Using the Diffusions Equation For Modeling Biological Anomalies in the Human Kidney: When Physics Faces Global Diseases at the Nano Level

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***Abstract*—We use Physics ideas and equations to explain and to provide quantitative results of a possible measurement of the charges of albumin in the human kidney. Basically we use the diffusion equation and it is interpreted as a charge density fluxing through out the last layers of the kidney in the urine formation space. This study is a combination of Physics ideas to solve and face concrete problems of global diseases by which the presence of novel and alternatives ideas would serve to tackle the possible complications of type-2 diabetes progress. Therefore the comprehension of the why of the progress of certain diseases might be seen from the Physics angle and thus to provide new alternatives to improve the quality of life of people.**

***Index Terms*—Diffusion's equation, Diabetic nephropathy, albumin proteins.**

I. Introduction

A. Motivation of the Paper

One of the most strong world-wide pandemic is known as the diabetes disease in their forms either type-1 or type-2 constitutes a permanent and threatening potential to continue with the degradation of the human phisiology in particular that of the renal apparatus, by which in most cases it turns out to be the diabetes kidney disease (DKD in short). In this manner novel techniques combining the criteria of medicine and engineering are needed. Clinically speaking, the apparition of DKD is featured for being asymptomatic since the first diagnosis of type-2 diabetes, for instance. Commonly, the diagnosis of DKD is given through the clinical test of albumin. For example, in the scenario of macroalbumin in diabetic patients, the clinical test would yield values of above of 300 mg/24 h, or around.

B. Contribution of the Paper

According to tests and biochemical studies is known that one of the reasons of the why of the progress of DKD is because the abundance of glucose permanently in blood so that their dipoles are continuously exerting the cancellation of electric charges in the intern and extern layers of the kidney resulting in the unstoppable flux of proteins through the glomerulus. This is translated as the feasibility of the pass of large bunches of negatively charged proteins through the layers of the renal glomerulus, and ending in the zone of urine formation. Clearly, an early identification of the very beginning of DKD might be advantageous from various angles in the sense that the nephrologist encounters solid positions for facing the disease in order to reconfigure the pharmacology or another early intervention. In this paper, we focus in the concrete task for solving the diffusion's equation for the bunches of albumin going through the different layers of glomerulus. Thus the diffusion's equation

$$\frac{\partial}{\partial t}\rho(\vec{\mathbf{r}},t) = D\vec{\nabla}^2\rho(\vec{\mathbf{r}},t) \tag{1}$$

where D the diffusion constant allows to model in our case the anomalous flux of albumin through the urine. The main hypothesis consists in the depletion of charges in the inner layers of glomerulus because the high dipole moment of glucose in those type-2 diabetes characterized by having a poor glucose's control in large periods. Under the assumption that the mobility of the bunches is due to the electrodynamics of the interaction between the charges of albumin and the ones located over the glomerular basement membrane (GBM) and podocytes. Then the solution of (1) leads to use the well know Gauss's law

$$\vec{\nabla}\mathbf{E}(\vec{\mathbf{r}},t) = \frac{1}{\epsilon_0}\rho(\vec{\mathbf{r}},t), \tag{2}$$

so that the knowledge of the charge density allows us to estimate the electric field of the charges of albumin leaving the glomerulus. By using the divergence theorem the total charge can be obtained in a straightforward manner

$$\frac{1}{\epsilon_0}\int_{\mathbf{V}}\rho(\vec{\mathbf{r}},t)dV = \frac{Q_T}{\epsilon_0}, \tag{3}$$

fact that lead us to use the well-known Poisson equation to formulate a equation based entirely in electrodynamics that would explain the transport of charges of albumin going to the zone of urine formation,

$$\mathcal{F} = \frac{Q_T Q_N}{4\pi\epsilon_0 r^2} \tag{4}$$

where Q_N becomes the noise charge exerting a Coulomb-like force with the albumin proteins. Clearly one notes the importance of the diffusion's equation to go through the electric phenomenology of central problem.

