

Scaling the U-net: Segmentation of biodegradable bone implants in high-resolution synchrotron radiation microtomograms

Ivo M. Baltruschat^{1,+,*}, Hanna Ćwieka^{2,+}, Diana Krüger², Berit Zeller-Plumhoff², Frank Schlünzen¹, Regine Willumeit-Römer², Julian Moosmann^{3,*}, and Philipp Heuser^{1,4}

¹Deutsches Elektronen-Synchrotron DESY, Notkestr. 85, 22607 Hamburg, Germany

²Institute of Metallic Biomaterials, Helmholtz-Zentrum hereon GmbH, 21502 Geesthacht, Germany

³Institute of Materials Physics, Helmholtz-Zentrum hereon GmbH, 21502 Geesthacht, Germany

⁴Helmholtz Imaging Platform, Deutsches Elektronen-Synchrotron DESY, Notkestr. 85, 22607 Hamburg, Germany

*ivo.baltruschat@desy.de

*julian.moosmann@hereon.de

+these authors contributed equally to this work

Supplementary Information

Illustration of the segmentation problem

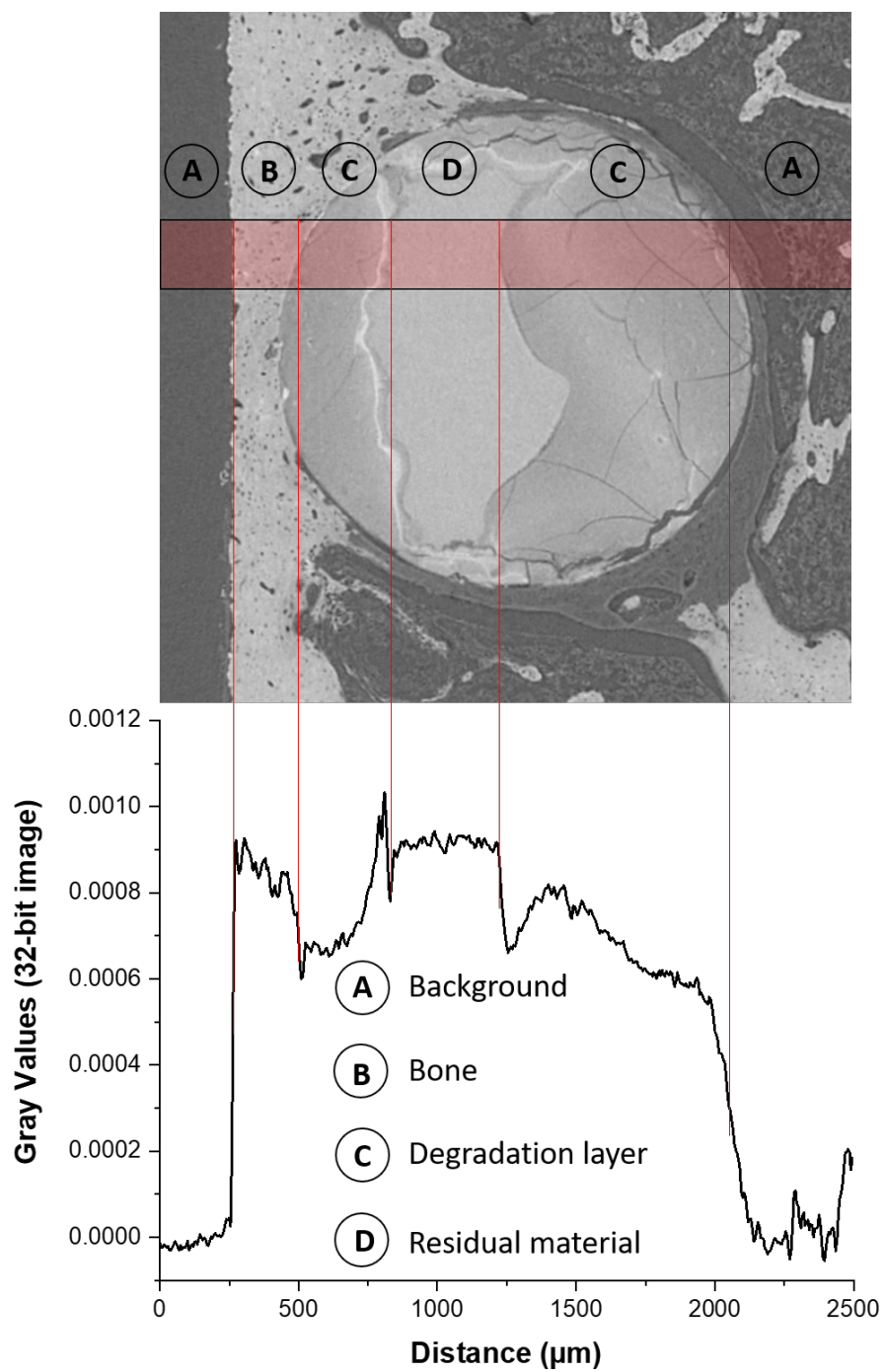


Figure S1. Gray value for each section: background, bone, degradation layer and residual material.

