

iScience, Volume 26

Supplemental information

Digital twin demonstrates significance of biomechanical growth control in liver regeneration after partial hepatectomy

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SUPPLEMENTAL INFORMATION

Varying mitotic index and threshold pressure for cell cycle progression.

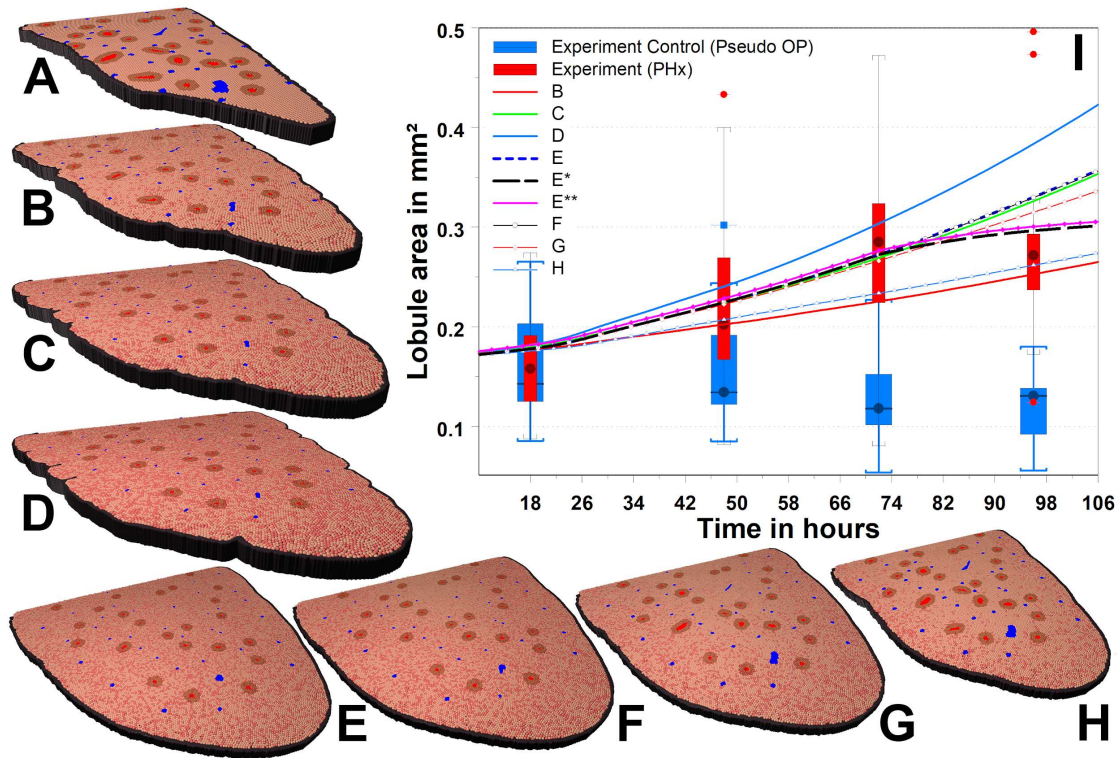


Figure S1. Parameter sensitivity analysis, related to Figure 4: A) Model of 4 cell layers height constructed from experimental images (see Fig.2) at $t=0$ days (initial state). B-D) Prediction of liver lobe pattern for different mitotic indices (achieved by varying pressure threshold) at $t=3$ days. Mitotic index: B) 0.3, C) 0.5 (as found in the experiments) and D) 0.8. Mitotic index = probability of a cell to start proliferating within 24h: Increasing the mitotic index defined as the probability of a cell to start proliferating within 24h (the experimentally found values was 0.5) not only increased the lobe in the simulation (see also (I)), but also led to small undulations at the Glisson capsule (grey color, its Young modulus is 5500Pa) reminiscent of buckling observed in the basal layer of skin or oral mucosa or in irradiated crypts (Drasdo & Loeffler, 2001). Buckling occurs when the stabilizing shear stress (or bending) force is outcompeted by the destabilizing cell proliferation (Drasdo, 2000). The more rigid the Glisson capsule was, the more unlikely was buckling to occur at a certain lobe size. This effect might be tested by increasing the cell cycle progression rate. (E-H) Model predictions for different proliferation inhibition thresholds w after $t = 5$ days: E) $w=300$ Pa (leads to a homogeneous distribution of proliferation as found in the experiments, see Fig.3), F) $w=200$ Pa, G) $w = 150$ Pa, H) $w = 100$ Pa. Furthermore, in these simulations the Young-modulus of the capsule was chosen $E = 20$ kPa. In comparison to A)-D) this led to a smoother Glisson capsule with no undulations. Only one half of the lobe was shown but all simulations were carried out for whole lobes. (E-H) shows that the fraction of cells entering the cell cycle also changed if the pressure threshold, at which a cell would exit the cell cycle, was modified: A lower pressure threshold results in a slower lobule growth speed (see also (I)) but only for $w < 200$ Pa (reference: 300Pa) the deviation was clearly detectable with a half as big lobule increase at day three. The reason is that below $w=200$ Pa the pressure for interior cells is above the proliferation threshold resulting in only growth close to the Glisson capsule (G/H). I) Model kinetics of B)-H) carried out to study the effect of the mitotic index and pressure-based inhibition of proliferation (E^*). In the curves E^* (black, dashed line) and E^{**} (magenta, solid line) the simulations were carried out with a global inhibition of proliferation once the original liver cell population size has been restored. Therefore, this simulation saturates after 3-4 days while the other simulations do not. In the curve E^{**} (magenta, solid line), the Young's modulus was increased by the factor 30 for small cell-cell distances to study the effect of various cell compressibility. Related to *Results and Limitations of the Study*.