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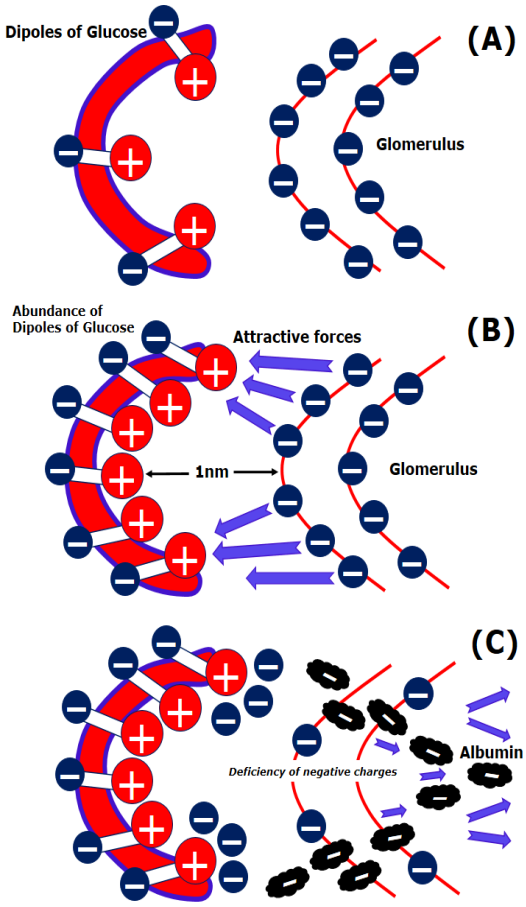

Fig. 1. Sequence which might explain the anomalous pass of bunches of proteins of albumin through the urine inside the human kidney. A possible cause for this would be the presence of an anomalous concentration of dipoles of glucose.

II. Model of Flux of Albumin Through the Glomerulus

A. The Very Beginning of DKD

Fig. 1 displays a possible scenario of the fluxing and dynamics of the proteins whose origin is the afferent vessels system and are pushed out the glomerular zone due to the following two-step sequence: (i) positive part of the dipole moment of glucose cancels the negative ones located in the intern part of the GBM, and (ii) bunches of albumin can surpass the region composed by podocytes and move on beyond the slit diaphragm. Albumin size might be of order of 5nm approximately, being this enough for passing the slit diaphragm efficiently. These proteins, (and others) can reach the convoluted tubule and be part of the urine formation. Thus, the radius r_1 and r_2 denote the variables which define the geometry of the glomerulus. The angular dependence of these cylinders doesn't apply any influence in the fluxing of albumin, so one can assume that there is symmetry along the variable θ. However, for ends of the numerical extraction of the equation's parameters, we kept the scenario where the cylinder has a height z.

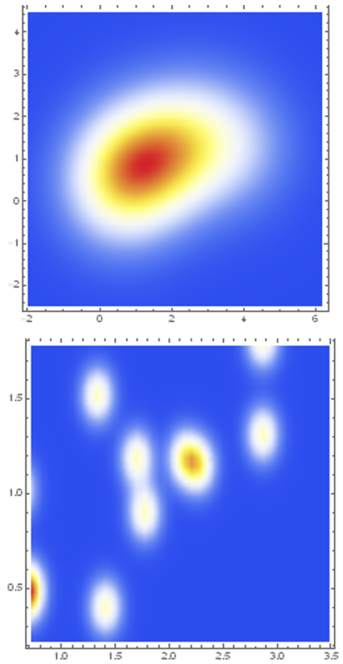

Fig. 2. Plotting of the radial part of the difusion's equation Eq.(9) being governed by integer-order Bessel 's functions as seen in the geometry of Fig.1. The small islets in the bottom panel is interpreted as singles bunches of albumin passing through the last layers of the human kidney.

