
Mean-intercept anisotropy analysis of porous media.

I. Analytic formulae for anisotropic Boolean models

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(Dated: April 7, 2017)
Abstract

Purpose: Structure-property relations, which relate the shape of the microstructure to physical properties such as transport or mechanical properties, need sensitive measures of structure. What are suitable fabric tensors to quantify the shape of anisotropic heterogeneous materials? The mean intercept length is among the most commonly used characteristics of anisotropy in porous media, for example, of trabecular bone in medical physics.

Methods: We analyze the orientation-biased Boolean model, a versatile stochastic model that represents microstructures as overlapping grains with an orientation bias towards a preferred direction. This model is an extension of the isotropic Boolean model, which has been shown to truthfully reproduce multi-functional properties of isotropic porous media. We explain the close relationship between the concept of intersections with test lines to the elaborate mathematical theory of queues, and how explicit results from the latter can be directly applied to characterize microstructures.

Results: In this series of two papers, we provide analytic formulas for the anisotropic Boolean model and demonstrate often overlooked conceptual shortcomings of this approach. Queuing theory is used to derive simple and illustrative formulas for the mean intercept length. It separates into an intensity-dependent and an orientation-dependent factor. The global average of the mean intercept length can be expressed by local characteristics of a single grain alone.

Conclusions: We thus identify which shape information about the random process the mean intercept length contains. The connection between global and local quantities helps to interpret observations and provides insights to the possibilities and limitations of the analysis. In the second paper of this series, we discuss, based on the findings in this paper, severe short-comings of the mean intercept analysis for (bone-)microstructure characterization. We will suggest alternative and better defined sensitive anisotropy measures from integral geometry.

Keywords: shape analysis, fabric tensors, mean intercept length, mean chord length, anisotropic porous media
Fabric tensors characterize the complex microstructure in both natural and man-made materials\(^1\), for example, in geology\(^2\), granular matter\(^3\), foams\(^4\), rough surfaces\(^5\), solids with cracks\(^6\), and trabecular bone\(^7-9\). The aim is to gain physical insight via a better understanding of the geometrical properties, for example, relating the mechanical properties of the material to its microstructure\(^2,10,11\). A common example from medical physics is the prediction of the mechanical stability or transport and migration properties of trabecular (or cancellous) bone by analyzing its complex structure\(^12-14\); see Fig. 1. Scalar measures, which are rotation- and translation-invariant quantities, like the volume fraction of the material or the area of the interface as the simplest example, may accurately describe isotropic media. However for anisotropic heterogeneous materials, like trabecular bone, so-called fabric tensors are needed to determine both the preferred orientation and strength of the anisotropic material.

For an understanding of tensorial physical properties, such as elasticity tensors, via a geometrical analysis, sensitive tensorial shape measures are needed. One of the first measures of anisotropy was the mean intercept length (MIL) tensor, by now one of the most common

![FIG. 1. Scanning electron microscopy image of trabecular bone (a) of a young male human bone and (b) of an elderly bone of a woman suffering from osteoporosis. Image courtesy of Hansma lab, USCB. Advanced measures of anisotropy can potentially help diagnose osteoporosis at an earlier stage.](image)
FIG. 2. The mean intercept length (MIL) is the mean length of the intercepts of test lines lying either within the void or the solid phase of a two-phase model: $\bar{L} = (\bar{L}_{\text{solid}} + \bar{L}_{\text{void}})/2$. The MIL is a function of the angle $\omega$ between the test line and the $x$-axis. It is usually plotted in a polar diagram (inset). The lines depict the analytic curves (given by Eq. (19)), the marks show numerical estimates.

approaches to quantify the anisotropy of composite materials\textsuperscript{7,15}.

The MIL analysis is applied in metallography\textsuperscript{16}, geology\textsuperscript{17,18}, mineralogy\textsuperscript{19}, food science\textsuperscript{20}, and biomechanics\textsuperscript{15}; for applications of the MIL analysis to digital images see Refs.\textsuperscript{9,17,22}. Especially in medicine, it has become a standard tool to characterize the structure of bone\textsuperscript{9,21–24}, which can be used for a diagnosis and a better understanding of the effects of osteoporosis\textsuperscript{25–27}; compare Figs. 1(a) and 1(b). The MIL fabric tensor has been used to relate the microstructure to the elasticity or compliance of the material to predict the mechanical properties\textsuperscript{8,28–31}. The distributions of intercept lengths, also known as chord-length distributions, can also be measured indirectly in scattering experiments, especially in small-angle scattering. They are related to the scattering intensity and therefore explicit formulas allow to construct and test models for physical and chemical materials (structured in the range of nano- to micrometers)\textsuperscript{32,33}. 

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The basic idea of a “mean-intercept analysis” is simple: to analyze a heterogeneous medium, parallel test lines are drawn through the sample intersecting the interface between the two phases; see Fig. 2. An intercept is an isolated segment within one phase. The MIL $\bar{L}$ is the mean length of these intercepts. In stochastic geometry, an intercept is also called a chord, and hence the mean intercept length is also known as the mean chord length. For further details on chord length distributions, coverage probabilities, and related properties, see also Ref. 33.

If the MIL varies with the orientation of the test lines, the medium has an anisotropic distribution of the interface. The orientation of a test line is either described by a unit vector $\mathbf{u}$ along the test line or by the angle $\omega$ between the test lines and the $x$-axis of the system. Usually, the polar diagram of the MIL $\bar{L}(\omega)$ is plotted, that is, the MIL for each orientation. A deviation from a circular shape implies interfacial anisotropy, see Fig. 2.

To gain insight in the orientation dependence of the MIL, we calculate in this series of papers both analytically and numerically the MIL of a versatile model for porous media, the so-called Boolean model. It is formed by overlapping grains that are distributed randomly in space. If the grains have a preferred direction, the system is a model for anisotropic heterogeneous materials. It is a common model in materials science and physics 11,33–36. A disordered two-phase medium can at least to some degree be reconstructed by choosing appropriate distributions of grain shape and orientation 19,37,38.

In the present paper, we discuss the analytic derivation of the MIL of anisotropic Boolean models in arbitrary dimensions $d$. Often the MIL analysis is applied to planar sections 7,39. However, modern tomography also provides three-dimensional data, of which the MIL can directly be estimated for all orientations on the unit sphere 20,22.

We highlight how the MIL of Boolean models is connected to a quite different field of research, queuing theory. The central idea is to interpret the test line as a “time axis” and intercepts of the test line with the heterogeneous material as “busy times” during which customers in a queue are served. Thus, spatial averages of the stochastic geometry model correspond to time averages in the queuing scenario. Well-known results from this elaborate theory about waiting times can be directly applied to the characterization of disordered microstructures. We thus identify the actual information about the random process that is contained in the MIL.