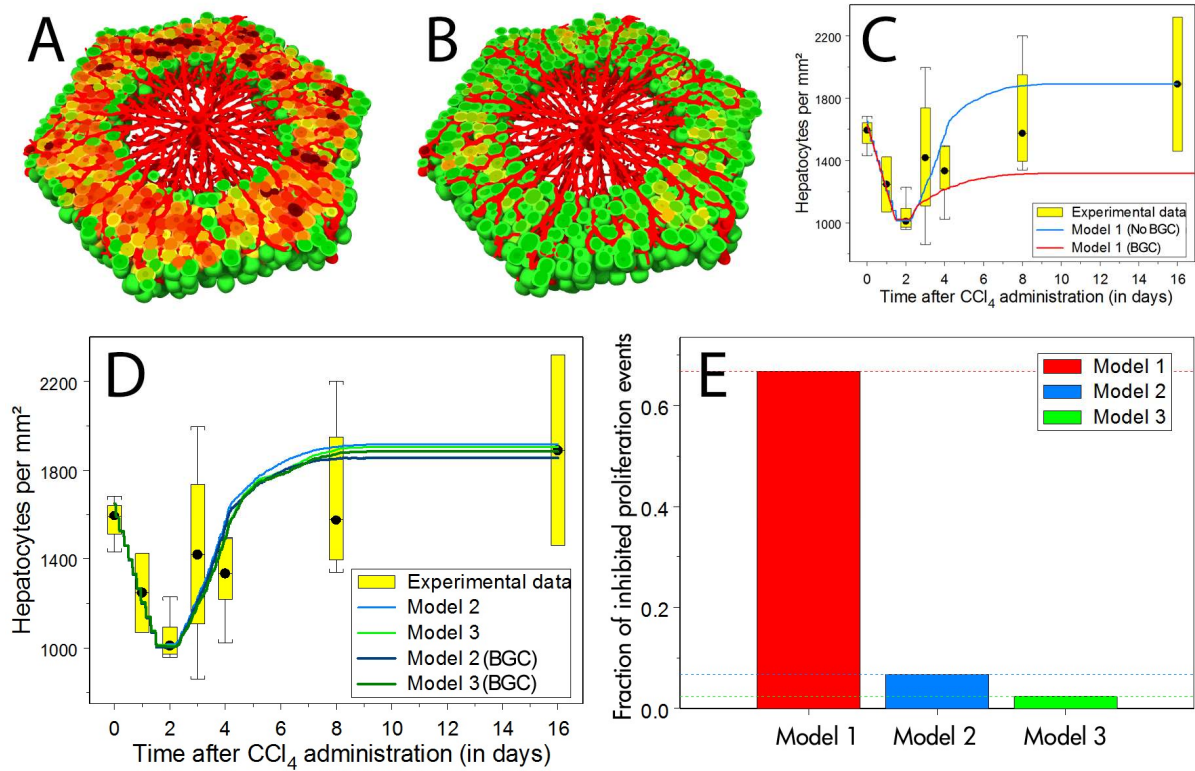


Figure S2. Consistency with liver regeneration after drug-induced liver injury, related to Figure 5: (A) Cell volume during regeneration after CCl₄ intoxication if unrealistic compression was not inhibited. (Green = the volume of an isolated sphere, Red = 0.3 times that volume) (B) The same simulation only with the assumption that entrance into the cell cycle is possible only, if the local pressure does not overcome a critical threshold. A Voronoi-based space partitioning analysis has been used to approximate the volume of the hepatocytes in the model. (C) Time course of cell population size per liver lobule in cases (A) and (B). (D): Time course of cell population size per liver lobule in models 2 and 3 with and without pressure inhibition by proliferation (BGC). (E): Fraction of cases in which proliferation impulses do not lead to proliferation due to pressure-controlled growth inhibition for models 1, 2 and 3 showing that the presence of a mechanism that inhibits proliferation by pressure (BGC) does not modify the regeneration dynamics of models 2 and 3 in (Hoehme *et al.*, 2010). Related to *STAR methods*.