Workflow segmentation

The procedure for workflow segmentation is as follows:

1. Import the reference and the preimplantation screw into Avizo with the correct pixel size for both data sets.
2. Register and resample the preimplantation screw onto the reference screw.
3. Import the corresponding explant with the correct pixel size, register and resample it on the preimplantation screw. As a result, we obtain 1200x1200x1000 lattice and 5 μm pixel size of preimplantation screw and explant data set. All next steps are performed on the registered and resampled data sets.
4. Convert the preimplantation screw into a label and attach it to the registered and resampled explant. As a result, the preimplantation screw is oriented in the same way as the explant screw.
5. Manually correct the mistakes where the preimplantation screw does not match the borders of the explant screw. As a result, we obtain segmented label of overall explant screw (residual material + degradation layer).
6. Create labels for residual material and degradation layer on the segmented overall explant screw and perform watershed segmentation. As a result, we obtain segmented labels of residual material and degradation layer.
7. Perform the automatic thresholding on the explant data set with locked label of explant screw. As a result, we obtain segmented label of bone.

Baseline U-net architecture

Table S1. (a) and (b) show the baseline encoder and decoder architecture, respectively. “Conv3x3BNAct“ refers to a convolution with a 3×3 kernel, batch normalization (BN), and activation function (i.e., in our case Mish). The columns “Resolution” and “#Channels” each represent the output dimensions of this operator. “#Layers” are the number of consecutive operator. “ConvTrans2x2” is a transposed convolution with a 2×2 kernel to upsample the image.

(a)					(b)				
Encoder					Decoder				
Block	Operator	Resolution [pixels]	#Channels	#Layers	Block	Operator	Resolution	#Channels	#Layers
1	Conv3x3BNAct	384×384	32	2	5	ConvTrans2x2	96×96	256	1
	MaxPooling2x2	192×192	32	1		Conv3x3BNAct	96×96	128	2
2	Conv3x3BNAct	192×192	64	2	6	ConvTrans2x2	192×192	128	1
	MaxPooling2x2	96×96	64	1		Conv3x3BNAct	192×192	64	2
3	Conv3x3BNAct	96×96	128	2	7	ConvTrans2x2	384×384	64	1
	MaxPooling2x2	48×48	128	1		Conv3x3BNAct	384×384	32	2
4	Conv3x3BNAct	48×48	256	2	Conv1x1Softmax	384×384	4	1	

Bone to implant contact

Bone to implant contact (BIC) is a parameter describing how much of the degraded implant is in contact with mineralized bone and is quantified by dividing the surface area being in contact with bone the overall surface area of the implant.

$$\text{BIC} = \frac{b}{a}, \quad (1)$$

where b is the total number of boundary voxel between the implant and bone and a is the surface area of the implant.

Table S2. Contact surface area b , surface area a and BIC for each sample obtained with different segmentation techniques

Sample	Segmentation	b [mm ²]	a [mm ²]	BIC [%]
Sample 1	WF	34.36	54.58	62.94
	HQ	35.53	56.43	62.97
	ML	38.83	55.12	70.44
Sample 2	WF	42.01	51.82	81.07
	HQ	45.93	57.25	80.22
	ML	47.73	59.44	80.30
Sample 3	WF	36.68	60.99	60.13
	HQ	30.62	67.82	45.14
	ML	29.85	57.83	51.61