Section I defines the Boolean model of overlapping grains as a versatile model of
anisotropic heterogeneous materials. In Sec. II, we begin the analytic calculation by defining the mean intercept lengths of the solid and the void phase, as well as other auxiliary quantities. The calculation of the MIL consists of two main steps. First, we determine the properties of single grain in Sec. III. Then, we identify the intersections of a test line in Sec. IV with a one-dimensional model. Thus, we derive in Sec. V the MIL of Boolean models with a fixed grain shape but arbitrary orientation distributions. In the appendix, Sec. A, we explain how queuing theories are closely connected to intersections of test lines with a heterogeneous two-phase media. The powerful results from queuing theory lead directly to explicit formulas for the characterization of microstructures.

In the second paper of this series, we compare the explicit formulas to simulation results. We especially focus on the functional form of the MIL as a function of the orientation of the test lines. We discuss in detail how the MIL depends on the mean number of grains and on their orientation distribution. Most importantly, we show that, in contrast to a widespread assumption, a large number of objects not all parallel to each other do not in general produce on average an elliptic global MIL figure. We reveal severe short-comings of the MIL analysis for (bone-)microstructure characterization. Instead of the MIL, we suggest rigorous and robust tensorial shape indices from integral geometry as alternative and better defined sensitive anisotropy measures.

I. THE ORIENTATION-BIASED BOOLEAN MODEL: A VERSATILE MODEL OF ANISOTROPIC POROUS MATERIALS

The Boolean model is a popular model to study heterogeneous materials; for example, wood composites, sedimentary rock, fractured materials or hydrating cement-based materials.

The construction of any Boolean model starts with a random point pattern. Non-interacting points are placed randomly in space, see Fig. 3. The points are therefore uncorrelated. The random number of points in a finite observation window follows a Poisson distribution. The expected number of points per unit square (number density) is called the intensity \( \rho \).

Then, each point is decorated with a grain. The Boolean model is therefore also known as a fully penetrable grain system, a homogeneous system of overlapping particles, a Poissonian
FIG. 3. The construction of the Boolean model: first, uncorrelated points are placed in the plane (a); then, a grain is assigned to each of these points (b). Here, the grains are ellipses with a fixed aspect ratio, but a random orientation. In two dimensions, the orientation can be characterized by the angle $\theta$ between the main axis of the grain and the $x$-axis of the system. The angle $\theta$ is drawn from a probability distribution $P$. The Boolean model is only isotropic if the orientation distribution $P(\theta)$ is uniform on $(-\pi/2, \pi/2]$; otherwise the model is anisotropic.

penetrable grain model, or a Poisson germ-grain model\cite{33}. For example, in Fig. 2 the grains are rectangles and in Fig. 3 they are ellipses. Both the shape and the orientation of the grain can be random, that is, drawn from a probability distribution. For example, the aspect ratio, size, or orientation of the ellipse could vary. In Fig. 3 the shape is fixed, but the orientation is randomly distributed with an orientation bias towards the $x$-axis. Different Boolean models can be created by choosing different grain distributions. We consider here only homogeneous Boolean models, that is, the intensity of the underlying point process is spatially constant and the grain distribution is independent of the position of the grain. This property is also called stationarity.

The distribution of the grains stores the local information of the Boolean model, that is, the characteristics of a single grain. The global Boolean model is defined as the union of all grains. The space is subdivided into two phases: first, the solid phase that is formed by the
union of the grains (it is also called the covered or occupied phase); second, its complement, which is not covered by the grains, the so-called void phase.

If the orientations are randomly and isotropically distributed, the Boolean model is also isotropic. If the single grains have an anisotropic shape and their orientation distribution is biased towards an axis, the resulting model is anisotropic.

The solid volume (or area) fraction $\Phi$ is defined as the volume (or area) of the solid phase divided by the total available space. For a Boolean model with grains of variable size, the mean value of this quantity is known analytically to be $\Phi = 1 - e^{-\rho\bar{V}} \in [0, 1]$ with $\bar{V}$ the mean volume (or area) of a single particle. For a fixed (deterministic) grain size $V$, the formula reduces to $\Phi = 1 - e^{-\rho V} \in [0, 1]$. The volume (or area) fraction of the void phase $\Phi_{\text{void}} := 1 - \Phi$ is called the porosity. Note that a dependence on the intensity always corresponds to a dependence on the solid volume fraction (or equivalently on the porosity).

For clarity, we concentrate in the following on Boolean models with a fixed grain shape and a random orientation. However the calculations can easily be generalized to more general grain distributions, essentially by replacing single grain characteristics by the corresponding averages. An example for a possible generalization are distributions of the grain size (leading to polydisperse systems).

In order to calculate the MIL, we need a more formal definition of the Boolean model. The random point pattern (with uncorrelated points placed randomly in space) is formally defined as a Poisson point process in $d$-dimensional Euclidean space $\mathbb{R}^d$ of intensity $\rho$. To each point $r_i \in \mathbb{R}^d$ in the point pattern a convex grain $K(r_i)$ is attached. We want to study the geometric properties of the Boolean model, which is defined as their union

$$B := \bigcup_i K(r_i). \quad (1)$$

Whereas the point pattern and thus the position of the grains is homogeneously distributed, we allow for an arbitrarily anisotropic orientation distribution $\mathcal{P}(\Omega)$ of $K_i$, where $\Omega$ denotes all necessary angles to fix orientation of $K_i$. In $2D$, $\Omega$ is simply the angle $\theta$ between the main axis of the grain and the $x$-axis; in $3D$, $\Omega$ is the polar and azimuthal angle of the direction of the main axis. If $\mathcal{P}(\Omega)$ is a uniform distribution, the Boolean model is said to be isotropic, but if the orientation distribution is in the extreme case a $\delta$ distribution, the grains are perfectly aligned. Any intermediate degree of orientation bias can be adjusted by choosing $\mathcal{P}(\Omega)$ appropriately.
II. MEAN INTERCEPT LENGTHS OF THE SOLID AND THE VOID PHASE

To determine the MIL of a Boolean model, parallel test lines are drawn through the sample, as described above, see Fig. 2. The length of the intercepts of the test line within the void or solid phase are denoted by $L_{\text{void}}$ or $L_{\text{solid}}$, respectively.

The MIL is the mean length of these intercepts

$$\bar{L} = \frac{\bar{L}_{\text{void}} + \bar{L}_{\text{solid}}}{2},$$

which is equal to the length of the test line divided by the number of intercepts$^{7,15}$. Another common normalization$^{17,45}$ is $\bar{L} = \bar{L}_{\text{void}} + \bar{L}_{\text{solid}}$, which corresponds to always combining an intercept in the solid phase with the following intercept in the void phase. In other words, the intersections only contribute if the line leaves the solid phase and enters the void phase (or vice versa).

The MIL of isotropic Boolean models is intensively studied and well known; see Refs.$^{11,19,33,46}$ and references therein. For convex grains, it is a function of the intensity and the mean surface area (or perimeter in two dimensions) of a single grain. More generally, it is related to the specific surface of an isotropic two-phase medium$^{11}$. Also for anisotropic and rather general Boolean models, the MIL has been derived; for example, see Ref. $^{47}$. Explicit formulas can be derived from the elaborate mathematical theory of queues$^{48}$, see Appendix A.

