



## 2 Allometric scaling law and ergodicity breaking in the vascular system

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### 6 Abstract

7 Allometry or the quantitative study of the relationship of body size to living organism physiology is an important area of  
8 biophysical scaling research. The West-Brown-Enquist (WBE) model of fractal branching in a vascular network explains  
9 the empirical allometric Kleiber law (the  $\frac{3}{4}$  scaling exponent for metabolic rates as a function of animal's mass). The WBE  
10 model raises a number of new questions, such as how to account for capillary phenomena more accurately and what are  
11 more realistic dependencies for blood flow velocity on the size of a capillary. We suggest a generalized formulation of the  
12 branching model and investigate the ergodicity in the fractal vascular system. In general, the fluid flow in such a system is  
13 not ergodic, and ergodicity breaking is attributed to the fractal structure of the network. Consequently, the fractal branching  
14 may be viewed as a source of ergodicity breaking in biophysical systems, in addition to such mechanisms as aging and  
15 macromolecular crowding. Accounting for non-ergodicity is important for a wide range of biomedical applications where  
16 long observations of time series are impractical. The relevance to microfluidics applications is also discussed.

17 **Keywords** Allometry · Ergodicity · Fractal branching · Capillaries · Cardiovascular system · Microfluidics

### 18 1 Introduction

19 Modern high throughput biomedical and bioinformatics  
20 methods often require in vivo observations of the temporal  
21 evolution of various parameters. In many cases, prolonged  
22 data acquisition from an object is impractical and it is sub-  
23 stituted by taking a snapshot from many similar objects. For  
24 this reason, understanding the ergodicity breaking mecha-  
25 nisms is particularly important for the study of biophysical  
26 fluid transport systems.

27 Ergodicity, or the equivalence of time and phase space  
28 (or ensemble) averages, is an important property of many  
29 dynamical systems. Roughly speaking, ergodic systems have  
30 no memory of their previous history, and they tend to attain  
31 all microstates available. Contrary to that, non-ergodic sys-  
32 tems demonstrate evolution with time or aging, which affects  
33 their ability to attain microstates with equal probability. The

concept of ergodicity was first introduced by Ludwig Boltz-  
mann, and it was further advanced in 1890 by Henri Poin-  
caré's Recurrence Theorem stating that phase-space volume-  
preserving systems will always return to a state identical or  
very close to their initial state.

George Birkhoff (1931) and von Neumann further  
extended the Ergodic theory, which became a central part  
of the theory of dynamical systems. Ergodicity is related to  
a number of important concepts in 20th century physics, such  
as the theory of spontaneous symmetry breaking and phase  
transitions. For example, it has been realized that a finite  
system returning to its initial position over a sufficiently long  
period of time makes phase transitions prohibitive in finite  
systems represented by Ising-type models (Kadanoff 2009).

Ergodicity has various implications for the theoretical  
aspects of dynamical system's behavior, such as its stability  
and quasi-periodic motion, and for its qualitative behavior  
(Arnold and Avez 1968, Arnold 1978), e.g., for identify-  
ing Lagrangian Coherent Structures (LCSs) in fluid flow  
(Rypina et al. 2011). Ergodicity is also crucial for practical  
aspects of measuring systems parameters, since sufficiently  
long observations of temporal behavior are often impossi-  
ble and, therefore, it should be substituted with finite time  
measurements (Guzman-Sepulveda et al. 2017; Magdziarz  
and Zorawik 2019).

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Author Proof

59 One area where ergodicity breaking is particularly  
 60 important is the biophysical transport of liquids. This  
 61 includes hemodynamics (blood flow dynamics), intra-  
 62 cellular and extracellular transport of complex media in  
 63 biological systems, such as cytoplasm and nucleoplasm,  
 64 and macromolecular biopolymer solutions (Kulkarni  
 65 et al. 2003; Földes-Papp and Baumann 2011; Manzo et al.  
 66 2015).

67 From the thermodynamic point of view, biological sys-  
 68 tems including the vascular system may be viewed as open  
 69 systems, so ergodicity is not expected in them, although  
 70 the assumption of ergodic behavior is often made. Ergo-  
 71 dicity breaking in biological fluids is associated with mac-  
 72 romolecular crowding, which causes anomalous diffusion.  
 73 According to the classical Einstein–von Smoluchowski  
 74 model, the mean-square displacement is a linear function  
 75 of the lag time,  $\langle r^2 \rangle \propto t$ . Contrary to that, the anomalous  
 76 diffusion results in the dependency which has the form of  
 77 a power law

$$78 \langle r^2 \rangle \propto t^\alpha \tag{1}$$

79 with  $\alpha < 1$  for the subdiffusion (which is the common case)  
 80 (Hofling and Franosch 2013).