B. Solving the Diffusion's Equation

In order to solve the diffusion's equation $\frac{\partial}{\partial t}u(\vec{\mathbf{r}},t) = D\vec{\nabla}^2 u(\vec{\mathbf{r}},t)$ where D the diffusion's constant, we proceed to use the cylindrical coordinate system by assuming that the glomerulus has the form as the one sketched in Fig. 1:

$$\frac{1}{D}\frac{\partial}{\partial t}u(\vec{\mathbf{r}},t) = \frac{1}{r}\frac{\partial}{\partial r}\left(r\frac{\partial}{\partial r}u(\vec{\mathbf{r}},t)\right)+\left(\frac{1}{r^2}\frac{\partial^2}{\partial\theta^2}+\frac{\partial^2}{\partial z^2}\right)u(\vec{\mathbf{r}},t). \tag{5}$$

The usage of the method of separation of variables lead us to write the function $u(\vec{\mathbf{r}},t) = R(r)\Theta(\theta)Z(z)T(t)$, in according to the variables belonging to the coordinate system. Thus, when $u(\vec{\mathbf{r}},t)$ is inserted in (1) and dividing both sides of equation by $R(r)\Theta(\theta)Z(z)T(t)$ [6], we can disengage the equations in the following manner

$$\frac{1}{DT(t)}\frac{dT(t)}{dt} = -\lambda \tag{6}$$

$$\frac{1}{rR(r)}\frac{\partial}{\partial r}\left(r\frac{\partial R}{\partial r}\right)+\left(\frac{1}{\Theta r^2}\frac{\partial^2\Theta}{\partial\theta^2}+\frac{1}{Z}\frac{\partial^2 Z}{\partial z^2}\right) = -\lambda. \tag{7}$$

Eq. (2) can be solved in a straightforward manner resulting in $T(t) = T_0\mathrm{Exp}(-\lambda Dt)$. However, Eq. (3) requires a refined methodology as to introduce new quantities that would guarantee its closed-form solution. For instance, $\frac{1}{Z}\frac{\partial^2 Z}{\partial z^2} = -m^2$ implying that the first side of Eq. (3) is written as $\frac{1}{rR(r)}\frac{\partial}{\partial r}\left(r\frac{\partial R}{\partial r}\right)+\frac{1}{\Theta r^2}\frac{\partial^2\Theta}{\partial\theta^2}+k^2$. Multiplying by r^2 and forcing to $\frac{1}{\Theta}\frac{\partial^2\Theta}{\partial\theta^2}=-\ell^2$ and accommodating conveniently we have

$$\phi^2\frac{d^2R}{d\phi^2}+\phi\frac{dR}{d\phi}+\left[\phi^2-\ell^2\right]R(r) = 0, \tag{8}$$

with $\phi = qr$, and $q = \sqrt{\lambda - m^2}$ and which is essentially the Bessel's equation, having as closed-form solution to $R(\phi) = \mathcal{E}_\ell J_\ell(\phi) + \mathcal{F}_\ell W_\ell(\phi)$ with J_ℓ and W_ℓ the Bessel and Weber functions. In the other hand, $\Theta(\theta) = \mathcal{C}_\ell \mathrm{Sin}(\ell\theta) + \mathcal{D}_\ell \mathrm{Cos}(\ell\theta)$ and $Z(z) = \mathcal{A}_m \mathrm{Sin}(mz) + \mathcal{B}_m \mathrm{Cos}(mz)$. With the boundary conditions, $m = \frac{n_1\pi}{z_1}$ and $\ell = \frac{n_2\pi}{\theta_1}$, with $n_{1,2}$ integer numbers, and z_1 and θ_1 values corresponding to the geometry of glomerulus. Throughout the paper, we will assume that $q = \sqrt{\lambda(1 - \frac{m^2}{\lambda})} \approx \sqrt{\lambda}$, implying that $\lambda >> (\frac{n_1\pi}{z_1})^2$. The solution of (1) can be written in the following form:

$$u(\vec{\mathbf{r}}, t) = T_0 \mathcal{Z}_0 \Theta_0 \sum_{\ell=-\infty}^{\infty} \frac{\mathrm{Exp}[-\lambda D(t - t_0)] \mathrm{Sin}\left(\frac{n_1\pi z}{z_1}\right) \mathrm{Sin}\left(\frac{n_2\pi\theta}{\theta_1}\right) [g_\ell(qr) J_\ell(qr) + h_\ell W_\ell(qr)]}{J_\ell(qr_2) W_\ell(qr_1) - J_\ell(qr_1) W_\ell(qr_2)} \tag{9}$$