Regeneration simulations varying lobule thickness and other parameters

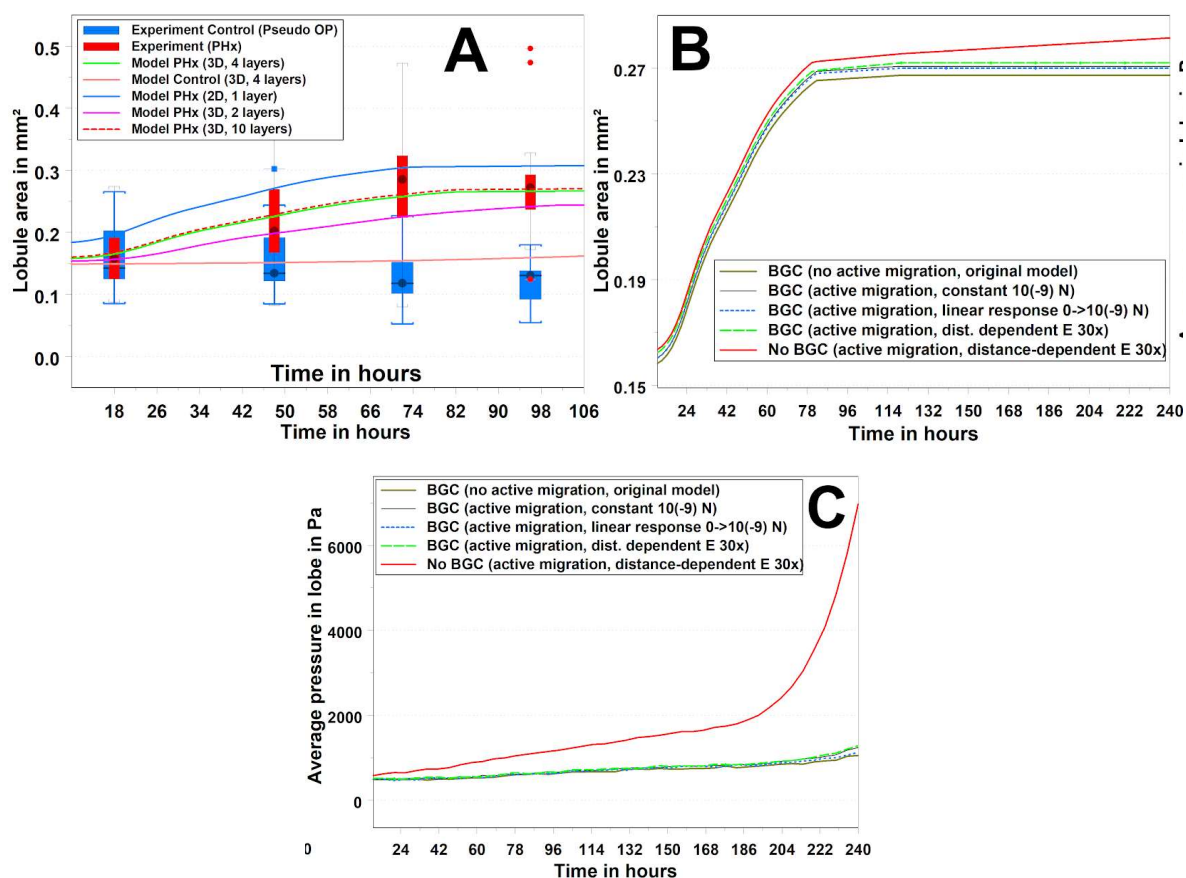


Figure S3. Effect of lobule thickness on simulation results, related to Figure 2 and STAR Methods: (A) Regeneration vs thickness (z -height) of the simulated lobes (1, 2, 4, 10 cells). (B) Comparison of area increase for different regeneration mechanisms (brown: original model, no active migration towards the Glisson capsule; black, blue, green: active migration towards the Glisson capsule, with constant micromotility force of 10^{-9} N (black), varying migration force (blue), distant-dependent cell Young modulus to mimic the strong repulsive force upon large cell compression (green), absence of BGC but with strong repulsive force upon large cell compression (red). (C) Comparison of average pressure in lobe for the models shown in (B). Related to *STAR methods*.

Simulated BrdU proliferating pattern

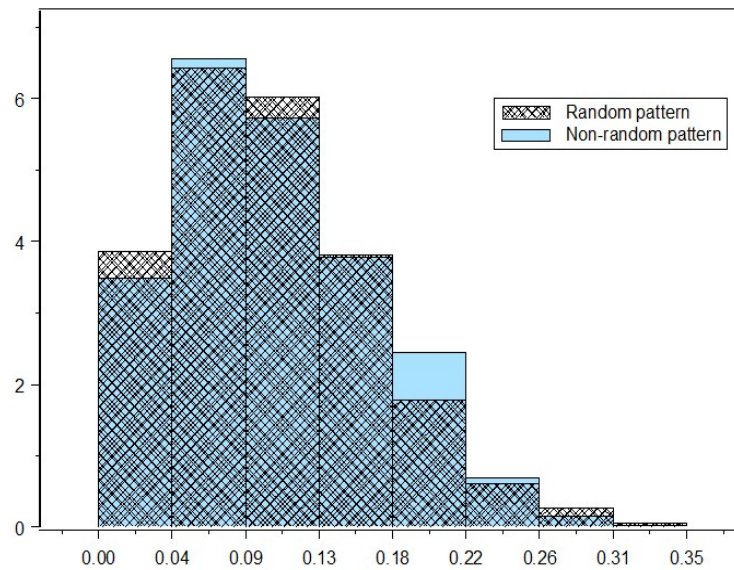


Figure S4. Number of proliferation neighbors of proliferating cells, related to Figure 5: Frequency histograms for the number of proliferating cells in the vicinity of a proliferating cell predicted by the model for BrdU staining (non-random pattern demarcates the BGC mechanism). BrdU only stains cells in the S-phase, which is about 8h long. Simulated was an experimental standard protocol where mice were sacrificed 2 hours after injection of BrdU. In that case, those cells that were in the S-phase during the injection and those cells that entered the S-phase within the two hours until the mice were sacrificed were BrdU-stained. The simulation results of the histogram equivalent to that in Fig.5C/D for KI-67 staining now shows only minor differences demonstrating that labeling S-phase only is insufficient to detect the BGC-generated specific growth pattern. Related to *STAR methods*.