81 The subdiffusion caused by aging can have several  
 82 underlying causes besides the macromolecular crowding.  
 83 This includes flowing through obstacles with a certain  
 84 density. Another cause can be the so-called “hydrody-  
 85 namic memory” when a particle’s effective mass should be  
 86 adjusted due to the deceleration caused by incessantly new  
 87 vortices diffusing slowly through the fluid. Consequently,  
 88 the friction force depends on the entire history of the par-  
 89 ticle’s trajectory, and it is related to the fractal nature of  
 90 a turbulent trajectory (Hofling and Franosch 2013). In all  
 91 these cases, the fractal behavior is responsible for ergodic-  
 92 ity breaking and for transport deceleration in comparison  
 93 with the classical diffusion law.

94 Besides the turbulence and random-walk diffusive  
 95 behavior both leading to the fractal geometry of the tra-  
 96 jectories, the self-similar or self-affine behavior could be  
 97 associated with another situation, which is rarely viewed  
 98 as a source of ergodicity breaking. This is the self-similar  
 99 tree-shaped flow in the cardiovascular or alveolar systems  
 100 (Bejan 2004), which is believed to be responsible for the  
 101 allometric scaling in living organisms.

102 The allometric scaling relationships were summarized by  
 103 the empirical Kleiber law. Kleiber (1932, 1947) compared  
 104 metabolism rates,  $B$ , in various species and found that it is  
 105 well approximated by a power-law scaling dependency on  
 106 the mass of an animal,  $B \propto M^{0.75}$ . The value of the exponent,  
 107  $a = 0.75$ , could not be explained until the seminal paper by  
 108 West et al. (1997) appeared, which used a fractal model of  
 109 the branching of blood vessels.

110 The theory by West et al. (1997), also referred to as the  
 111 West-Brown-Enquist (WBE) model, caused some discus-  
 112 sions in the literature (Savage et al. 2004; Kozłowski and  
 113 Konarzewski 2004; Bejan 2004; Brown et al. 2005; Etienne  
 114 et al. 2006, 2008; Banavar et al. 2010); however, despite its  
 115 shortcomings, the WBE model remains the main explana-  
 116 tion of the allometric scaling exponents. At the same time,  
 117 the WBE model has never been viewed as an underlying  
 118 reason for ergodicity breaking in hemodynamics. While  
 119 dealing with capillaries, the WBE model does not take into  
 120 account the physico-chemical capillary phenomena, such as  
 121 the effect of the surface tension, associated with the flow of  
 122 such a multi-component liquid as blood. Instead, the WBE  
 123 model relies solely on macroscale fluid mechanics consider-  
 124 ations. In the present paper, we extend the allometric model  
 125 to include the capillary phenomena and investigate ergodic-  
 126 ity breaking caused by the fractal nature of the capillary  
 127 branching model. 128

## 2 Scaling relationships for a branching capillary system 129 130

131 Scaling relationships traditionally play a significant role in  
 132 biophysics, since scaling considerations define the size and  
 133 properties of living cells (Fabry et al. 2003; Bormashenko  
 134 and Voronel 2018). A particularly important area of bio-  
 135 physical scaling is the allometry or the quantitative study of  
 136 the relationship of body size to living organism physiology.

### 2.1 Branching with area and volume conservation 137

138 West et al. (1997) suggested an allometric scaling law for  
 139 a branching cardiovascular network based on the assump-  
 140 tions of area- and volume-preserving branching (the WBE  
 141 model). The concept of the area-preserving branching has  
 142 been known in biology for a long time. Already Leonardo  
 143 da Vinci suggested that in trees, the total cross-section area  
 144 of branches is conserved across branching nodes. This struc-  
 145 ture is believed to be self-similar and optimized to resist  
 146 wind-induced loads (Eloy 2011). The volume preservation  
 147 implies that the same volume is served equally by branches  
 148 of different sizes.

149 According to the WBE model, when a tube with the  
 150 length  $l_k$  and radius  $r_k$  branches into  $n$  tubes with the lengths  
 151  $l_{k+j} = \gamma l_k$  and radii  $r_{k+j} = \beta r_k$ , the volume served by the next  
 152 generation tubes and their cross-section area should be con-  
 153 served, which leads to the scaling relationships  $\gamma \propto n^{-1/3}$  and  
 154  $\beta \propto n^{-1/2}$ . The volume is preserved because the same vol-  
 155 ume in the organism is served by blood vessels of different  
 156 hierarchical levels. The area is preserved on the assumption  
 157 of the constant rate of the fluid flow at different hierarchical  
 158 levels (Fig. 1).