where las functions $g_\ell(qr)$ and $h_\ell(qr)$ are given by $R_2 W_\ell(qr_1) - R_1 J_\ell(qr_2)$ and $R_1 J_\ell(qr_2) - R_2 J_\ell(qr_1)$, respectively. The inner and outer radius r_1 and r_2 denote the radial distances or displacements made by the compound described by $u(\vec{\mathbf{r}}, t)$. A simple illustration is seen in Fig.2. The sum over all integer number Bessel functions is applied on ℓ, by which we are accepting all contributions. In this formulation of the solution of $u(\vec{\mathbf{r}}, t)$ we can define that the beginning of the dynamics starts with $T_0 = 0$. The boundary conditions taken for the solution of (1) has demanded $Z(0) = Z(z_1) = 0$ as well as $\Theta(0) = \Theta(\theta_1) = 0$. In addition, the part radial: $R(qr_1) = R_1$ and $R(qr_2) = R_2$ indicating that the compound of proteins have values when is moving out from the microvascular veins to the slit diaphragm and podocytes. The solution of (1) actually follows the common procedure when the differential equation contains the main structure of a Bessel's function. In general, from (5) we can anticipate that the mathematical shape of any compound might be governed by radial and temporal term, fact which leads us to write $u(\vec{\mathbf{r}}, t) \approx \mathrm{Exp}[-\lambda D t] J_\ell(qr)$. This form was obtained in [7] from a phenomenological derivation.

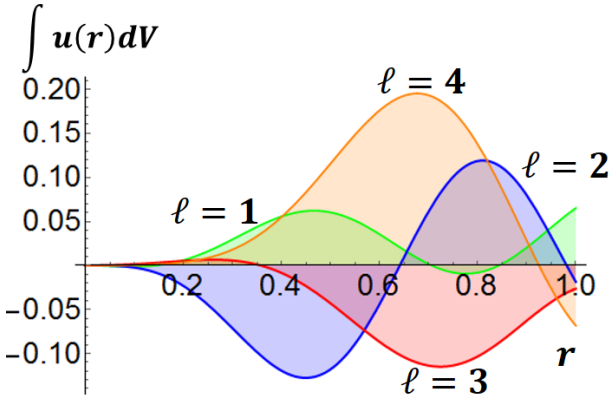

Fig. 3. In top panel, different curves for the values of the integer number ℓ=[1-4], of the closed-form solution of the diffusion's equation (1) $u(r, t = 1)$ for the first nanometer of displacement is shown. In bottom panel, by assuming that the bunching described by $u(r, t = 1)$ has a total charge, the integration over the volume (in cylindrical coordinates) is plotted.