The distribution of the length of a typical intercept can be related to the linear contact distribution$^{33}$, which is also called lineal path function$^{11}$, see also Ref. $^{49}$.

Our calculations provide another concise analytic derivation and discussion of the MIL of Boolean models that give an easier insight for applied scientists into which information is contained in the MIL.

The MIL is determined by drawing one-dimensional test lines. Their orientation can be parametrized by a unit vector $\mathbf{u}$ along the line and their position by the perpendicular distance vector $\mathbf{s} \perp \mathbf{u}$ to the origin $\mathbf{O} \in \mathbb{R}^d$. We here denote such a test line by $\mathcal{L}^\mathbf{u}(\mathbf{u})$; see Fig. 4.

A test line intersects a given grain $\mathbf{K}$ if and only if it intersects the projection of the grain onto a hyperplane perpendicular to the test line, due to the definition of a projection. A line between the projection $\mathbf{p}_\mathbf{z}$ and the original point $\mathbf{z}$ in $\mathbf{K}$ must be perpendicular to the hyperplane (or in other words, the line is parallel to $\mathbf{u}$). In 2D, the hyperplane is simply a
III. SINGLE GRAIN CHARACTERISTICS

Before we derive the global average for the union of all grains, we first need to derive the average characteristics of a single grain $K$. The simplest geometric property is $V[K]$, the volume of a three-dimensional or the area of a two-dimensional grain.
The length of an intercept $L[K \cap L^s(\mathbf{u})]$, that is, the length of the intersection of $K$ with the test line $L^s(\mathbf{u})$, depends on the position $\mathbf{s}$ of the test line. If a random line with orientation $\mathbf{u}$ is drawn through the sample such that it intersects the grain $K$ (with no preferred positions $\mathbf{s}$), the probability density function of the length $l$ of an intercept is proportional to the integral over all points $\mathbf{s}$ on the hyperplane $H^\perp$, for which $L[K \cap L^s(\mathbf{u})]$ is equal to $l$:

$$P_u[l; K] \propto \int_{H^\perp} \mathrm{d}\mathbf{s} \, \delta(l - L[K \cap L^s(\mathbf{u})])$$

for $0 < l \leq l_{\text{max}}(\mathbf{u})$, where $l_{\text{max}}$ is an upper bound of the intercept length, the length of the projection of $K$ onto the line $L^s(\mathbf{u})$. Note that the length $l_{\text{max}}(\mathbf{u})$ is only a function of the orientation of the test lines, but does not depend on their position $\mathbf{s}$.

A normalization of the distribution of the intercept lengths $l$ is needed such that $\int_0^{l_{\text{max}}} \mathrm{d}l \, P_u[l; K] = 1$. The normalizing constant in Eq. (3) is given by the integral over test lines that intersect the grain $K$ or equivalently over all positions $\mathbf{s}$ for which $L[K \cap L^s(\mathbf{u})] > 0$.

As discussed above this is, by definition, equal to an integral over the perpendicular projection $K_u^\perp$. We denote by $S^\perp[\mathbf{u}; K]$ the size of the perpendicular projection $K_u^\perp$: in 2D this is its length; in 3D, it is the area of the projection; and in arbitrary dimension $d$, it is proportional to the so-called intrinsic volume $V_{d-1}$ of $K_u^\perp$.

The distribution of the intercept length $l$ in a single grain $K$ with lines along $\mathbf{u}$ is thus given by

$$P_u[l; K] = \frac{1}{S^\perp[\mathbf{u}; K]} \int_{H^\perp} \mathrm{d}\mathbf{s} \, \delta(l - L[K \cap L^s(\mathbf{u})])$$

Now, we can calculate the mean length $L^\parallel[\mathbf{u}; K]$ of an intercept in a single grain $K$. We exchange the order of integration (using Fubini’s theorem), and because the integral over the projection weighted by the length of the intercept is equal to the volume $V[K]$ of the grain $K$, we derive

$$L^\parallel[\mathbf{u}; K] = \int_0^{l_{\text{max}}} \mathrm{d}l \, P_u[l; K] \cdot l = \frac{1}{S^\perp[\mathbf{u}; K]} \int_{H^\perp} \mathrm{d}\mathbf{s} \, L[K \cap L^s(\mathbf{u})] = \frac{V[K]}{S^\perp[\mathbf{u}; K]}.$$ 

Figure 5 gives an intuitive explanation for this formula.

So far, we have considered a grain $K$ with a fixed orientation, for which we have defined the size $S^\perp[\mathbf{u}; K]$ of the perpendicular projection $K_u^\perp$ and derived the mean length of intercepts $L^\parallel[\mathbf{u}; K]$. 

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FIG. 5. (Color online only) Intuitive explanation of Eq. (5): a grain $K$ with area $V$ is projected onto the plane $H^\perp$ perpendicular to the unit vector $u$; the size of the projection is $S^\perp$. Test lines in direction of $u$ intersect the grain (yellow bars in figure on left-hand side). The length $l$ of these intercepts varies with the position $s$ of the test lines (orange line in figure on right-hand side). $L^\parallel$ is the average of this length, that is, the integral of the curve $l(s)$ divided by the size of the projection $S^\perp$. The area enclosed by this curve is the area $V$ of the grain, because the line segments were moved to the $s$-axis but did not change their length; therefore, $L^\parallel = V/S^\perp$. An alternative geometric construction follows the rule that the area below the red line indicating $L^\parallel$ must be the same as below $l(s)$, that is, $L^\parallel \cdot S^\perp = V$.

By construction, these quantities depend on the relative orientation between the grain $K$ and the direction $u$ of the test lines (in contrast to scalar measures like the volume). The grains are randomly oriented following the distribution $P(\Omega)$. We therefore define the
FIG. 6. (Color online only) The section of a test line $L_s(u)$ with the Boolean model $B$ is again a one-dimensional Boolean model $B_u^{(1)}$. The intercepts of the single rectangles are highlighted (colored yellow), their endpoints are marked by a dot. They overlap like the original two-dimensional grains (colored blue).

orientational averages of the perpendicular projection and the mean length of intercepts:

$$\bar{S}^\perp[u] = \int_{S^{d-1}} d\Omega \, \mathcal{P}(\Omega) \, S^\perp[u; K],$$  \hspace{1cm} (6)

$$L^\parallel[u] = \int_{S^{d-1}} d\Omega \, \mathcal{P}(\Omega) \, L^\parallel[u; K]$$

$$= V \int_{S^{d-1}} d\Omega \, \mathcal{P}(\Omega) \frac{1}{S^\perp[u; K]} \neq \frac{V}{\bar{S}^\perp[u]}. \hspace{1cm} (7)$$

Equation (5) states that, for a fixed grain, the mean length of an intercept $L^\parallel[u; K]$ is proportional to the inverse of the size of the perpendicular projection $S^\perp[u; K]$. That relation does not hold for the orientational averages of a single grain.