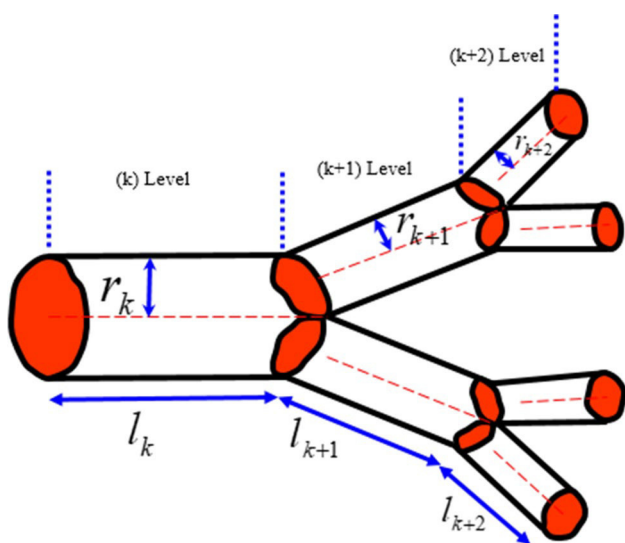


Fig. 1 Branching of a vascular network; three levels are shown

159 The volume of fluid at a certain  $k$ -th level of the branching hierarchy  $V_k = \pi r_k^2 l_k n^k = V_0 (n\gamma\beta^2)^k$ , where  $V_0 = \pi r_0^2 l_0$ .  
 160 The total volume of fluid is given by the sum of the geometric series  $V = \sum_{k=0}^N \pi r_k^2 l_k n^k = V_0 \frac{1 - (n\gamma\beta^2)^{N+1}}{1 - n\gamma\beta^2}$ , where  $N$  is the  
 161 total number of branch generations. Since  $n\gamma\beta^2 < 1$  and  
 162  $N \gg 1$ , a good approximation is  $V = V_0 \frac{1}{1 - n\gamma\beta^2} = V_c \frac{(\gamma\beta^2)^{-N}}{1 - n\gamma\beta^2}$   
 163 where  $V_c = V_0 / (\gamma\beta^2)^{-N}$  is a certain elementary volume (e.g., volume served by a capillary) (West et al. 1997).  
 164 Therefore, the volume scales as  $V \propto (\gamma\beta^2)^{-N}$ . From this, the scaling dependency of the total number of capillaries as a  
 165 function of volume is  
 166  $n^N \propto V^a \propto (\gamma\beta^2)^{-Na} \propto (n^{-4/3})^{-Na} \propto n^{4Na/3}$  yielding  $a = 3/4$ ,  
 167 the well-established empirical results known as the Kleiber law.  
 168

169 The total volume of fluid in the cardiovascular network was further assumed to be linearly proportional to the mass  
 170 of the organism. At the same time, the number of capillaries  
 171  
 172  
 173  
 174  
 175

is proportional to the flow rate and to the rate of metabolic processes in general. This leads to various conclusions, for example, that the lifespan scales with the mass of an animal as  $M^{1/4}$  (Bejan 2012).

## 2.2 Considering more realistic scaling dependencies

Note that the WBE branching model takes into account neither the physico-chemical capillary effects due to the interfacial tension of the liquids, nor the tortuosity of the capillaries. Human blood is a non-Newtonian multi-component fluid consisting of liquid plasma (55% of total blood volume, consisting of water by 95% with various dissolved substances), red blood cells or erythrocytes (flexible disks of 6–8  $\mu\text{m}$  diameter), white blood cells or leucocytes of different types (of 7–30  $\mu\text{m}$  diameter), and platelets (of 2–3  $\mu\text{m}$  diameter). However, the WBE model does not properly consider the effect of such a complex flow. Moreover, the radius of blood vessels The radius of blood vessels varies by about 3000 times from 15 mm in the aorta to 5  $\mu\text{m}$  in the capillaries, while the flow velocity changes by about 1300 times from 0.4 m/s in the aorta to 0.3 mm/s in the capillaries. This is in striking contradiction with the assumption of the constant rate of the fluid flow at different hierarchical levels. Therefore, more accurate scaling dependencies than those of the WBE model should be studied.

Computation Fluid Dynamics (CFD) simulations demonstrate that even simple branching (bifurcation,  $n = 2$ ) of a vessel results in a complex flow velocity profile. Thus, Fig. 2 shows CFD modeling results for bifurcation of a blood vessel for typical blood flow conditions at the peak systolic phase. The velocity profile and flow streamlines are far from being uniform. Therefore, the scaling assumption for velocities in a branching network can be satisfied only approximately.

