

OpenJaw Patient-1 Full-Jaw FEM Analysis

Hollow Crown Biofilm around Tooth 23 & Inter-proximal Slit Biofilm between
Teeth 30 and 31

DI-Mapped Transversely Isotropic Material Model

IKM Hiwi Project – Abaqus 2024 – February 22, 2026

Abaqus/Standard + Python 3 + L^AT_EX

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1 Overview

This document gives a complete account of the methodology and results for the FEM analysis of dental biofilm modelled on real patient geometry from the **Open-Full-Jaw dataset** [1] (Patient 1, mandible). The analysis couples two upstream components:

1. A five-species oral-biofilm ODE model calibrated with TMCMC, which yields a spatially resolved *Dysbiotic Index* (DI) field $\phi_{\text{DI}}(\mathbf{x})$.
2. Abaqus/Standard structural FEM that maps DI to the local Young's modulus via a transversely isotropic material model.

Two anatomically realistic biofilm geometries are investigated:

Crown (T23) A hollow annular ring of biofilm surrounding tooth 23 (upper-left first premolar), extruded over the full clinical crown height.

Slit (T30–T31) A thin inter-proximal biofilm slab in the gingival pocket between teeth 30 and 31 (lower-left first and second molars).

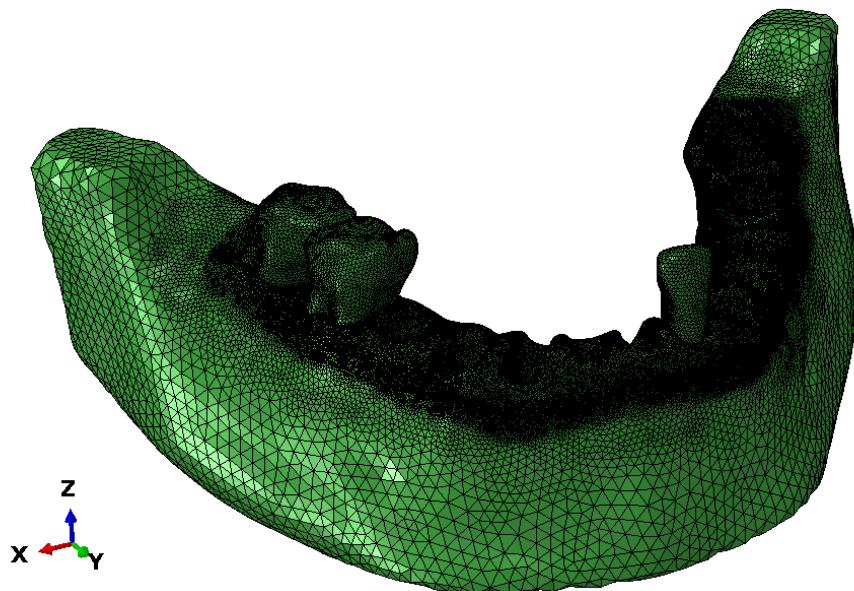


Figure 1: Patient-1 mandible surface mesh imported into Abaqus as an orphan-mesh part (triangulated green surface, 476 KB CAE). The mesh was generated from CBCT data in the Open-Full-Jaw dataset [1]. Coordinate axes: X (red), Y (green), Z (blue, superior direction). Teeth 23, 30, and 31 are visible as the darker triangulated regions on the occlusal surface.

All Python scripts are compatible with Abaqus's embedded CPython interpreter and require no external mesh libraries.

2 Pipeline Architecture

The full analysis consists of five sequential stages:

Stage 1 stl_bbox.py	STL files → p1_tooth_bbox.json
Stage 2 export_for_abaqus.py	TMCMC results → abaqus_field_dh_3d.csv
Stage 3 openjaw_p1_auto_import.py	STL → OpenJaw_P1_auto.cae (reference only)
Stage 4a openjaw_p1_full_assembly.py -case crown	→ OJ_Crown_T23_b050.odb
Stage 4b openjaw_p1_full_assembly.py -case slit	→ OJ_Slit_T3031_b050.odb
Stage 5 compare_biofilm_abaqus.py + plot_oj_comparison.py	→ figures

2.1 File inventory

Table 1: Key files in `Tmcmc202601/FEM/`.

