equations

3. Qualitative analysis

Existence and uniqueness result Positivity and asymptotic behaviour of the solution

4. Numerical tests

Results & biological interpretation

Motivation

Normally, the immune system

- identifies the difference between foreign cells and our own cells;
- protects against germs, like bacteria and viruses;
- recognizes foreign invaders and sends out cells to attack them.

An **autoimmune disease** is a condition in which our immune system wrongly attacks our own cells.

In many cases, it is **chronic**, and patients alternate periods of **relapse** having **suffering** symptoms, with periods of **remittance** in which symptoms are **absent**.

Our objective

To construct a mathematical model of **kinetic type** in order to describe the **immune system interactions** in the context of **autoimmune disease**.

State of the art

It is well known that the immune system can be regarded, at the cellular level, as a system constituted by a large number of cells, belonging to several interacting populations.

Cellular interactions can modify the behaviour or **activity** of cells and can also modify the **size** of populations.

The behaviour can be modelled within a **kinetic theory** approach in terms of the statistical distribution of all states possessed by each cell population.

State of the art

After the pioneering work

Jager & Segel (1992), for population of social organisms,

Kinetic modelling approaches have been used to describe tumor-immune system interactions and immune competition

Bellomo & Forni (1994) Arlotti & Bellomo (1995) Arlotti & Lachowicz & Latrach (1996) Arlotti & Bellomo & Latrach (1999) Delitala (2002) Kolev (2003, 2005) Kolev & Nikolova (2007) Angelis & Lods (2008) Bellouquid & Angelis (2011) Conte & Groppi & Spiga (2018)

Cell populations

We consider three interacting populations in the autoimmune competition

(SAPCs) Self Antigen Presenting Cells (A) (SRTCs) Self Reactive T cells (R) (ISCs) Immunosupressive Cells (S)

SRTCs are activated when they encounter a SAPC that has digested a self-antigen.

(ISCs) regulate the activity of SRTCs and SAPCs.



Assumptions

- Only binary interactions between cells are significant.
- Interactions are instantaneous and homogeneous in space.
- The functional state of each population is described by the biological activity variable, *u* ∈ [0, 1];
- Interactions can be conservative, proliferative and destructive.

Cellular activity

The behaviour of cells is described by distribution functions

$$f_i \colon [0,\infty] \times [0,1] o \mathbb{R}^+$$
, $i = 1,2,3$

and the expected number of cells of the i-population at time t is given by

$$n_i(t) = \int_0^1 f_i(t, u) \, \mathrm{d}u, \qquad i = 1, 2, 3.$$
 (1)

Cellular activity (meaning)

(SAPCs) Self Antigen Presenting Cells

their activity u is the ability to stimulate and activate SRTCs

u=0 means that the simulation by SAPCs does not activate SRTCs does not induce an autoimmune response



Cell activity

(SRTCs) Self Reactive T cells

their activity u is the secretion of cytokines

u = 0 means that the SRTCs do not produce cytokines SRTCs are tolerant to SAPCs no inflammatory process is triggered



Cell activity

(ISCs) Immunosupressive Cells

their activity u is the ability to inhibit the autoimmune response suppressing the activity of SAPCs and SRTCs or eliminating SAPCs and SRTCs



Kinetic equations

$$\frac{\partial f_i}{\partial t}(t,u) = G_i[f](t,u) - L_i[f](t,u) + S_i[f](t,u), \quad i = 1, 2, 3,$$

where

$$f=(f_1,f_2,f_3)$$

and

- $G_i[f](t, u) L_i[f](t, u)$ corresponds to conservative interactions
- $S_i[f](t, u)$ corresponds to proliferative or destructive interactions

The cellular interaction terms have the structure

$$G_{i}[f](t, u) = \sum_{j=1}^{3} \int_{0}^{1} \int_{0}^{1} \eta_{ij}(v, w) \psi_{ij}(v, w; u) f_{i}(t, v) f_{j}(t, w) dv dw$$

$$L_{i}[f](t, u) = f_{i}(t, u) \sum_{j=1}^{3} \int_{0}^{1} \eta_{ij}(u, v) f_{j}(t, v) dv$$

$$S_{i}[f](t, u) = f_{i}(t, u) \sum_{j=1}^{3} \int_{0}^{1} s_{ij}(u, v) f_{j}(t, v) dv$$

where

 $\eta_{ij}(v, w) \ge 0$ is the **encounter rate** of a conservative interaction $s_{ij}(u, v)$ is the **proliferation** or **destruction rate** $\psi_{ij}(v, w; u) \ge 0$ is the **transition probability density** and satisfies

$$\int_0^1 \psi_{ij}(v,w;u) du = 1, \ i,j = 1,2,3, \ v,w \in [0,1]$$

Cellular interactions (from biological considerations)