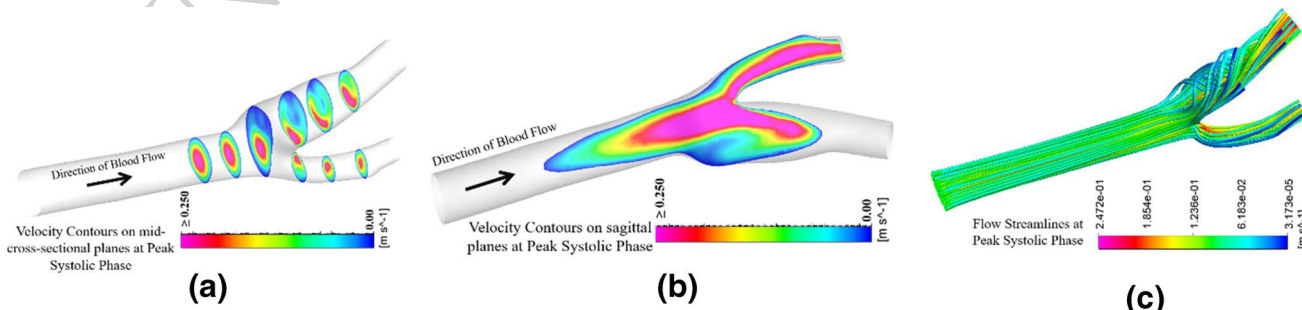


Fig. 2 CFD simulation of blood flow through a bifurcating (branching) vessel shows complex dependencies of velocity, which cannot be approximated by a simple scaling relationship. Velocity contours

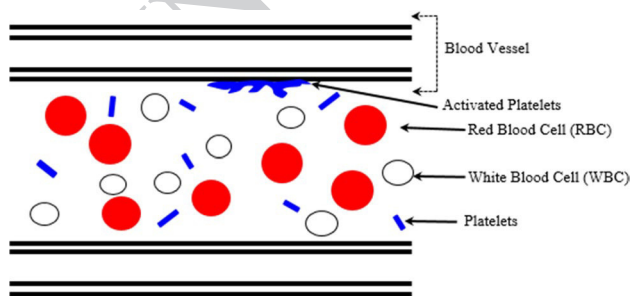
in (a) a perpendicular and (b) a parallel cross-section along with (c) flow streamlines for the peak systolic phase are shown



Due to the liquid volume preservation postulate,  $\pi r_k^2 u_k = \pi r_{k+1}^2 u_{k+1}$ , the velocity scales as  $\frac{u_k}{u_{k+1}} = n \frac{r_{k+1}^2}{r_k^2} = n\beta^2$ . Under the assumption of cross-sectional area preservation,  $\beta \propto n^{-1/2}$ , this leads to a constant value of the flow velocity in the system,  $u_k = u$ ; however, experimental data indicate that the flow velocity may be different at different branching levels, as was discussed in the preceding section. As suggested by the CFD simulations and experimental data, the decrease of the flow speed is roughly of the same order as vessel radius and can be captured with the scaling assumption  $\beta \propto n^{-1/3}$ .

The surface tension of blood is rarely discussed in biomedical literature, although it is significantly lower than that of water: about 56 mN/m at room temperature, while water surface tension is about 72 mN/m. The surface tension of blood has biological and medical implications, thus, it has been associated with the genesis of the decompression sickness and other processes in the human organism (Hrnčič and Rosina 1997; Krishnan et al. 2005). Therefore, it is important to pay attention to blood surface tension.

The superhydrophobicity, or the surface roughness-induced non-wetting, has been studied intensively in two recent decades (Nosonovsky and Rohatgi 2012). This brought attention to related ideas of the surface roughness-induced self-cleaning in the liquid flow, the oleophobicity (repelling organic liquids such as oils), underwater oleophobicity to reduce fouling, and the shark skin effect (flow drag reduction due to specially oriented micro-riblets). Maani et al. (2015) suggested the micro/nanostructure-controlled adhesion in blood flow for cardiovascular applications, where it is desirable to reduce stagnation and clotting of blood. The complex structure of blood vessel surface layers combined with a complex multiphase composition of blood may result in significant surface-induced effects (Fig. 3) Biomedical “hemophobic” applications can prevent blood clotting and thrombosis by controlling the surface pattern at a wall of a catheter or stent (Ramachandran et al. 2016).



**Fig. 3** Schematic of blood flow in a blood vessel showing layers of the blood vessel and various components of blood. The interaction with the blood vessel wall is important due to its medical significance and hemodynamic effects (Maani et al. 2015)

Taking into account the surface effect may modify the law of cross-sectional area preservation for small capillaries, leading to the alternate assumption that  $\beta \propto n^{-1}$ .

Times spent by a particle or molecule at different levels of branching hierarchy form a geometric sequence with the ratio

$$\frac{T_{k+1}}{T_k} = \frac{l_{k+1} u_k}{u_{k+1} l_k} = \gamma n \beta^2 \tag{2}$$

To accommodate for the vascular resistance, the Hagen–Poiseuille equation is often used, which states that the resistance to the blood flow scales as  $r^{-4}$ , or the Thurston (1976) equation, which scales the flow resistance as  $r^{-3}$ . There are different ways to account for the size effect due to the capillary phenomena; however, in general, the assumption of the dependencies of  $\gamma$  and  $\beta$  on  $n$  should be modified.