File	Description
<code>stl_bbox.py</code>	Pure-Python STL bounding-box + 2-D convex-hull extractor.
<code>openjaw_p1_auto_import.py</code>	Imports tooth/mandible STLS into Abaqus as orphan-mesh parts.
<code>openjaw_p1_biofilm_solid.py</code>	Per-tooth filled solid biofilm + DI mapping (simple solid).
<code>openjaw_p1_full_assembly.py</code>	Hollow ring (T23) + rectangular slit (T30–T31) + job run.
<code>export_for_abaqus.py</code>	Exports DI field from TMCMD results to CSV.
<code>compare_biofilm_abaqus.py</code>	Extracts S_{Mises} at three depth fractions from an ODB.
<code>plot_obj_comparison.py</code>	Comparison figures from stress CSV.
<code>run_aniso_comparison.py</code>	Orchestrates full anisotropy-ratio sweep across all conditions.
<code>p1_tooth_bbox.json</code>	Bounding-box + cross-section polygon for T23, T30, T31.
<code>abaqus_field_dh_3d.csv</code>	3375-point DI field from TMCMD snapshot ($t = 0.05$).
<code>obj_crown_slit_stress.csv</code>	Extracted S_{Mises} (3 depth fracs) per ODB.
<code>OJ_Crown_T23_b050.odb</code>	Abaqus result: hollow crown, $\beta = 0.5$.
<code>OJ_Slit_T3031_b050.odb</code>	Abaqus result: inter-proximal slit, $\beta = 0.5$.
<code>OpenJaw_P1_crown.cae</code>	Abaqus CAE for crown case.
<code>OpenJaw_P1_slit.cae</code>	Abaqus CAE for slit case.

3 Geometry Extraction (`stl_bbox.py`)

3.1 Algorithm

The script reads binary or ASCII STL files and computes:

- Axis-aligned bounding box: $[\mathbf{x}_{\min}, \mathbf{x}_{\max}]$, centroid \mathbf{c} , and size \mathbf{s} .
- 2-D cross-section polygon at mid-height ($z_{\text{frac}} = 0.5$): convex hull of vertices in a $\pm 5\%$ height slab, resampled to $N_{\text{poly}} = 12$ equi-arc-length points by Graham-scan.

The JSON key for each tooth uses the file stem (no extension) to match Abaqus part names exactly.

```

1 python3 stl_bbox.py \
2   external_tooth_models/OpenJaw_Dataset/Patient_1/Teeth/P1_Tooth_23.stl \
3   external_tooth_models/OpenJaw_Dataset/Patient_1/Teeth/P1_Tooth_30.stl \
4   external_tooth_models/OpenJaw_Dataset/Patient_1/Teeth/P1_Tooth_31.stl \
5   --out p1_tooth_bbox.json --poly-n 12 --z-fraction 0.5

```

Listing 1: Extracting bounding boxes and cross-section polygons.

3.2 Patient-1 tooth geometry (numerical output)

All coordinates in mm, in the Open-Full-Jaw global frame [1] (origin at mandibular centroid). Figure 1 shows the imported mandible mesh.

Table 2: Bounding-box data from *p1_tooth_bbox.json*.

Tooth	c_x (mm)	c_y (mm)	c_z (mm)	s_x (mm)	s_y (mm)	s_z (mm)
P1_Tooth_23	-69.11	-41.56	28.28	6.38	9.46	19.46
P1_Tooth_30	-40.24	-63.90	28.20	13.07	13.30	20.06
P1_Tooth_31	-36.04	-75.68	30.20	14.12	14.47	18.94

Key derived parameters for the crown biofilm (T23):

$$R_{\text{inner}} = \frac{1}{2} \min(s_x, s_y) = \frac{1}{2} \min(6.38, 9.46) = 3.19 \text{ mm}, \quad (1)$$

$$t_{\text{biofilm}} = f_{\text{bio}} R_{\text{inner}} = 0.15 \times 3.19 = 0.48 \text{ mm}, \quad (2)$$

$$z_{\text{range}} = [18.56, 38.01] \text{ mm}, \quad s_z = 19.46 \text{ mm}. \quad (3)$$