In the isotropic case, the average size of the perpendicular projection of a grain $\bar{S}^\perp$ is equal to its surface area $S[K]$ (or perimeter in two dimensions)$^{50}$.

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IV. DIMENSIONAL REDUCTION: INDUCED ONE-DIMENSIONAL BOOLEAN MODEL

In the previous Section, we have derived the average characteristics of a single grain $K$. Now, we determine the mean intercept length for the union of all grains $\mathcal{B}$, which is the Boolean model.

Therefore, we intersect the one-dimensional test line $\mathcal{L}^s(\mathbf{u})$ with the $d$-dimensional realization of the Boolean model $\mathcal{B} = \bigcup_i K(\mathbf{r}_i)$

$$\mathcal{B}_{\mathbf{u}}^{(1)} := \mathcal{L}^s(\mathbf{u}) \cap \mathcal{B}.$$  \hfill (8)

In contrast to the previous Sec. III, which considered only a single grain, here a collection of many particles with different orientations is analyzed. The union of intercepts $\mathcal{B}_{\mathbf{u}}^{(1)}$ is again a Boolean model in one-dimension: random intersections with single grains are distributed along the test line; they are overlapping and form clusters; their unions are the final intercepts of the test line with the Boolean model; see Fig. 6.

Notice the two different types of intercepts: first, the intersections of the test line with a single grain $K$, which we call “segment” (marked by $\ast$ in Fig. 6). They can be seen as the one-dimensional grains in the one-dimensional Boolean model with varying length $L[K \cap \mathcal{L}^s(\mathbf{u})]$. Second, an intercept in the solid phase of the Boolean model formed by the union of a cluster of segments (marked by $\ast\ast$ in Fig. 6), their length is denoted by $L_{\text{solid}}$. $L_{\text{void}}$ is the length of the void intercepts in the one-dimensional model along the test line $\mathcal{L}^s(\mathbf{u})$. Their average intercept lengths directly determine the MIL $\bar{L}$, which we want to derive.

However, we first need to determine the intensity of the segments in the one-dimensional Boolean model and the distribution of their lengths.

The intensity $\rho_{\mathbf{u}}^{(1)}$ of the one-dimensional Boolean model $\mathcal{B}_{\mathbf{u}}^{(1)}$ is the average number of segments per unit length. The probability for a grain to intersect the line depends on the orientation of the grain. Therefore, the average number of intercepts varies for different orientations.

We first determine the intensity $\rho_{\mathbf{u}}^{(1)}[K]$ for a fixed grain $K$. Put differently, we calculate the average number of segments per unit length if all grains are decorated with a grain $K$ with the same orientation; see Fig. 7. As discussed above, only those grains intersect the line for which the projection intersects the line. From Fig. 7 can be seen that this is equivalent...
to the condition that the center of a grain falls in a region that extends parallel to the line and that has a width equal to the size of the perpendicular projection. The average number of grains in such a region with length $t$ parallel to the line is $\rho \cdot S^\perp \cdot t$ by definition of the intensity $\rho$, and the average number of intersections per unit length is therefore

$$\rho_u^{(1)} [K] = \rho S^\perp [u; K].$$  \hfill (9)

If the grain orientation is not fixed, but their orientations are distributed according to $P(\Omega)$, the intensity $\rho_u^{(1)}$ of the one-dimensional Boolean model is simply the orientational average of Eq. (9):

$$\rho_u^{(1)} = \int_{S^{d-1}} \Omega (\omega) \rho_u^{(1)} [K] = \rho S^\perp [\omega].$$ \hfill (10)

FIG. 7. (Color online only) The test line $L^s$ intersects the grains $K(r_1)$ and $K(r_2)$ but not grain $K(r_3)$. Accordingly, the perpendicular projections $K_u^\perp$ of the first two grains intersect the line $L^s$ in contrast to the projection of $K(r_3)$. Therefore, the grain $K$ with fixed orientation intersects the line if and only if its center (marked by a dot) lies within the highlighted band (between the dash-dotted lines; colored orange). The width of the band is by definition equivalent to the size $S^\perp [u; K]$ of the perpendicular projection.
Obviously, not only the length of the intercepts $L_{\text{solid}}$ varies, but also the length $L[K \cap \mathcal{L}(u)]$ of the segments (i.e., of the one-dimensional grains). What is the probability density function $P_u^{(1)}[l]$ of the length $l$ of such a segment?

Only if the grains have a fixed orientation, the length $l$ of a segment follows the probability density function $P_u^{(1)}[l] = P_u[l; K]$ given by Eq. (4). If the orientation of the grains is drawn from a non-trivial distribution $\mathcal{P}(\Omega)$, the density function is different from only an orientational average of $P_u[l; K]$. In the previous Sec. III, we have considered a given grain $K$ and determined the average length of intersections with lines hitting the grain. Here, the line is given, and we ask for the distribution of the lengths of the intersections with all grains hitting the line. This distribution is different because grains with different orientations are differently probable to hit the line. The distribution must be weighted by the fraction $\rho_u^{(1)}(K)/\rho_u^{(1)}$ of grains $K$ with orientation $\Omega$ among all grains intersecting the line; see Eqs. (9) and (10).

\[
P_u^{(1)}[l] = \int \delta(l - L[K \cap \mathcal{L}(u)])
\]

Therefore, also the mean length of a segment $\bar{L}^{(1)}[u]$ (i.e., of the intersection of a grain with the line) is different from the mean length of an intercept of a line with a grain $\bar{L}^\parallel[u]$ given by Eq. (7). Similar to the calculation in Eq. (5), we get

\[
\bar{L}^{(1)}[u] := \int_0^\infty dl P_u^{(1)}[l] \cdot l
\]

\[
= \frac{1}{\bar{S}^{\perp}[u]} \int \mathcal{P}(\Omega) \int_{H^+} ds \delta(l - L[K \cap \mathcal{L}(u)])
\]

\[
= \frac{\bar{V}}{\bar{S}^{\perp}[u]}. \tag{12}
\]

Note, that the mean length of a segment $\bar{L}^{(1)}[u]$ is different from the single grain characteristic $\bar{L}^\parallel[u]$, that is, from the mean length of a segment conditional on the fact that the line hits the grain.