In addition, capillaries are not straight tubes. The influence of capillary tortuosity or curvature can be scale-dependent. To account for various above-mentioned effects and the corresponding various possible values for the scaling rates, we can consider more general scaling relationships  $\gamma \propto n^{-b}$  and  $\beta \propto n^{-c}$ . In other words, since different assumptions lead to different relationships between  $\gamma$ ,  $\beta$  and  $n$ , we will now consider a general case of the relationships. Repeating the same derivation as in the preceding section, one now obtains  $n^N \propto V^a \propto (\gamma \beta^2)^{-Na} \propto (n^{-b-2c})^{-Na} \propto n^{Na(b+2c)}$  leading to the power exponent

$$a = 1/(b + 2c) \tag{3}$$

The relationship is given by Eq. 3 is based on the fractal geometry of branching vessels, and in the case of  $b = 1/3$ ,  $c = 1/2$  it produces the same result as the WBE model,  $a = 3/4$ .

### 3 Ergodicity breaking analysis

Let us now concentrate on the ergodicity of the blood flow in the vascular system. For that end, we will calculate the fraction of time that a blood cell spends in a certain fraction of the total volume of the circular system, and, after that, we will compare the temporal and volumetric fractions.

The total time that a blood particle (including cells or molecules) spends in the circulatory system is given by the sum of the infinite geometric series with the ratio obtained from Eq. 2 as  $T_{k+1}/T_k = \gamma n \beta^2 = n^{1-b-2c}$ . The sum is given by (Wolfram 2020)

$$T = \sum_{k=1}^{\infty} T_k = \sum_{k=1}^{\infty} \frac{l_k}{u_k} = \frac{l_1}{u_1 (1 - n^{1-b-2c})} \tag{4}$$

292 where  $l_1$  is the length of the highest hierarchical level. For  
 293  $b = 1/3$  and  $c = 1/2$ , Eq. 4 yields  $T = \frac{l_1}{u(1-1/\sqrt[n]{n})}$ .

294 Let us calculate the time, which a blood particle spends at  
 295 the levels of the system starting from  $k = m$  to  $k = \infty$  using the  
 296 formula of a partial sum of a geometric series. The assumption  
 297 behind this calculation is that only blood vessels  $k = m, \dots, \infty$   
 298 serve the volume defined by the length  $l_k$  (the volume itself is  
 299 given by the sphere  $32\pi l_m^3/3$ ). Consequently, the ratio of the  
 300 time spent at the levels  $k = m, \dots, \infty$  to the total time in the  
 301 vascular system,  $T$ , is given by the time fraction

302 
$$\theta_m = \left(\frac{T_{k+1}}{T_k}\right)^{m-1} = n^{(1-b-2c)(m-1)} \quad (5)$$

303 Note that for  $b = 1/3$  and  $c = 1/2$ , Eq. 5 yields  
 304  $\theta_m = n^{-(m-1)/3}$ .

305 Consider a region with the radius  $= 2l_m$ , which corre-  
 306 sponds to the volume  $32\pi l_m^3/3$  in the organism, served by  
 307 capillaries of the levels  $k \geq m$ . This volume constitutes the  
 308 fraction of the total volume

309 
$$\rho_m = \frac{l_m^3}{l_1^3} = \gamma^{3(m-1)} = n^{-3b(m-1)} \quad (6)$$

310 The volume distribution of the capillaries is uniform,  
 311 therefore, the probability to find a liquid molecule or cell/  
 312 particle in a given volume is supplied by  $\rho_m$ . On the other  
 313 hand, the time fraction spent by a single blood cell or mole-  
 314 cule at a given volume  $32\pi l_m^3/3$  is given by  $\theta_m$ , and thus  
 315 the ratio of the probability to find a single cell or molecule  
 316 within a certain volume during its motion to the fraction of  
 317 molecules in this volume is

318 
$$\frac{\theta_m}{\rho_m} = \frac{n^{(1-b-2c)(m-1)}}{n^{-3b(m-1)}} = n^{(1+2b-2c)(m-1)} \quad (7)$$

319 In general, the ratio supplied by Eq. 7 is dependent on  $m$ ,  
 320 and, therefore, it is dependent on the size of the volume thus  
 321 indicating that the motion is not ergodic. Due to the fractal  
 322 nature of the capillary system, a particle tends to spend much  
 323 more time in smaller volumes in comparison to the volume  
 324 fraction. Note that for  $b = 1/3$  and  $c = 1/2$ , Eq. 7 yields