Hepatocyte-sinusoidal interface as order parameter for the regenerating lobe

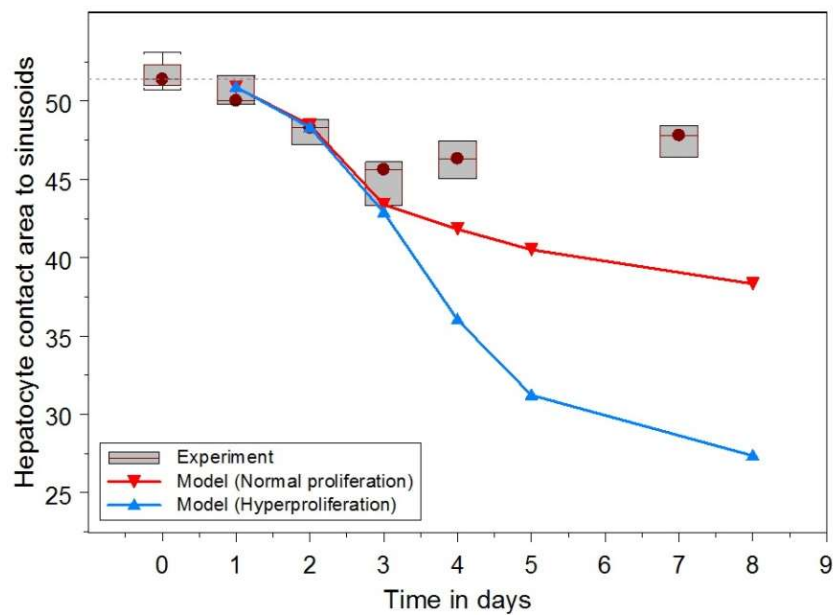


Figure S5. Hepatocyte-sinusoid contact area in regenerating lobe, related to Discussion: Confocal scans of a regenerating liver after PHx indicates a decrease of hepatocyte-sinusoid interface area in the first three days (points) that the model captures quantitatively (red, blue lines). Neo-vascularization results from day 4 in a slow recovery of the hepatocyte-sinusoidal interface area hence the reorganization within the liver lobe is delayed compared to recovery of liver mass, as this was already the case for regeneration after drug-induced liver injury (Hoehme *et al.*, 2010). Our model of the regenerating lobe does not consider neo-vascularization so cannot capture the recovery phase. However, the model predicts that hyperproliferation (blue curve) would not affect the order parameter in the first 3 days after PHx. Related to *Results*.