Conservative interactions

Interactions SAPCs–ISCs decrease the activity of SAPCs Interactions SRTCs–ISCs decrease the activity of SRTCs Interactions SAPCs–SRTCs increase the activity of SAPCs

and also that of SRTCs

Proliferative interactions

Interactions SRTCs–SAPCs increase the number of SRTCs and also the number of SAPCs (autoimmune cascade) Interactions SAPCs–ISCs increase the number of ISCs

Destructive interactions

Interactions ISCs–SAPCs result in the elimination of SAPCs Interactions ISCs–SRTCs decrease the number of SRTCs

Cellular interactions (from biological considerations)

In proliferative interactions, we consider that

the newborn cells inherit the same aggressive state as the mother cells the proliferation rates are constant

In destructive interactions, we consider that

the destructive rates are constant

For the population of ISCs, we consider that

the distribution function is independent of its functional state

The kinetic equations are given by

Population p_1 of **SAPCs**

•
$$\frac{\partial f_1}{\partial t}(t, u) = 2c_{12} \int_0^u (u - v) f_1(t, v) dv \int_0^1 f_2(t, w) dw$$
$$-c_{12}(u - 1)^2 f_1(t, u) \int_0^1 f_2(t, w) dw$$
$$+2c_{13} f_3(t) \int_u^1 (v - u) f_1(t, v) dv - c_{13} u^2 f_1(t, u) f_3(t)$$
$$+p_{12} f_1(t, u) \int_0^1 f_2(t, w) dw$$
$$-d_{13} f_1(t, u) f_3(t)$$

Populations p_2 of **SRTCs** and **populations** p_3 of **ISCs**

•
$$\frac{\partial f_2}{\partial t}(t, u) = 2c_{21} \int_0^u (u - v) f_2(t, v) dv \int_{w^*}^1 f_1(t, w) dw$$

 $-c_{21}(u - 1)^2 f_2(t, u) \int_0^1 f_1(t, w) dw$
 $+2c_{23} f_3(t) \int_u^1 (v - u) f_2(t, v) dv - c_{23} u^2 f_2(t, u) f_3(t)$
 $p_{21} f_2(t, u) \int_0^1 f_1(t, w) dw - d_{23} f_2(t, u) f_3(t)$
• $\frac{df_3}{dt}(t) = p_{31} f_3(t) \int_0^1 f_1(t, w) dw$

 w^* is a parameter related to **tolerance** of SRTCs to SAPCs For this system, we consider the following initial data

 $f_1(0, u) = f_1^0(u), f_2(0) = f_2^0(u), f_3(0) = f_3^0, \text{ with } f_i^0 > 0, \text{ for } i = 1, 2, 3.$

The macroscopic equations

From the **kinetic equations** we formally derive balance equations for the **cellular density of each population**.

Integrating over the biological activity variable, $u \in [0,1]$, we obtain

$$\dot{n}_1(t) = p_{12}n_1(t)n_2(t) - d_{13}n_1(t)n_3(t)$$

$$\dot{n}_2(t) = p_{21}n_2(t)n_1(t) - d_{23}n_2(t)n_3(t)$$

$$\dot{n}_3(t) = p_{31}n_3(t)n_1(t)$$

As usual, **we loose the effects of conservative interactions**. For this system, we consider the following initial data

$$n_1(0) = n_1^0, n_2(0) = n_2^0, n_3(0) = n_3^0, \text{ with } n_i^0 > 0, \text{ for } i = 1, 2, 3.$$

Wellposedeness of the IVP (kinetic)

A result of paper [1], for η_{ij} and ψ_{ij} real valued, measurable and uniformly bounded, implies

Theorem 1 (local existence)

Assume initial data $f_i(0)$ in $L^1[0, 1]$. Then, there exists $T_0 > 0$ such that a unique positive solution to the Cauchy problem for our **kinetic system** exists in $L^1[0, 1]$, for $t \in [0, T_0]$.

[1] L. Arlotti, N. Bellomo, K. Latrach. Mathl. Comput. Modelling, 30, 15-40 (1999).

Kinetic versus macro

Thanks to a result of paper [2],

• the **boundedness** of the solution to the **macroscopic** system implies the **boundedness** of the solution to the **kinetic** system

• if the solution to the **macroscopic** system **blows up** then so does the solution to the **kinetic** system

The basic assumptions are

- constant destruction and proliferation rates
- cloned cells (proliferative encounters) **inherit the** same aggressive state as their mother cells

Therefore, the basic information about our kinetic system can be "extracted" from the corresponding macroscopic equations.

[2] L. Arlotti, M. Lachowicz, Mathl. Comput. Modelling, 23, 11–29 (1996).