325 
$$\frac{\theta_m}{\rho_m} = n^{2(m-1)/3} \quad (8)$$

326 Using  $3b(m-1)\ln n = -\ln \rho_m$  we find  
 327  $m-1 = -\ln \rho_m / (3b \ln n)$ . By further substituting the value  
 328 of  $m$  into Eq. 7 and finding a logarithm, we obtain

329 
$$\ln \theta_m = \frac{b-1+2c}{3b} \ln \rho_m + \ln(n^{-1+b+2c}) \quad (9)$$

330 The number of the hierarchical level  $m$  is eliminated from  
 331 Eq. 9, which presents the dependency of the time fraction

332 spent in a certain volume upon its volume fraction of the  
 333 total volume. By interpolating it (i.e., assuming continuous  
 334 rather than discrete ranges of  $\theta$  and  $\rho$ ), one finds the depend-  
 335 ency of the probability for a particle to be found in a certain  
 336 volume based on the time spent there to the probability to  
 337 find a particle in that volume based on the volume fraction

338 
$$\theta = \rho^{\frac{b-1+2c}{3b}} \quad (10)$$

339 Ergodicity implies that the ensemble average equals the  
 340 time average. For blood particles (such as blood cells or  
 341 molecules), this requires a comparison of how many parti-  
 342 cles (as a fraction of the total number) are found in a certain  
 343 volume vs. how much time (as a fraction of the total time)  
 344 one particle spends in the volume. For a given volume, the  
 345 space-average probability to find a particle is proportional  
 346 to that volume. Note that  $\rho$  is the fractional volume of the  
 347 tissue, which is served by capillaries. When experimental  
 348 observations are performed to trace a particle, the parameter  
 349 of interest is the volume of the tissue. The volume of liquid  
 350 in the vascular circulatory system, which serves the volume  
 351 of the tissue, is a different volume. The capillaries in our  
 352 model (similarly to the WBE model) provide equal access to  
 353 all tissues. Consequently, the ensemble-averaged probability  
 354 to find a blood particle in a certain volume of tissue,  $\rho$ , is  
 355 just proportional to the volume. Contrary to that, the time  
 356 fraction,  $\theta$ , is not necessarily proportional to the volume of  
 357 the tissue. This is because a particle spends more time in  
 358 smaller regions due to the self-similar scaling of a fractal  
 359 branching network.

360 Three dependencies of the time fraction spent in a cer-  
 361 tain volume upon its volume fraction,  $\theta(\rho)$ , are shown in  
 362 Fig. 4a for different values of  $a$  and  $b$ . Note that for  $b = 1/3$   
 363 and  $c = 1/2$ , Eq. 10 yields a non-linear (and, therefore, non-  
 364 ergodic) dependency  $\theta = \sqrt[3]{\rho}$ .

365 The ergodicity condition would imply equal time spent in  
 366 equal volumes and, therefore, a linear dependency between  
 367 corresponding variables,  $\theta \sim \rho$ . This is achieved when the  
 368 following condition is satisfied

369 
$$b = c - \frac{1}{2} \quad (11)$$

370 For example, in Fig. 4a, the linear dependency for  
 371  $b = 1/4, c = 3/4$  is the ergodic case. Combining Eqs. 3 and  
 372 11 gives  $a = 2/(6c - 1)$ . For volume-preserving branching,  
 373  $b = 1/3$ , this yields  $c = 5/6$  and  $a = 1/2$ . This is inconsis-  
 374 tent with the Kleiber law, which relates the metabolic rates to  
 375 the animal mass,  $B \propto M^a$  as  $a = 3/4$ . On the other hand, the  
 376 Kleiber law,  $a = 3/4$ , is satisfied when  $b = 25/22 \approx 1.136$   
 377 and  $c = 18/11 \approx 1.636$ , which contradicts the volume-pre-  
 378 serving branching assumption. We conclude that for realistic  
 379 situations (the volume-preserving branching and the Kleiber  
 380 law), the model predicts non-ergodic behavior.