This difference $\bar{L}^\parallel[u] \neq \bar{L}^{(1)}[u]$ can be illustrated by a simple example of rectangles with only two possible orientations: with equal probability a rectangle is either oriented along (↔) or perpendicular (↕) to $x$, see Fig. 8; the side-lengths of a rectangle are $a = 2p$ or $b = 2q$. Then, for a test line along $x$ the mean size of the projection $\bar{S}^{\perp} = (a+b)/2$ is by
FIG. 8. Illustration to explain the difference between the mean length of a segment \( \bar{L}^{(1)}[\mathbf{u}] \) [see Eq. (12)], which includes the probability for a grain to hit the line \( L^s(\mathbf{u}) \), and the mean length of an intercept of a single grain with the test line conditional on the line hitting the grain: \( \bar{L}^\parallel = (a+b)/2 \) [see Eq. (7)]. With equal probability a rectangle is either oriented along (↔) or perpendicular (↕) to \( \mathbf{u} \). However, a vertically aligned rectangle (with a smaller segment length) is more likely to hit the line. Therefore, the mean length of a segment \( \bar{L}^{(1)}[\mathbf{u}] = 2/(1/a + 1/b) \) is smaller than \( \bar{L}^\parallel \).

coincidence equal to the mean length \( \bar{L}^\parallel \) of an intercept conditional on the line hitting the grain in Eq. (7). In other words, the latter is the arithmetic mean of the side lengths of a rectangle

\[
\bar{L}^\parallel = \frac{a + b}{2}.
\]  

However, the probability to hit the test line is larger for the vertically (↕) than for the horizontally (↔) aligned grains. According to Eq. (12) the mean length of a segment is therefore

\[
\bar{L}^{(1)}[\mathbf{u}] = \frac{2ab}{a + b} = \frac{2}{\frac{1}{a} + \frac{1}{b}} \leq \bar{L}^\parallel,
\]

because the harmonic mean \( \bar{L}^{(1)}[\mathbf{u}] \) of the side lengths is smaller than their arithmetic mean \( \bar{L}^\parallel \) (except for squares with \( a = b \), for which of course both averages are trivially equal to \( a \)).

Recall that for a fixed grain \( K \) the mean intercept length \( L^\parallel[\mathbf{u}; K] \) is the volume of the grain divided by the size of the perpendicular projection \( S^\perp[\mathbf{u}; K] \), see Eq. (5), but this does
not hold for the orientational averages $\bar{L}^\parallel[u]$ and $\bar{S}^\perp[u]$; see Eq. (7). Instead, the volume divided by the average size of the perpendicular projection is equal to the mean length of a segment $\bar{L}^{(1)}[u]$. We show below that the MIL is therefore not a function of $\bar{L}^\parallel[u]$, but of the average size of the perpendicular projection $\bar{S}^\perp[u]$.

In other words, we must not average over the mean length of an intercept with a grain $L^\parallel[u;K]$, but instead average over its inverse $S^\perp[u;K]/\nu$ to derive the inverse of the mean length of a segment $\bar{L}^{(1)}[u]^{-1} = \frac{\bar{S}^\perp[u]}{\nu} \neq (\bar{L}^\parallel[u])^{-1}$.

The average length of a segment $\bar{L}^{(1)}[u]$ can also be seen as the average size of the one-dimensional grains in $B^{(1)}_u$. Together with its intensity $\rho^{(1)}_u$ from Eq. (10), we can now calculate directly the void probability of the one-dimensional Boolean model, which is the probability that an arbitrary point on the test line $L^*$ is not covered by any grain. It equals the fraction of length of the void phase, which is known to be $e^{-\rho^{(1)}_u L^{(1)}[u]}$, as mentioned above. Inserting Eqs. (10) and (12), we see that, as expected, this is in the $d$-dimensional Boolean model equal to the porosity (which is the volume fraction of the void phase $\Phi_{\text{void}} = e^{-\rho V}$).

A crucial step for the calculation of the MIL is the use of another well-known formula for one-dimensional Boolean models, the complementary cumulative distribution function of the void intercepts $L_{\text{void}}$ (see Fig. 2). It is the probability to find voids $v$ larger than $L_{\text{void}}$ given the one-dimensional intensity $\rho^{(1)}_u$:

$$\text{Prob}[v > L_{\text{void}}] = e^{\rho^{(1)}_u L_{\text{void}}}. \tag{14}$$

The probability density function of the void intercepts $L_{\text{void}}$, that is, the distribution of the length of the intercepts of the test lines with the void phase, is then simply the negative of the derivative w.r.t. $L_{\text{void}}$:

$$\mathcal{P}_{\text{void}}(L_{\text{void}}) = \rho^{(1)}_u \cdot e^{-\rho^{(1)}_u L_{\text{void}}} \tag{15}$$

with the normalization $\int_0^\infty dL_{\text{void}} \mathcal{P}_{\text{void}}(L_{\text{void}}) = 1$. Knowing the probability density function of the lengths of the void intercepts finally allows us to determine the mean length of the void intercepts

$$\bar{L}_{\text{void}} = \int_0^\infty dL_{\text{void}} \mathcal{P}_{\text{void}}(L_{\text{void}}) \cdot L_{\text{void}}$$

$$= \int_0^\infty dL_{\text{void}} e^{-\rho^{(1)}_u L_{\text{void}}} \cdot \rho^{(1)}_u L_{\text{void}}$$

$$= \frac{1}{\rho^{(1)}_u} \int_0^\infty dz e^{-z} \cdot z = \frac{1}{\rho^{(1)}_u}. \tag{16}$$

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The mean void length is the inverse of the one-dimensional intensity.

The calculation of the mean length of the void intercepts $L_{\text{void}}$ is the first part in calculating the total mean intercept length $\mathcal{L}$, which is the average of the mean void length $L_{\text{void}}$ and the mean length of the intercepts in the solid phase $L_{\text{solid}}$; see Eq. (2).

The distribution of the length $L_{\text{solid}}$ in the solid phase is much more difficult to calculate explicitly. It is the length between two adjacent void regions and consists of many overlapping segments of different length $L[K \cap \mathcal{L}^s(u)]$. If, however, the line $\mathcal{L}^s$ is interpreted as a time axis and the beginning of a segment $K \cap \mathcal{L}^s(u)$ as the arrival of a customer with a job of length $L[K \cap \mathcal{L}^s(u)]$, the one-dimensional Boolean model can be described as a queue, where the customers arrive independently of each other and there are infinitely many servers, i.e., no customer has to wait. Queuing theory calls such a system a $M/G/\infty$-queue. Then, the length $L_{\text{solid}}$ in the solid phase can be interpreted as the busy time of the server, which is well-known in queuing theory. Its relation to the distribution of the length $L_{\text{solid}}$ in the solid phase is explained in Sec. A.

Because we are here only interested in the mean solid length and not in its distribution, we can in the following express the MIL $L$ from Eq. (2) by properties of the void phase only, by applying the so-called formula of the mean, and thus explicitly derive the MIL with methods from stochastic geometry.