C. Implication of the Bessel's Function in their Interpretation as Diffusion of the Bunches of Albumin

According to Eq.3 once we know the charge density of albumin then we proceed to calculate the total charge. In Fig 3, up to 4 different scenarios of the morphology of the charges or compounds of proteins of albumin as function of radial variable are plotted. For this exercise, we have assumed the following numerical values: r_1=10nm, r_2=50nm, R_1 = 1 r.u, R_2 = 2r .u, (r.u=radial units), Θ_0=25rad, $\mathcal{Z}_0$=10nm, T_0=1, n_1=2, n_2=3, z_1=π and $\Theta_1 = \pi/4$. Thus, we can evaluate now for the variables in the following values: $\theta = \pi/5$rad, and $z = 5/2$nm. The diffusion's constant D is set to 0.14 or a 50% of the H_2O value (0.28 in 25°C). We only left to the variables r and t to be the independent ones for analysis. In fact, Fig. 3 displays up to 4 different values of the integer number ℓ. We have plotted $u(r, t)$ for $\ell = [1, 4]$. All these distributions are showing their peaked morphology which indicates that there exists a prominent bunching of albumin proteins. In praxis, from the peaked distribution we can link this with the anomalous accumulation of proteins and therefore, the albumin excretion rate might be estimated approximately. For instance the case where $\ell = 1$ the peak value reaches 0,40 a.u. Another peak is seen in r=0.8 a.u. radial for $\ell = 2$. According to the frame explained in Fig. 1, it is interpreted as the quantity of proteins which has surpassed the area populated by podocytes [8]. Finally, the case of $\ell = 4$ indicates that $u(r, t)$ would be the case of the most prominent peak in r=0.7. The peaked bunches of albumin might be considered hypothetically as the very beginning of the DKD. This is founded on the basis that the size of these bunches (≈10 nm) are passing through the slit diaphragm whose size is of order of 5 to 15 nm [9]. Therefore, the filtration of these bunches is imminently an alert of degree of degradation of the glomerular layers of kidney. Indeed a noise given by others proteins are also expected. From Fig. 3 the integration over a finite cylindrical volume displays a total negative charge for $\ell = 4$, fact that can be intrerpreted as the screening of positive proteins such as the Tamm-Horsfall. It is actually connected with the idea of electrodynamics that states that $\vec{\nabla} \cdot \vec{E}_{\mathrm{AL}} = \frac{u(r,t)}{\epsilon}$, with ϵ permittivity of medium, and $\vec{E}_{\mathrm{AL}}$ is interpreted as the electric field of the bunch of albumin leaving the glomerulus. Indeed, the electric potential can also be estimated with $\rho_{\mathrm{AL}} = -\epsilon \vec{\nabla}^2 \Phi(\vec{\mathbf{r}})$.

D. Physics of the Detection of Albumin and Tamm-Horsfall Proteins

By assuming that the product of charge densities is governed by the Coulomb force as written in Eq. 4 the expected signal leaving the real glomerulus, we write below the master equation,

$$\mathcal{F}(t) = \mathcal{G}_{\rm GM}(t) \otimes \mathcal{G}_{\rm GL}(t) + \mathcal{G}_{\rm THP}(t) \tag{10}$$

with $\mathcal{G}_{\rm GM}(t)$ and $\mathcal{G}_{\rm GL}(t)$ the contributions of charge denoting the renal glomerulus and glucose, respectively. The main criterion is that the dipole moment of glucose induces asymmetry in the charge densities located along the glomerulus [9]. It should be noted that the $\mathcal{G}_{\rm THP}(t)$ models the THP (Tamm Horsfall Proteins THP). The term $\mathcal{F}(t)$ contains explicitly the charged albumin proteins which are proportional to the charge density of the product of glomerulus and glucose respectively. To note that this analogue to the intensity of the Coulomb-like electric force. Below is presented the following expressions for signal approximation $\mathrm{Exp}(-\frac{k}{T}xt) \rightarrow \mathrm{Exp}(-at)$ with $a = \frac{k}{T}x$,

$$\left[\mathcal{G}_{\rm GM}(t) \otimes \mathcal{G}_{\rm GL}\right]_{m\times n}(t) = \int\int d\omega d\beta J_m(\beta t)\mathrm{Exp}(-a\beta)\times$$

$$\times \left[\beta^n \delta(\alpha\beta t - \omega)\right]. \tag{11}$$

Where the Bessel functions are in according to Eq. 9 the radial solution of the Diffusion's equation. With the simplest case when the diagonal is considered, we can make more concrete our proposal,

$$\mathbf{Diag}\{\left[\mathcal{G}_{\rm GM}(t) \otimes \mathcal{G}_{\rm GL}\right]_{m\times n}(t)\} =$$

$$\int\int d\omega d\beta J_n(\beta t)\mathrm{Exp}(-a\beta)\left[\beta^n \delta(\alpha\beta t - \omega)\right]. \tag{12}$$