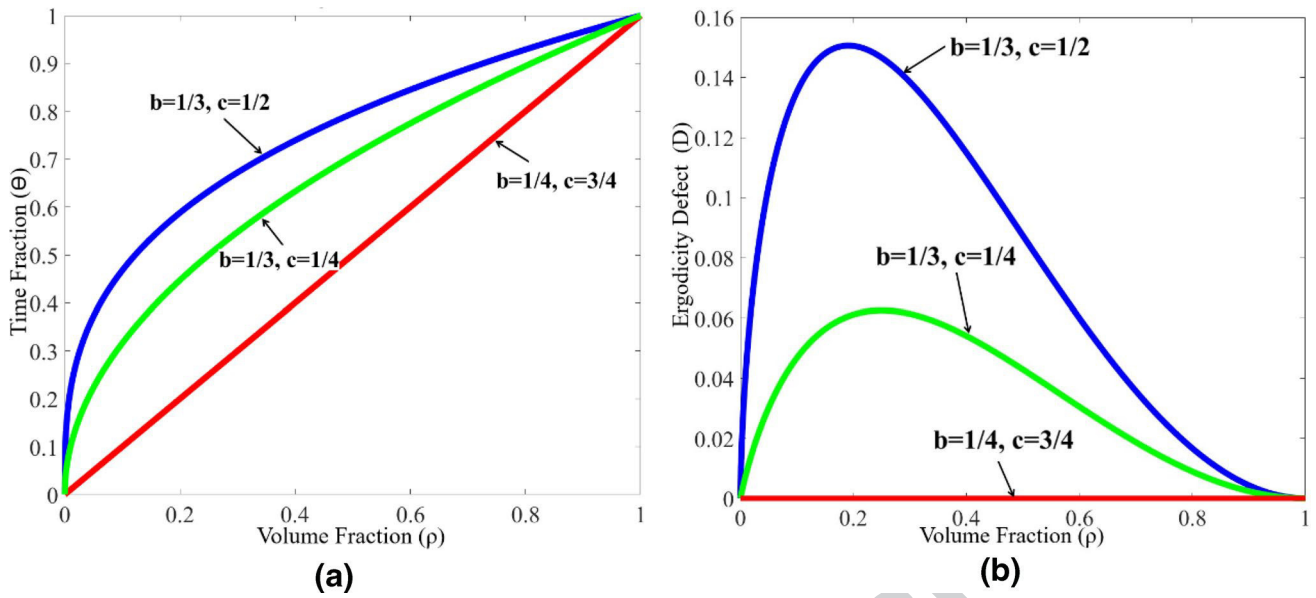


Fig. 4 a Time fraction and b ergodicity defect as a function of the volume fraction for three combinations of parameters  $a$  and  $b$

388 Several measures of deviation from the ergodic behavior  
 389 have been suggested in literature. Földes-Papp and Baumann  
 390 (2011) suggested decoupling the effects of the molecular  
 391 crowding and the temporal heterogeneity by presenting the  
 392 power exponent, which controls the dynamics of the interac-  
 393 tion network, as a product of these two factors.

394 Scott et al. (2009) suggested the ergodicity defect  $D$ ,  
 395 defined at different scales (on a map  $T$ ) with respect to a basis  
 396 of functions  $f$  given by an integral of the square of space and  
 397 time averages  $D(f, T) \propto \int (f^*(x, T) - \bar{f})^2 dx$ , where  $f^*$  and  $\bar{f}$   
 398 are the time and space averages. The ergodicity defect defined  
 399 in this manner can be used to identify the structure of the solu-  
 400 tion, such as Lagrangian coherent structures (Rypina et al.  
 401 2011).

402 Using Eq. 10, one can suggest defining the ergodicity defect  
 403 for our case as

$$404 D = (\theta - \rho)^2 = \rho^2 \left( \rho^{\frac{-2b-1+2c}{3b}} - 1 \right)^2 \quad (12)$$

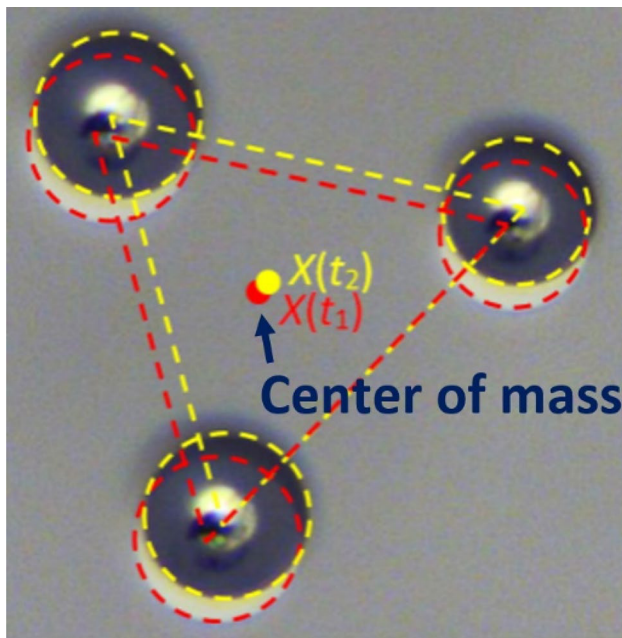
405 Note that Eq. 12 does not involve the integration over space  
 406 (i.e., L2 norm) because the parameters  $\theta$  and  $\rho$ , as obtained  
 407 from Eq. 10, do not depend on spatial variables. Figure 4b  
 408 shows a plot of the ergodicity defect vs. the volume fraction  
 409 for the values of the parameters used in Fig. 4a.  
 410