V. EXPLICIT EXPRESSION FOR THE MIL OF BOOLEAN MODELS

The volume fraction $\Phi_{\text{void}}$ of the void phase, which is the ratio of the area of the void phase and the sum of the areas of void and solid phase, is equal to the ratio of the length of the intercepts in the void phase and the total length of the test lines, which is the sum of the intercepts in both phases. Because every intercept in the void phase is followed by one in the solid phase, the number of intercepts is equal. Therefore, the volume fraction $\Phi_{\text{void}}$ is equal to the ratio of the mean length of the intercepts in the void phase $L_{\text{void}}$ and the sum of the mean lengths of the intercepts in both phases $L_{\text{void}} + L_{\text{solid}}$:

$$\Phi_{\text{void}} = \frac{L_{\text{void}}}{L_{\text{void}} + L_{\text{solid}}},$$

which is confirmed by the results from queuing theory in Sec. A, compare Eqs. (16) and (A15). Inserting the definition of the MIL $L = (L_{\text{void}} + L_{\text{solid}})/2$ provides a simple relation
between the mean void length given in Eq. (16) and the MIL\textsuperscript{1,21}: 

$$\bar{L} = \frac{L_{\text{void}}}{2\Phi_{\text{void}}}.$$  \hspace{1cm} (17)

The volume fraction of the void phase in a Boolean model with grains of variable size is

$$\Phi_{\text{void}} = e^{-\rho V},$$  \hspace{1cm} (18)

where \(\bar{V}\) the mean volume (or area) of a single particle\textsuperscript{50}; if the grain size is constant equal to \(V\), the mean \(\bar{V}\) is trivially equal to \(V\).

Inserting Eqs. (10), (16), and (18) in Eq. (17), we find the mean intercept length (or mean chord length) of the homogeneous Boolean model as a function of the orientation of the test lines along \(u\):

$$\bar{L}(u) = \frac{L_{\text{void}}}{2} \cdot e^{\rho V} = \frac{1}{2\rho^{(1)}_u} \cdot e^{\rho V}$$

$$= \frac{V}{\tilde{S}^\perp[u]} \cdot \frac{e^{\rho V}}{2\rho V}.$$  \hspace{1cm} (19)

The MIL of the Boolean model is a global property in that it is defined on the union of all grains. Here, it is expressed by local properties, that is, by single grains characteristics \(V\) and \(\tilde{S}^\perp[u]\) and the intensity of the particle process.

Moreover, the formula for the MIL of Boolean models separates into an orientation and an intensity dependent factor. The first only depends on the properties of a typical grain, the latter only on the solid volume fraction \(\Phi\). A change of the intensity \(\rho\) (and hence of the porosity \(\phi\)) only represents a uniform scaling of the MIL figure. Here, we choose to include the volume of the particle in the orientation dependent factor so that its unit is length, like for the MIL \(\bar{L}\), while the intensity dependent factor is a prefactor without unit.

Its shape, that is, the orientational dependence on \(u\), is solely given by the mean length of an intersection of a single grain with a given test line

$$\bar{L}^{(1)}[u] = \frac{V}{\tilde{S}^\perp[u]}$$  \hspace{1cm} (20)

which is the volume \(V\) of the grain divided by the orientational average \(\tilde{S}^\perp[u]\) of the size of the perpendicular projection; see Eqs. (6) and (12) and Fig. 5. Therefore, \(\tilde{S}^\perp[u]\) contains the complete anisotropy information of the MIL analysis.
This means that measuring the global average of the MIL of the union of all grains for all orientations provides access to the average shape of a single grain, in the sense, that it allows us to determine the average size $\bar{S}_\perp$ of the projection of a single grain as a function of the orientation of the test lines up to a proportionality constant. For example, if a porous medium is built up by the successive addition of inclusions, this single grain characteristic allows for a better understanding of the formation of this porous medium, because the average shape of such an inclusion can be approximated. Moreover, this allows to adjust the Boolean model to the experiment by choosing an appropriate grain distribution.

As predicted above, the mean intercept length $\bar{L}[\mathbf{u}]$ of a single grain from Eq. (7) does not enter the expression, because it does not take into account the probability to hit a line. To calculate the MIL, we must therefore not determine the average of $L[\mathbf{u}; K]$, but of its inverse $S^{-1}[\mathbf{u}; K]$; see Eq. (5).

In the plane, the projected length of a fixed grain $K$ is given by

$$S^{-1}[\mathbf{u}; K] = |\mathbf{u}^\perp \cdot \mathbf{r}^{(1)}(\varphi) - \mathbf{u}^\perp \cdot \mathbf{r}^{(2)}(\varphi)|, \quad (21)$$

where $\mathbf{u}^\perp$ is the vector perpendicular to $\mathbf{u}$, and $\mathbf{r}^{(0)}(\varphi) \in \partial K$ are the points on the boundary of $K$ which are projected on the boundary of $K_\mathbf{u}^\perp \subset H^{\perp}(\mathbf{u})$; in other words, $\mathbf{r}^{(0)}(\varphi)$ are the extrema of $\mathbf{u}^\perp \cdot \mathbf{r}(\varphi)$ for all $\mathbf{r}(\varphi) \in \partial K$. For polygons these points are identical to the corners of the polygon. $S^{-1}[\mathbf{u}; K]$ in Eq. (21) then needs to be averaged according to the orientation distribution $\mathbf{P}$ of the grain $K$ to determine $\bar{S}^{-1}[\mathbf{u}]$. Its inverse inserted in Eq. (19) provides an explicit formula for the MIL of the anisotropic Boolean model.

VI. CONCLUSIONS

Orientation-dependent mean intercept or chord length analyses are the most commonly used tools to quantify anisotropy in porous bone materials\cite{7,15,21} despite several weaknesses of this spatial structure measure\cite{45}. Here, we provided clarification on the interpretation or the morphological information content of these measures, by exploiting an analytic formula derived for an important model for anisotropic microstructures, namely the anisotropic Boolean model; see Eq. (19).

We have pointed out the close connections between $M/G/\infty$-queuing theories and intersections of test lines with a heterogeneous two-phase media, see Sec. A. The powerful
results and explicit formulas from queuing theory can directly be applied to characterize microstructures.

We have shown how the orientation and intensity dependence of the MIL separates into two factors; see Eqs. (19) and (20). The latter is only a function of the porosity and independent of the specific Boolean model. The orientation dependent factor $\bar{L}^{(1)} [u]$ from Eq. (20) determines the shape of the MIL figure. Interestingly, the average length of an intercept with a typical grain does not enter the expression of $\bar{L}^{(1)} [u]$. Instead, it is a function only of the volume and the average size of the projection of a single grain.

We expressed the global MIL by only local single grain characteristics. The whole anisotropy information of the MIL figure is thus contained in the average size of the projection of a single grain. This corresponding relation can be used to interpret measurements of the MIL. Also the connection of the MIL of Boolean models to the seemingly quite different field of research about queues provides further insights in the connection between local and global structure information in the MIL analysis.

Further analytic calculations of intercept lengths, possibly aided by results from queuing theory, could include additional explicit formulas or improved approximations for other models of porous media, like Gaussian random fields, or cellular systems, like Voronoi tessellations. Going beyond the Poisson process and overlapping grains could help to deepen our understanding about the information content of the MIL analysis.

ACKNOWLEDGMENTS

Financial support by the Deutsche Forschungsgemeinschaft (DFG) through the Research Unit “Geometry and Physics of Spatial Random Systems” (GPSRS) under grants ME1361/11, SCHR1148/3, HU1874/3-2, and LA965/6-2 is gratefully acknowledged.