The closed-form integration [10], for the signal $\mathcal{G}_{\rm GM} \otimes \mathcal{G}_{\rm GL}(t)$ = $\mathcal{G}_{\rm S}(t)$ reads

$$\mathcal{G}_{\rm S}(t) = A_1 \frac{(\frac{1}{\alpha t})^n}{\left[\left(\frac{1}{\alpha t}\right)^2 + \left(\frac{a}{\alpha t^2}\right)^2\right]^{n+\frac{1}{2}}}. \tag{13}$$

with $A_1 = \frac{2^n\Gamma(n+1/2)}{(\alpha t^2)^n\sqrt{\pi}}$. For the THP, we considered the same structure as given by the signal, but without the presence of the parameters α,

$$\mathcal{G}_{\rm THP}(t) = \int J_n(\beta t)\mathrm{Exp}(-a\beta)\beta^n d\beta. \tag{14}$$

We perform the integration in a straightforward manner resulting in

$$\mathcal{G}_{\rm THP}(t) = A_2 \frac{t^n}{[a^2 + t^2]^{n+1/2}}, \tag{15}$$

con $A_2 = \frac{2^n\Gamma(n+1/2)}{\sqrt{\pi}}$. We can see that the parameters a in given inside of signal and noise, however α does only with signal. It is because the modeling of signal is derived from the fact that the albumin flux has as origin the electric interaction between glomerulus and glucose.

E. Near-to-End Model: Quantifying the Efficiency and Purity of Proteins Detection

Here we introduce the definitions of efficiency and purity, as part of a near-to-end model which would be required to be consistent with previous ideas as given in [1]. Consider the net amount of negatively charged proteins leaving the glomerulus $\mathcal{P}_1$ and the total composition of charges coming from others electrical sources (cations) $\sum_j \mathcal{C}_j$, and the efficiency of senses charges can be written as

$$\mathrm{E_f} = \frac{\mathcal{P}_1}{\sum_j \mathcal{C}_j}. \tag{16}$$

We define the purity as the ratio between the signal plus noise and the total charged compounds which has the chance of being filtering by the glomerulus,

$$\mathrm{P_f} = \frac{\mathcal{P}_1 + \mathcal{P}_2}{\mathcal{P}_1 + \mathcal{P}_2 + \sum_j \mathcal{C}_j}. \tag{17}$$

The received signal is maximum when the product of the purity and efficiency does it in the same manner, independently with or without any attenuation since we assume that these quantities exhibits their maximum values during the first times when albumin is filtering. In this manner the received signal can be estimated as the product of the purity and efficiency and reads $\Psi = \mathrm{E_f} \times \mathrm{P_f}$

$$\Psi = \frac{\mathcal{P}_1}{\sum_j \mathcal{C}_j} \times \frac{\mathcal{P}_1 + \mathcal{P}_2}{\mathcal{P}_1 + \mathcal{P}_2 + \sum_j \mathcal{C}_j},$$

$$\Psi \approx \frac{\mathcal{P}_1^2 + \mathcal{P}_1\mathcal{P}_2}{\sum_j \mathcal{C}_j(\mathcal{P}_1 + \mathcal{P}_2)}. \tag{18}$$

The approximation as seen in (16) is due to the neglecting of the quadratic term in $(\sum_j \mathcal{C}_j)^2$. In this manner we obtain that the received signal is made of two terms, one belonging to the pure signal coming from the charges of albumin and the second signal which can be understood as noise,

$$\Psi \approx \frac{\mathcal{P}_1^2}{\sum_j \mathcal{C}_j(\mathcal{P}_1 + \mathcal{P}_2)} + \frac{\mathcal{P}_1\mathcal{P}_2}{\sum_j \mathcal{C}_j(\mathcal{P}_1 + \mathcal{P}_2)}. \tag{19}$$

It is interesting note that the derivation is phenomenological but it valids the argument that the product of negatively charged albumin and THP plays the role as noise including to the albumin itself. Again, the received signal derived from simple statistical arguments is in agreement with the the phenomenon of repulsion which would occur between albumin and THP little later both have passed to the subsequent processes of formation of urine. Eq. 17 can be used in order to acquire a most precise view of the prospective detection of proteins through a nanosensor located few mm near to kidney. Clearly one expects the detection made a nanosensor with a resolution of 1 per mile. We use Eq. 11 and 13 whereas the free parameters are obtained from a stochastic manner since most of them are related with the random nature of the dynamics of the proteins. In Fig,4 up three scenarios of detection of charged proteins are plotted. The best scenario of signal detection is seen in the bottom panel when signal surpasses notably the noise or background distribution for the first second of