#### 4 Discussion

411 The calculations in the preceding section demonstrate that  
 412 flow systems with fractal branching exhibit non-ergodic  
 413 behavior. Such systems, including vascular networks, involve  
 414 the flow, which covers a 3D volume delivering fluid to the  
 415 vicinity of every point of the volume (every cell) with equal  
 416 probability. In addition to covering the volume with equal  
 417 probability, they should supply the fluid continuously in the  
 418 temporal domain. However, due to the fractal organization of  
 419 the vascular network, the flow “decelerates” at small length  
 420 scales. Consequently, particles (including molecules and  
 421 cells) spend more time at small volumes, in comparison with  
 422 the volumetric fraction of these volumes. We interpret this  
 423 feature of fractal behavior as ergodicity breaking.  
 424

425 While traditional sources of ergodicity breaking in bio-  
 426 physical fluid transport systems include time evolution or  
 427 aging of the particles and macromolecular crowding, it is not  
 428 uncommon that fractal geometry of a trajectory results in an  
 429 effective deceleration of a motion. One example would be the  
 430 “hydrodynamic memory,” which slows down the diffusion  
 431 (Hofling and Franosch 2013). Another example is the so  
 432 called “dissipative anomaly” in the turbulent flow when the  
 433 dissipation does not approach zero even at the zero viscosity





**Fig. 5** Oscillations of a small levitating droplet cluster, which vibrates as a whole (Fedorets et al. 2019b)

434 limit so that fractal trajectories lead to deceleration (De Lellis and Székelyhidi 2019; Shnirelman 2000).

436 Ergodicity breaking due to scale-dependent behavior  
 437 is also significant for small systems of colloidal or droplet  
 438 clusters (Nosonovsky and Roy 2020). These systems are  
 439 used for in situ tracking of biomolecules and bioaerosols  
 440 (Fedorets et al. 2019a). Lim et al. (2019) reported the transi-  
 441 tions from sticky to ergodic configurations in six-particle  
 442 and seven-particle systems of hard spheres. Fedorets et al.  
 443 (2019b) studied small oscillations of a microdroplet cluster  
 444 levitating in an ascending vapor stream and found that the  
 445 cluster tends to oscillate as a whole. They showed that the  
 446 synchronization of droplets' trajectories is not caused by the  
 447 interactions between droplets, but by external fluctuations  
 448 with the characteristic length scale much larger than the  
 449 size of the droplets. The center of mass of the entire cluster  
 450 produces the same motion as single micro-droplets, indicat-  
 451 ing ergodic behavior. Ergodicity breaking, in this case, is  
 452 related to the scale ratio of the external fluctuation and of  
 453 the system (Fig. 5).

454 Understanding the ergodicity breaking in the fluid flow of  
 455 branching vascular networks is also relevant to micro/nano-  
 456 fluidic applications, such as the artificial biomimetic vas-  
 457 cularized tissues. Such tissues are being developed for both  
 458 medical applications of tissue-engineered constructs (Hasan  
 459 et al. 2014) and for applications such as self-healing materi-  
 460 als where a flow of liquid agent is required (Nosonovsky  
 461 and Rohatgi 2012).

## 5 Conclusions

462 Fractal models of branching cardiovascular networks 463  
 464 involve two elements: the ability of a network to serve 465  
 466 homogeneously a 3D volume (the volume preservation) 467  
 468 and the conservation of the flow through the 2D cross-sec- 469  
 470 tions after branching (the area preservation). These mod- 470  
 471 els explain empirical allometric laws, such as the power 471  
 472 exponent of  $\frac{3}{4}$  in the Kleiber law, which relates metabo- 472  
 473 lic rates to the animal mass. At the same time, these models 473  
 474 raise new concerns, such as the need for more accurate 474  
 475 accountability for capillary phenomena and more realistic 475  
 476 dependencies for the blood flow velocity with decreasing 476  
 477 size of vessels. We suggested a generalized formulation 477  
 478 of the branching model (Eq. 3) and investigated the ergo- 478  
 479 dicity of the fluid flow in a vascular network described 479  
 480 by such a model. Generally, the fractal structure of such 480  
 481 models makes them non-ergodic because a particle of the 481  
 482 fluid spends more time in small 3D regions comparing 482  
 483 with the volumetric fraction of these regions. The time 483  
 484 fraction corresponds to the temporal average, while the 484  
 485 volumetric fraction corresponds to the ensemble average. 485

486 The mechanism studied in the present paper can be a 486  
 487 factor which contributes to the ergodicity breaking in bio- 487  
 488 physical systems, as follows from Eq. 10, in addition to 488  
 489 such well-established mechanisms as aging and macro- 489  
 490 molecular crowding. Accounting for the non-ergodicity 490  
 491 is important for a wide range of biomedical applications 491  
 492 where long observations of time series are impractical. 492

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