DISCLOSURE OF CONFLICTS OF INTEREST

The authors have no relevant conflicts of interest to disclose.
Appendix A: The one-dimensional Boolean model and queueing theory

The one-dimensional Boolean model is known to be connected to a queue with infinitely many servers and independent customers\textsuperscript{33,46}. The latter is studied in queueing theory; e.g., see\textsuperscript{60}. We explain how results from queueing theory have directly been adopted for the one-dimensional Boolean model; e.g., see Ref.\textsuperscript{46}. Here the most important example is the distribution of the length $L_{\text{solid}}$ of the intercepts in the solid phase.

1. Standard Queueing Models

In queues, both the arrivals of new customers and the required service time are typically not deterministic but stochastic in nature. The prediction of waiting times in queues is almost as old as probability theory. However, it was only in 1909 when Agner Erlang published the first detailed work on queueing theory in which he tries to understand the theoretical requirements of an efficient telephone network. In 1953, David Kendall introduced the current standard notation $A/S/N$ for a queueing model with the interarrival time distribution $A$, the service time distribution $S$ and the number of servers $N$. Extensive reviews can be found in standard textbooks; for example, see Refs.\textsuperscript{48,60–64}.

The basic queueing model is defined in several steps that specify the different parts and processes:

- **N number of servers**: the two limiting cases are $N = 1$, where only one customer is served at a time, and $N = \infty$, where each customer is immediately served when arrived.

- **A arrival process**: we assume that customers arrive independently with a distribution density $P^{(A)}(t_A)$ of the time $t_A$ between two arrivals. The mean arrival time is denoted by $\bar{t}_A$. The arrival rate, i.e., the average number of arrivals per unit time, is

$$\lambda = \frac{1}{\bar{t}_A}, \quad (A1)$$

- **S service process**: we assume that the time $t_S$ needed to serve a customer is for all customers independent and identically distributed. Its probability density function is denoted by $P^{(S)}(t_S)$. (We do not consider the case, that $P^{(S)}(t_S)$ depends on the length of the queue or the arrival process.) The mean service time is denoted by $\bar{t}_S$. The
occupation rate

\[ \tau = \frac{\bar{t}_S}{N\bar{t}_A} < 1 \]

is defined as the fraction of time when the server is busy. It is assumed to be smaller than 1. Otherwise, the mean queue length diverges because new customers arrive faster than they are served.

In the following, we consider standard models of queueing theory that we denote by \( A/S/N \). Analyses of the performance of queues are interested in the following quantities:

- \( t_w \) waiting time of a customer and its distribution \( P^{(W)}(t_w) \).
- \( t_w^+ \) sojourn time, which is the waiting time plus the service time: \( t_w^+ = t_w + t_S \).
- \( t_B \) busy time of the server and its distribution \( P^{(B)}(t_B) \). It is the period during which the server is working continuously.
- \( L \) number of customers in the system including those in service.
- \( L^q \) number of customers that are waiting in the queue; \( L = L^q + N \) if \( L^q \geq 1 \).

These quantities depend on the choice of \( N \), \( P^{(A)}(t_A) \) and \( P^{(S)}(t_S) \).

2. Correspondence between covering and queuing processes

There is an intuitive correspondence between the induced one-dimensional Boolean model from Sec. \( IV \) and a so-called \( M/G/\infty \)-queue with independent customers who are immediately served.

The test line on which the one-dimensional Boolean model is defined can be interpreted as a time axis. The intersections of the test line with a single grain (which corresponds to a segment) can be interpreted as a time interval. At its beginning, a new customer arrives and is immediately accepted if there are infinitely many servers. The length \( l \) of the segment then corresponds to the service-time \( t_S \). Its probability density function is therefore given by Eq. \((11)\). The arrivals of new customers, or equivalently the intersections of grains with the test line, form a Poisson point process on the line. The time between two subsequent customers is therefore exponentially distributed. Both the arrival time and the service time of different customers are independent of each other.
An intercept in the solid phase of the Boolean model formed by the union of a cluster of segments then corresponds to a time frame during which at least one server is active. This is the busy time $t_B$. It corresponds to the length $L_{\text{solid}}$ of an intercept in the solid phase, that is, in the phase covered by grains.

3. $M/G/\infty$ Queue

In contrast to most of the queueing models, one can explicitly derive the distribution $P^{(B)}(t_B)$ of the busy time $t_B$ for a queue with unlimited service potential\(^{51-53}\).

The arrival process is a (one-dimensional) Poisson point process, the service time follows an arbitrary probability density function $P^{(S)}(t)$, and thus an arbitrary distribution function

$$D^{(S)}(t) = \int_0^t d\tau' P^{(S)}(\tau') .$$ (A2)

a. Laplace transform and n-fold convolution

It is convenient to use the so-called Laplace transform

$$\mathcal{L}(f)(s) = \int_0^\infty dt \; f(t)e^{-st}$$ (A3)

for a function $f(t)$ defined for positive times $t \geq 0$. We here assume that the following integrals actually exist, which is the case for the distribution functions discussed in Sec. A 3 b. The inverse of the Laplace transform is given by

$$f(t) = \frac{1}{2\pi i} \lim_{T \to \infty} \int_{\gamma-iT}^{\gamma+iT} ds \; e^{st} \cdot \mathcal{L}(f)(s) \quad \text{with} \quad \gamma \in \mathbb{R}_+ .$$ (A4)

The Laplace transform is convenient, because the derivatives can be expressed by

$$\frac{d}{ds} \mathcal{L}(f)(s) = -\mathcal{L}(tf)(s) ,$$

$$\mathcal{L}\left( \frac{d}{dt} f \right)(s) = s \mathcal{L}(f)(s) - f(0) .$$ (A5)

Therefore, the distribution function $D(t)$ and its density $P(t) = D'(t)$ (e. g., see Eq. (A2)) are simply related by

$$\mathcal{L}(P)(s) = s \mathcal{L}(D)(s)$$ (A6)

because $D(0) = 0$. 