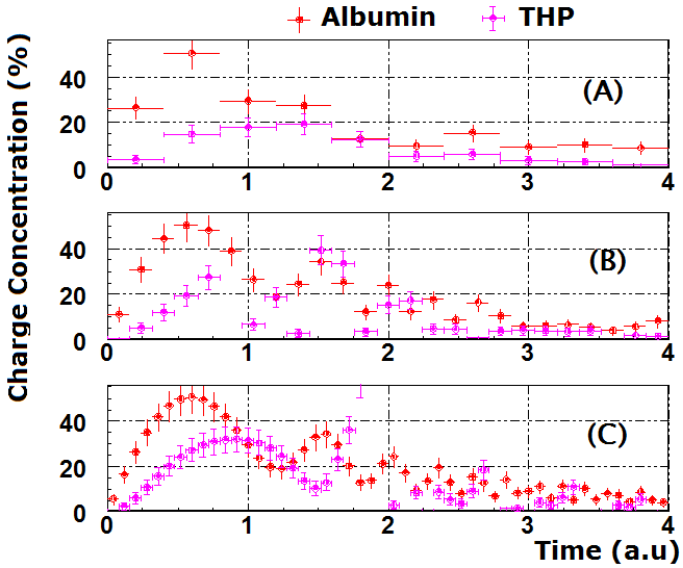

Fig. 4. Charge concentration of albumin and Tamm Horsfall proteins when both are simultaneously sensed by an expected nano sensor.

detection. From the third second of detection both proteins are fully indistinguishable each other. It is interesting that this can be explained in terms of the Coulomb forces in the sense that same sign charges are repulsed each other and move away of the range of the nanodetector. It makes a very small charge concentration measurement of order of less than 10% as seen in Fig.6 (C). One can see that the input-output view can approximately reach interesting results which to some extent can be also interpreted in the Physics side.

III. Estimation of the Albumin Excretion Rate

The peak of the distribution $\int u(r)dV$ for $\ell = 4$ shown in Fig. 3 yields a value of order of 0.2. It is interpreted as the maximum value per glomerulus. Now we pass to estimate the AER from the value Max[$\int u(r)_{\ell=4}dV$]=0.2. For this end, we use the expression

$$\mathrm{AER} = \frac{\mathrm{M_{PR}}}{v_{\mathrm{PR}} \times s} \times \mathrm{V_{TOT}} \tag{20}$$

where $\mathrm{M_{PR}}$ mass of protein of albumin, $\mathrm{V_{TOT}}$ total volume for both kidneys, and v_{PR} full volume of proteins. Firstly, we assume that the net number of human glomerulus is 10^6 (both kidneys). Thus, we can estimate $\mathrm{V_{TOT}}$= 0.2 64 $(10\mu\mathrm{m})^3$ 10^6, where 0.2=$p_{\ell=4}$ denotes the estimated of the peak of curve when ℓ=4 as seen in Fig. 3 bottom panel. The value of 0.64 is obtained from the case of cylindrical geometry. On the other hand, v_{PR}=$\pi(2\mathrm{nm})^2$ 2nm = 8π $(\mathrm{nm})^3$ (assuming a cylindrical geometry). Finally, $\mathrm{M_{PR}}$= 1,6 $(1\mathrm{nm})^3$kg, which is the albumin's mass. A straightforward calculation, yields AER≈0.82 (1n)kg/s, where 1n=10^{-9}. This value is actually of order of 150 mg/day and, in somewhat, can be interpreted as the very beginning of the DKD in patients having an older diagnosis of type-2 diabetes of order of 10 years [10]. The error of calculation is given by