Liver and liver lobule size in pig

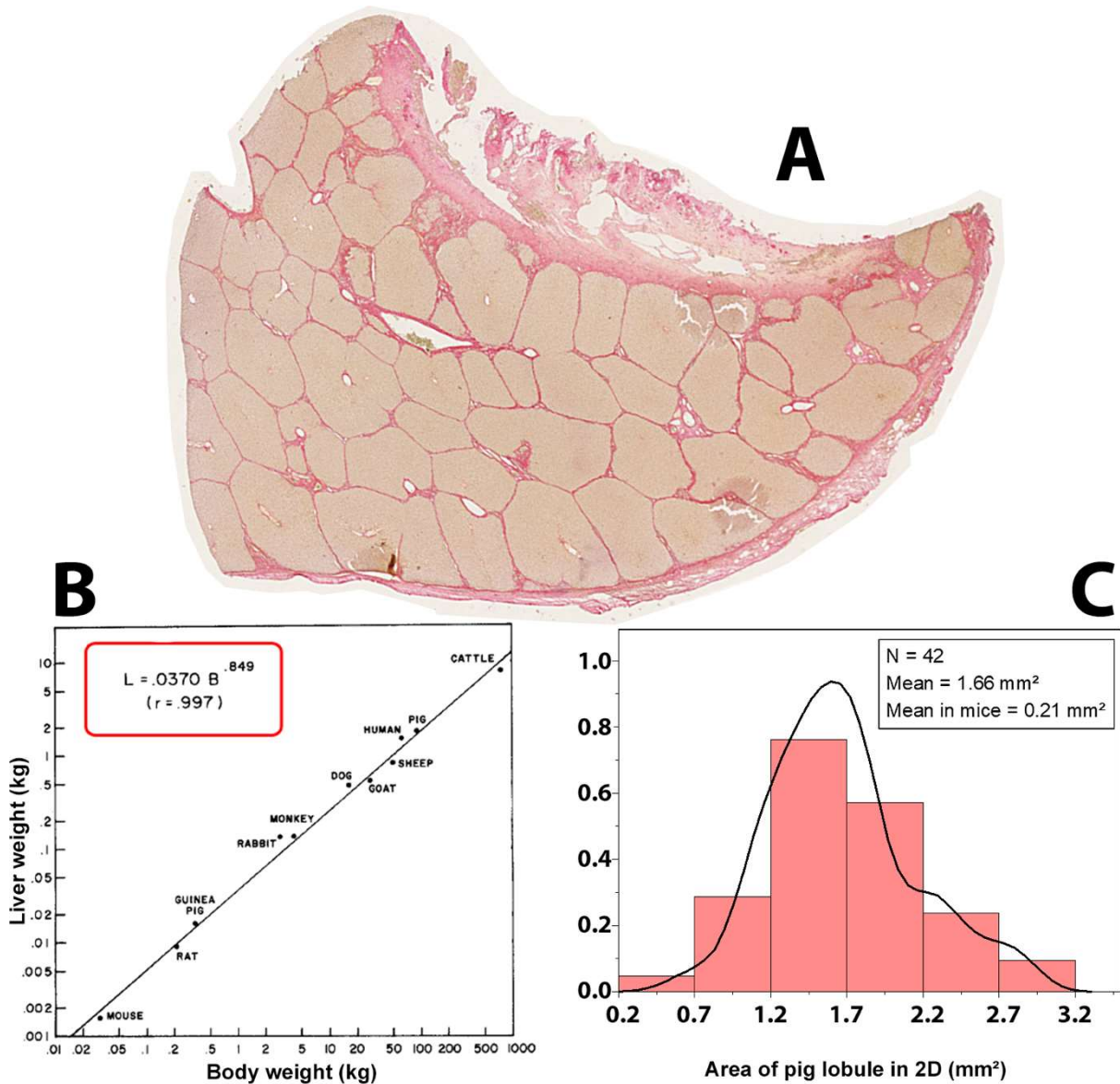


Figure S6. Liver architectural parameters in pigs, related to Figure 6: (A) Whole slide scan of a part of a pig liver lobe stained with Sirius Red for collagen in the portal field (B) Liver weight for mice and larger animals, including pig and human. (C) Area of pig liver lobules quantified from images similar to (A). Related to *STAR methods*.

Table S1: Lobule parameters for mouse and pig, related to STAR Methods and all Figures.

| Parameter | Mouse | | Pig | |
|---|--|--|---|--|
| | Source | Value ± Standard deviation | Source | Value ± Standard deviation |
| Number of analyzed datasets | - | 26 | - | 4 |
| Lobule | | | | |
| Confocal scanning depth | Confocal metadata | 95 ± 57 μm | Confocal metadata | 60.21 ± 9.11 μm |
| Lobule height in the model | 10 Cell layers | 250 ± 0 μm | 5 Cell layers | 90 ± 0 μm |
| Lobule area (2D slice) | Bright field microscopy | 0.21 ± 0.05 mm ² | Bright field whole slides (Sirius Red) | 1.66 ± 0.84 mm ² |
| Lobule radius in model (2D slice) | $R = \sqrt{\frac{2 \cdot A}{3 \cdot \sqrt{3}}}$ A... lobule area, assuming a regular hexagon | 284.3 ± 56.9 μm (12.2 ± 2.4 hepatocytes) | Calculations as in mouse | 799.33 ± 260.7 μm (43.0 ± 14.6 hepatocytes) |
| Area of necrotic lesion before regeneration | Image analysis | 0.073 ± 0.011 mm ² | - ⁽¹⁾ | - |
| Radius of necrotic lesion before regeneration | $R_{nec} = \sqrt{\frac{A_{nec}}{\pi}}$ (assuming a circular necrotic lesion) | 149 ± 22 μm (6.4 ± 1.0 hepatocytes) | - ⁽¹⁾ | - |