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For two functions \( f(t) \) and \( g(t) \) defined for positive times \( t \geq 0 \), their convolution is defined as

\[
(f \ast g)(t) := \int_0^t d\tau \ f(\tau)g(t - \tau) .
\]

The \( n \)-fold convolution of the function \( f(t) \) is then given by

\[
f^{(n)}(t) := \int_0^t dt_1 \int_0^{t_1} dt_2 \cdots \int_0^{t_{n-1}} dt_n 
\]

\[
f(t_n) f(t_{n-1} - t_n) \cdots f(t_1 - t_2) f(t - t_1) .
\]

The Laplace transform of the convolution \( f \ast g \) is simply the product of the Laplace transforms of \( f \) and \( g \):

\[
\mathcal{L}\{f \ast g\}(s) = \int_0^\infty dt \int_0^t d\tau \ f(\tau)g(t - \tau)e^{-st}
\]

\[
= \int_0^\infty d\tau \ f(\tau)e^{-st} \int_0^\infty dt \ g(t - \tau)e^{-st}
\]

\[
= \int_0^\infty d\tau \ f(\tau)e^{-st} \int_0^\infty dt \ g(t)e^{-st}
\]

\[
= \mathcal{L}\{f\}(s) \cdot \mathcal{L}\{g\}(s) .
\]

By induction follows straightforwardly that

\[
\mathcal{L}\{f^{(n)}\}(s) = (\mathcal{L}\{f\}(s))^n .
\] (A7)

In other words, the Laplace transform of an \( n \)-fold convolution is the product of \( n \) Laplace transforms.

\[b. \quad \text{Distribution of Waiting Times}\]

Given the distribution \( D^{(S)} \) of the service time \( t_S \), we define the 'capacity'

\[
C(t) := 1 - e^{-\frac{t}{\bar{t}_A}} \int_0^t dt' (1 - D^{(S)}(t')) ,
\]

\[
c(t) := C'(t)
\]

\[
= \frac{(1 - D^{(S)}(t))(1 - C(t))}{\bar{t}_A} .
\] (A8)

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Using Eqs. (A1), (A2), and (A5), the Laplace transform can be written as

\[
\mathcal{L}\{C\}(s) = \frac{1}{s} - \int_0^\infty dt \, e^{-st - \lambda} \int_0^t \int_0^r P_S(r') \, dr'\, \, dr,
\]

\[
\mathcal{L}\{c\}(s) = s \mathcal{L}\{C\}(s)
\]

\[
= 1 - s \int_0^\infty dt \, e^{-st - \lambda} \int_0^t \int_0^r P_S(r') \, dr'\, \, dr,
\]

\[
= 1 - s \int_0^\infty dt \, e^{-st - \lambda} \int_0^t \int_0^r P_S(r') \, dr'\, \, dr.
\]

The distribution of the busy times is given by\textsuperscript{53}

\[
D^{(B)}(t_B) = 1 - \bar{t}_A \sum_{n=1}^\infty e^{\lambda n}(t_B)
\]

\[
\mathcal{L}\{D^{(B)}\}(s) = \frac{1}{s} - \bar{t}_A \sum_{n=1}^\infty (\mathcal{L}\{c\}(s))^n
\]

\[
= \frac{1}{s} - \bar{t}_A \frac{\mathcal{L}\{c\}(s)}{1 - \mathcal{L}\{c\}(s)}.
\]

(A9)

Using Eq. (A9), we get

\[
P^{(B)}(s) = s \mathcal{L}\{D^{(B)}\}(s) = 1 - \bar{t}_A s \frac{\mathcal{L}\{c\}(s)}{1 - \mathcal{L}\{c\}(s)}
\]

\[
= 1 + \bar{t}_A s \left(1 - \frac{1}{1 - \mathcal{L}\{c\}(s)}\right)
\]

\[
= 1 + \bar{t}_A s - \int_0^\infty dt \, e^{-st - \lambda} \int_0^t \int_0^r P_S(r') \, dr'\, \, dr.
\]

(A10)

The proof is straightforward and can be found, for example, in Refs.\textsuperscript{48,51–53}.

c. Mean Busy Time

The mean value of the busy time is with Eq. (A10) and the relations in Eq. (A5) given by

\[
\bar{t}_B = \int_0^\infty dt_B \, t_B \mathcal{L}\{D^{(B)}\}(t_B) = \mathcal{L}\{t_B P^{(B)}\}(s)|_{s=0}
\]

\[
= \frac{d}{ds} \left(-\mathcal{L}\{P^{(B)}\}(s)\right)|_{s=0} = \frac{d}{ds} \left(-s \mathcal{L}\{D^{(B)}\}(s)\right)|_{s=0}
\]

\[
= \bar{t}_A \frac{\mathcal{L}\{c\}(0)}{1 - \mathcal{L}\{c\}(0)},
\]

(A12)
where in the last equation we assumed that \( L(c)(0) \neq 1 \) and \( L(c)'(0) \) is finite. This is certainly the case if we assume that the distribution of the service time has a compact support, i.e., that a maximum service time \( t_S^{\text{max}} \) exist with \( P^S(t > t_S^{\text{max}}) = 0 \) but \( P^S(t < t_S^{\text{max}}) \neq 0 \). From Eq. (A9), we derive

\[
L(c)(0) = 1 - \lim_{s \to 0} s \int_0^\infty dt \left( e^{-st} \int_0^{t_S^{\text{max}}} dt' P^S(t') \cdot \text{Min}(t, t') \right) = 1 - \lim_{s \to 0} s \int_0^{t_S^{\text{max}}} dt' P^S(t') \cdot \text{Min}(t, t') = 1 - \lim_{s \to 0} s \int_0^{t_S^{\text{max}}} dt' P^S(t') \cdot \text{Min}(t, t') = 1 - e^{-\bar{t}_S / \bar{t}_A} .
\]

Inserting this result in Eq. (A12) provides the mean busy time

\[
\bar{t}_B = \frac{\bar{t}_A L(c)(0)}{1 - L(c)(0)} = \bar{t}_A \left( \frac{\bar{t}_S}{e^{\bar{t}_S / \bar{t}_A}} - 1 \right) .
\]

The \( M/G/\infty \) queue with an arrival rate \( \frac{1}{\bar{t}_A} \) and a probability density function \( P^S(t_S) \) of the service time corresponds to the induced one-dimensional Boolean model from Sec. IV with intensity \( P_u^1(l) \) and a probability density function \( P_u^1[l] \) of the length of a segment as defined in Eq. (11). The mean service time \( \bar{t}_S \) corresponds to the mean length \( \bar{L}^1[u] \) of a segment, and the busy time \( t_B \) corresponds to the solid interception length \( L_{\text{solid}} \). Therefore, the mean length \( \bar{L}_{\text{solid}} \) of the intercepts in the solid phase follows immediately from Eq. (A14) using Eqs. (10) and (12):

\[
\bar{L}_{\text{solid}} = \frac{1}{P_u^1} \left( e^{P_u^1[L^1[u]]} - 1 \right) = \frac{1}{P_u^1} \left( e^{\rho V} - 1 \right) .
\]

Comparing it to the mean length \( \bar{L}_{\text{void}} \) of the void intercepts from Eq. (16) and using the solid area fraction \( \Phi = 1 - e^{-\rho V} \) from Sec. I, we see that, as expected, \( \bar{L}_{\text{solid}} / \bar{L}_{\text{void}} = \Phi / (1 - \Phi) \). The ratio of the mean length of the one-dimensional intercepts is equal to the ratio of the two-dimensional area fractions of the two phases. This well-known relation can also be used to derive the mean length \( \bar{L}_{\text{solid}} \) of the intercepts in the solid phase without evaluating their full distribution.

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M. A. Klatt, Morphometry of random spatial structures in physics, Ph.D. thesis, Friedrich-Alexander-Universität Erlangen-Nürnberg (2016), Parts of this article are from this PhD thesis of one of the authors.