Result example for sample 1

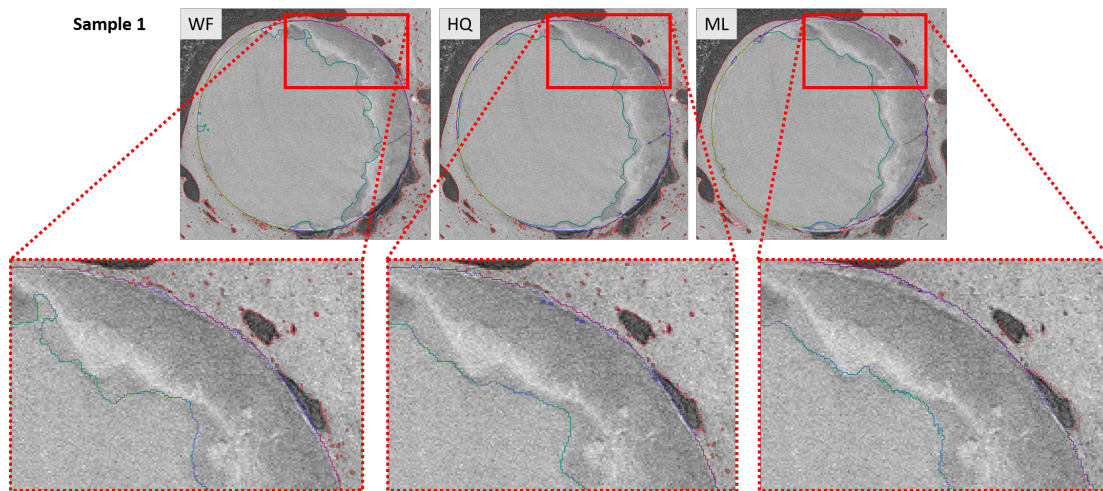


Figure S2. Sample 1. Comparison of the quality of different types of segmentation (shown as outline): semi-automatic workflow (WF), high-quality (HQ), and machine learning (ML). HQ is the reference segmentation.

Result example for sample 2

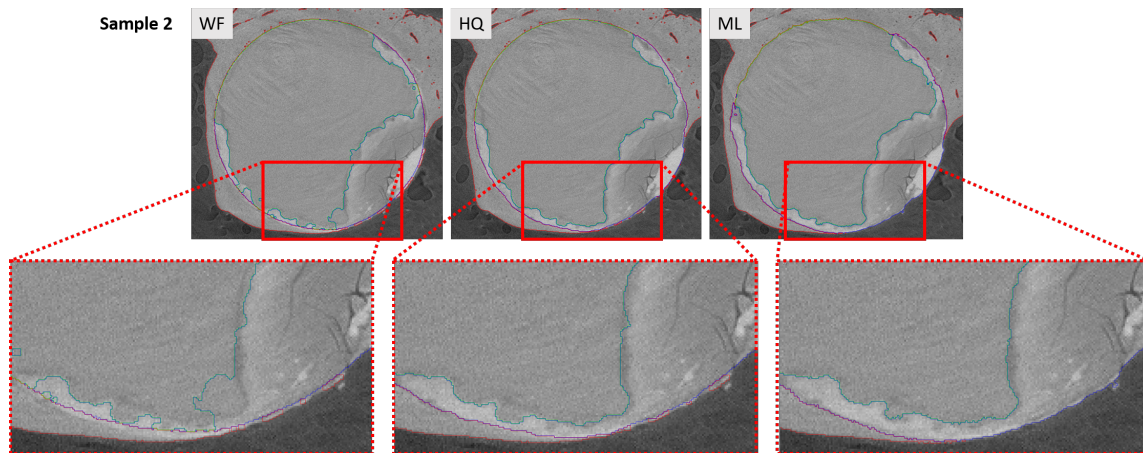


Figure S3. Sample 2. Comparison of the quality of different types of segmentation (shown as outline): semi-automatic workflow (WF), high-quality (HQ), and machine learning (ML). HQ is the reference segmentation.

Result example for sample 3

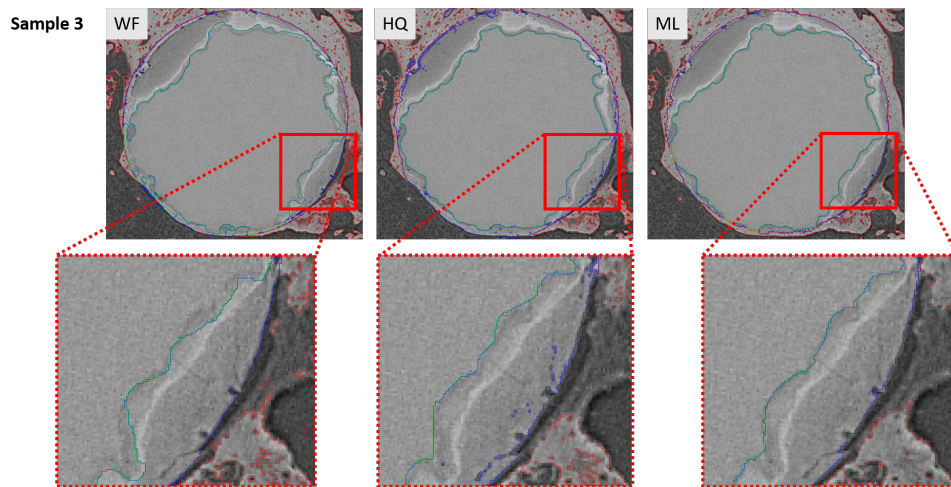


Figure S4. Sample 3. Comparison of the quality of different types of segmentation (shown as outline): semi-automatic workflow (WF), high-quality (HQ), and machine learning (ML). HQ is the reference segmentation.