$$\frac{\Delta\mathrm{AER}}{\mathrm{AER}} = \sqrt{\left(\frac{\Delta p_\ell}{p_\ell}\right)^2 + \left(\frac{\Delta \mathrm{V_{TOT}}}{\mathrm{V_{TOT}}}\right)^2 + \left(\frac{\Delta v_{\mathrm{PR}}}{v_{\mathrm{PR}}}\right)^2} \tag{21}$$

where the main source of error would come from the capacity of the model to make predictions of peak of the maximum quantity of albumin bunches leaving the renal glomerulus. However the volumes as written in (6) can also be subject to systematic errors either by measurement or theoretical model. A rapid calculation of ΔAER yields 7%, roughly.

On the other hand in Fig. 5, up to 4 smooth density histograms for t = 0.22s (top panels), t = 0.72s (middle plots), and t = 1.7s (bottom panels) are displayed. Yellow arrows indicate the presence of noise. Although we use bandwidth plotting the displaying of these distribution might be interpreted to some extent as signal and noise. These plots are actually showing their time evolution of the charged bunches going to the convoluted tubule, previous to the urine formation. These plots are expressing the different bandwidth used in this exercise. We have employed 0.1, 0.15 and 0.3. The case of a bandwidth of 0.1 is showing the complexity in the diffusion of the proteins leaving the glomerulus. Actually, the importance of this resolution is perceived as a kind of advantage from the point of view of the nano networking which demands the deployment of very sensitive nanodetectors around the last layers of glomerulus. The reason of such deployment has its ground in the fact that these prospective nanodevice might produce emissions of THz waves, as alarm when the patient is under events of high excretion of albumin into the urine.

IV. Conclusion

In this paper, we have solved as closed-form the diffusion's equation in cylindrical coordinates and its interpretation is given in terms of the evolution of compound passing through the renal glomerulus. The compound is understood to be a bunch of proteins of albumin. These giant proteins are leaving the glomerulus because the electrodynamics with the shielding of charges over the inner and outer layers of glomerulus. These results would support the idea that the deployment of a nanosensor near to the glomerulus might be advantageous for the anticipation of the very beginning of DKD, by assuming the central hypothesis that the dynamics of the bunches of albumin is entirely governed for repulsion and attraction electric forces. Finally we have added to this study a view from the input-output theory and adapted to the phenomenology of anomalous transport of charged proteins resulting in possibles curves of charges concentration detection of both signal and noise. This approach turns out to be valid since explains also the electrodynamics of the bunches of charges expelled by the kidney due to the presence of high concentrations of glucose.

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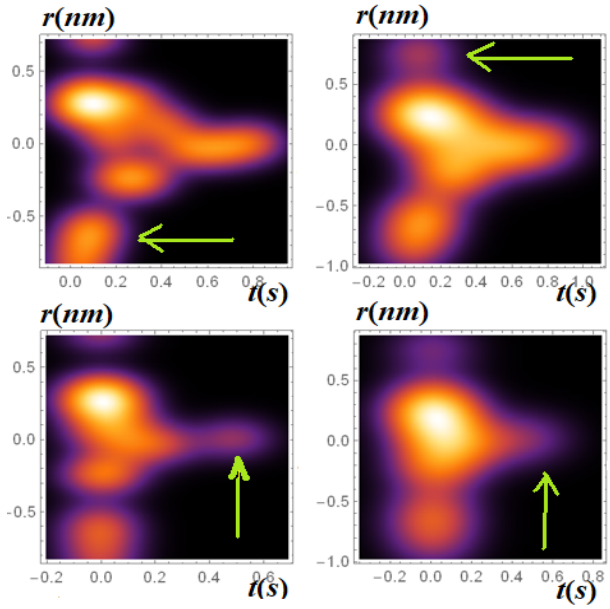

Fig. 5. Smooth density histograms as a possible result of charge detection for t = 0.22s (top panels), and t = 0.72s (middle plots) with the numerical values of the curve $\int u(r)dV$ for $\ell = 1$. Yellow arrows indicate the location of noise such as THP being also excreted together with the urine.

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