| Sinusoids | | | | |
| Radius of sinusoid vessels | Volume analysis | 4.75 ± 2.25 μm | Volume analysis | 8.85 ± 3.11 μm |
| Orthogonal minimal vessel distance | Volume analysis | 16.45 ± 4.22 μm | Volume analysis | 25.7 ± 8.28 μm |
| Non-branched segment length | Volume analysis | 43.1 ± 18.9 μm | - ⁽²⁾ | - |
| Mean branching angles | Volume analysis | 32.5° ± 11.2° | - ⁽²⁾ | - |
| Vessel volume in lobule | Volume analysis | 7.4 ± 1.1% | Volume analysis | 11.1 ± 2.6% |
| Hepatocytes | | | | |
| Hepatocyte volume | Volume analysis | 1.2653·10 ⁻⁵ ± 3.915·10 ⁻⁶ mm ³ | Volume analysis | 0.6838·10 ⁻⁵ ± 8.133·10 ⁻⁶ mm ³ |
| Hepatocyte diameter | Volume analysis | 23.3 ± 3.1 μm | Volume analysis | 18.6 ± 4.7 μm |
| Hepatocyte density | Image analysis | 1889 ± 341 cells/mm ² | Volume analysis | 2631 ± 397 cells/mm ² |
| Next neighbor distance | Volume analysis | 21.6 ± 13.1 μm | Volume analysis | 17.4 ± 11.5 μm |
| Diameter of hepatocyte nucleus | Image analysis | 9.3 ± 4.4 μm | - ⁽¹⁾ | - |
| Central vein | | | | |
| Length in Volume | Volume analysis | 107 ± 69 μm | - ⁽¹⁾ | - |
| Radius | Volume analysis | 41.2 ± 32.1 μm | Manual analysis | 45.3 ± 52.1 μm |
| Inclination to viewing plane | Volume analysis | 6.6° ± 4.1° | - ⁽¹⁾ | - |
| Capsule | | | | |
| Capsule thickness | Manual analysis (IfaDO, 5 datasets in 2D) | 10.75 ± 1.14 μm | Manual analysis (IfaDO, 5 datasets in 2D) | 24.96 ± 9.06 μm |