Positivity of the existing solution

Theorem 2

If $(n_1(t), n_2(t), n_3(t))$ is a solution to the Cauchy problem for the **macroscopic equations** defined on the time interval [0, T], with $0 < T < \infty$, then this solution is **positive**, that is

 $n_1(t) > 0, \ n_2(t) > 0, \ n_3(t) > 0, \ t \in [0, T].$

Existence, uniqueness and asymptotic behaviour

Theorem 3

If the proliferative rates p_{21} , p_{31} are such that $p_{21} < p_{31}$, then the **Cauchy problem** for the **macroscopic equations** has a unique global solution $(n_1(t), n_2(t), n_3(t))$ defined on all \mathbb{R}^+ . This solution is **bounded** and

$$\lim_{t\to\infty} n_1(t) = 0,$$
$$\lim_{t\to\infty} n_2(t) = 0,$$
$$\lim_{t\to\infty} n_3(t) = \alpha < +\infty,$$

whatever are the corresponding initial data.

Simulations

We **solve** numerically the kinetic system, by **discretizing** the equations in the **activation** variable and using a **quadrature** rule (trapezoidal).

Objective

Investigate the influence of certain parameters on the behaviour of the solution.

Idea

Which **trends** or **reactions** typical in autoimmune diseases can be reproduced by our kinetic model?

Numerical scheme

The discretization of the activation state variable u, combined with quadrature approximations, leads to a system of 2(m+1)+1 ODEs,

$$\begin{aligned} \frac{df_1^k}{dt}(t) &= 2c_{13}f_3(t) \left(\mathcal{Q}_k^m[vf_1(t,v)] - u_k \mathcal{Q}_k^m[f_1(t,v)] \right) - c_{13}u_k^2 f_1^k(t) f_3(t) \\ &+ c_{12} \left[2 \left(u_k \mathcal{Q}_0^k[f_1(t,v)] - \mathcal{Q}_0^k[vf_1(t,v)] \right) - (u_k - 1)^2 f_1^k(t) \right] \mathcal{Q}_0^m[f_2(t,v)] \\ &+ p_{12}f_1^k(t) \mathcal{Q}_0^m[f_2(t,v)] - d_{13}f_1^k(t) f_3(t), \qquad k = 0, \dots, m, \end{aligned}$$

$$\begin{aligned} \frac{df_2^k}{dt}(t) &= 2c_{23}f_3(t) \left(\mathcal{Q}_k^m[vf_2(t,v)] - u_k \mathcal{Q}_k^m[f_2(t,v)] \right) - c_{23}u_k^2 f_2^k(t) f_3(t) \\ &+ c_{21} \left[2 \left(u_k \mathcal{Q}_0^k[f_2(t,v)] - \mathcal{Q}_0^k[vf_2(t,v)] \right) \mathcal{Q}_\ell^m[f_1(t,v)] - (u_k - 1)^2 f_2^k(t) \mathcal{Q}_0^m[f_1(t,v)] \right] \\ &+ p_{21}f_2^k(t) \mathcal{Q}_0^m[f_1(t,v)] - d_{23}f_2^k(t) f_3(t), \qquad k = 0, \dots, m, \end{aligned}$$

Trending to illness

ISCs are unable to regulate the autoimmune reaction. The result is a full autoimmune cascade and trending to illness.



Mass proliferation of very active SRTCs due to insufficient regulation by ISCs or insufficient destruction of SRTCs and SAPCs by ISCs or low tolerance of SRTCs to self-antigens.

 $p_{12}=20, p_{21}=19, p_{31}=20,$ $d_{13}=0.35, d_{23}=0.025, w^{*}=1/30.$

Immunosupression

ISCs are efficient in aborting the autoimmune reaction. The result is the suppression of the autoimmune reaction.



Very low proliferation of active SRTCs due to an efficient regulation by ISCs

SAPCs are less efficient in increasing the activity of SRTCs

 $p_{12}=20, p_{21}=19, p_{31}=22,$ $d_{13}=0.35, d_{23}=0.025, w^{*}=1/30.$

Immunotolerance

SRTCs become more tolerant to SAPCs

The result is a lowering effect on the number of SRTCs with high activity



Very low proliferation of active **SRTCs SRTCs** become more tolerant to **SAPCs** $p_{12}=20, p_{21}=19, p_{31}=20,$ $d_{13}=0.35, d_{23}=0.025, w^*=5/6.$

Perspectives

Work in progress

- An immunotherapy treatment was introduced in the description
- \bullet A fourth population of Interleukin-2 (IL-2) is considered to induce the proliferation of <code>ISCs</code>
- An artificial inlet representing an external drug therapy is introduced

Future work

- Other biological relevant populations can be introduced in the model
- A time delay can be included in the model to describe the **chronicity** of the autoimmune disease.

Thank you for your attention!