⁽¹⁾ Not relevant for current simulations

⁽²⁾ Not yet possible with current datasets (too limited sinusoid tracking)

Related to *Results*.

Table S2: Simulation parameters, related to STAR Methods and Figures 2, 4, 5, 6 (all simulations).

| Parameter / Symbol | Unit | Value (Range in sensitivity analysis) | Source |
|---|------------------------------|---|---|
| Cell diameter l_{Cell} | μm | 23.3 | A |
| Sinusoid vessel diameter l_{Sinu} | μm | 4.75 | A |
| Intrinsic cell cycle time τ | h | 24 | (Vintermyr & Døskeland, 1987) |
| Reference energy F_T | J | 10^{-16} | (Beysens <i>et al.</i> , 2000) (Schienbein <i>et al.</i> , 1994) |
| Hepatocyte Young-Modulus E_{Cell} | Pa | 450 (300-1000) | (Davidson <i>et al.</i> , 1995) (Lekka <i>et al.</i> , 1999) |
| Sinusoids Young-Modulus E_{Sinu} | Pa | 600 (300-1000) | B |
| Glisson capsule Young-Modulus E_{Gli} | kPa | 15 (10-50) | B |
| Hepatocyte Poisson ratio ν_{Cell} | - | 0.4 | (Alcaraz <i>et al.</i> , 2003) (Mahaffy <i>et al.</i> , 2000) |
| Sinusoids Poisson number ν_{Sinu} | - | 0.4 | B |
| Glisson capsule Poisson number ν_{Sgli} | - | 0.45 | B |
| Hepatocyte diffusion constant D_i^C for all i | $\text{cm}^2 \text{ s}^{-1}$ | $2 \cdot 10^{-12}$ ($2 \cdot 10^{-13} - 2 \cdot 10^{-11}$) | (Beysens <i>et al.</i> , 2000) |
| Receptor surface density ρ_m For hepatocyte-hepatocyte interaction (Sinusoids are non-adhesive, i.e. $\rho_m = 0$ for interactions involving sinusoids) | m^{-3} | $\approx 10^5$ ($10^{14} - 10^{16}$) | (Chesla <i>et al.</i> , 1998) (Piper <i>et al.</i> , 1998) |
| Binding energy single bond W_s | | $\approx 25k_B T$ | (Beysens <i>et al.</i> , 2000) |
| Friction coefficients ξ_{\parallel}^{CC} ξ_{\perp}^{CC} ξ_{\parallel}^{CS} ξ_{\perp}^{CS} | Ns / m^3 | 10^7 | B |
| Morphogen diffusion coefficient D_M | cm^2 / s | 10^{-6} ($10^{-5}-10^{-7}$) | (Casciari <i>et al.</i> , 1988) |
| Active migration force F_{AM} | nN | 30 (0-100) | B |
| High compression $\tilde{E}_{ij}(\alpha)$ | Pa | 450 - 13500 (450-22500) | B |
| BGC threshold | Pa | 675 (475-4500) | B |
| A ... Quantitative analysis of 3D confocal datasets B ... Value assumed | | | |
| Model parameters. Parameter ranges in parentheses in the last but one column denote the range over which we have varied the respective parameter to test the robustness of our simulation results with regard to the model parameters. Related to STAR methods. | | | |