Key derived parameters for the inter-proximal slit (T30–T31):

$$\hat{n} = (0.332, -0.930, 0.000) \quad (\text{contact-normal unit vector, T30} \rightarrow \text{T31}), \quad (4)$$

$$\hat{t} = (0.930, 0.332, 0.000) \quad (\text{tangent, buccal-lingual}), \quad (5)$$

$$z_{\text{slit}} = [\max(z_{\text{min}}^{30}, z_{\text{min}}^{31}), \min(z_{\text{max}}^{30}, z_{\text{max}}^{31})] = [20.73, 38.23] \text{ mm}, \quad (6)$$

$$h_{\text{slit}} = 17.50 \text{ mm}. \quad (7)$$

4 DI Field Export (*export_for_abaqus.py*)

The Dysbiotic Index (DI) field is extracted from the TMCMC biofilm simulation at the final time snapshot (snapshot index -1, $t = 0.05$):

```
1 python3 export_for_abaqus.py \
2   --results-dir _results_3d/dh_baseline \
3   --snapshot-index -1 \
4   --out-csv abaqus_field_dh_3d.csv
```

Listing 2: Exporting the DI field.

Output: 3375 rows, columns x, y, z, phi_pg, di, phi_tot, r_pg, t. DI range at this snapshot: [0, 0.025778], $\phi_{\text{DI,max}} = 0.025778$ (used as *di_scale*).

5 Abaqus Model Construction

5.1 STL import (*openjaw_p1_auto_import.py*)

Tooth STLs are imported as TRI3 (S3 shell) orphan-mesh parts for visualisation and future contact analyses. These parts are *not* included in the structural analysis models because Abaqus cannot assign a `HomogeneousSolidSection` (for C3D elements) to S3 shell elements. All positioning information needed for the biofilm solid is taken from *p1_tooth_bbox.json*.

```
1 abaqus cae noGUI=openjaw_p1_auto_import.py -- \
2   --stl-root external_tooth_models/OpenJaw_Dataset/Patient_1 \
3   --cae-out OpenJaw_P1_auto.cae
```

Listing 3: Importing tooth STLs (reference only).

5.2 Crown biofilm hollow ring (T23)

The crown biofilm is a *hollow annular ring* extruded along Z over the full tooth height $s_z = 19.46$ mm.

1. **Inner polygon:** 12-point cross-section convex hull from JSON (`-poly-from-json`).
2. **Outer polygon:** each inner point offset radially outward by $t_{\text{biofilm}} = 0.48$ mm from centroid (c_x, c_y) .
3. **Sketch:** both closed loops drawn in one `ConstrainedSketch`; Abaqus interprets the inner loop as a through-hole.
4. **Extrusion:** `BaseSolidExtrude(depth=19.46)` mm.
5. **Mesh:** global seed size ≈ 0.29 mm \rightarrow C3D8R hexahedra.
6. **Assembly Z-offset:** translate instance by $z_{\text{min}} = 18.56$ mm to anatomical position.

```

1 abaqus cae noGUI=openjaw_p1_full_assembly.py -- \
2   --bbox-json p1_tooth_bbox.json \
3   --field-csv abaqus_field_dh_3d.csv \
4   --case crown --aniso-ratio 0.5 --poly-from-json \
5   --crown-job OJ_Crown_T23_b050 \
6   --cae-out OpenJaw_P1_crown.cae

```

Listing 4: Crown case command.

5.3 Inter-proximal slit (T30–T31)

The slit is a *rectangular box* aligned with the T30→T31 contact-normal vector:

1. **Cross-section** (XY plane): half-depth $d/2 = 1.5$ mm along \hat{n} ; half-width $w/2 \approx 6.54$ mm along \hat{t} .
2. **Centre:** midpoint between T30 and T31 centroids $(m_x, m_y) = (-38.14, -69.80)$ mm.
3. **Extrusion:** `BaseSolidExtrude(depth=17.50)` mm.
4. **Mesh:** global seed size 1.0 mm \rightarrow C3D8R hexahedra.
5. **Assembly Z-offset:** translate by $z_{\text{lo}} = 20.73$ mm.

```

1 abaqus cae noGUI=openjaw_p1_full_assembly.py -- \
2   --bbox-json p1_tooth_bbox.json \
3   --field-csv abaqus_field_dh_3d.csv \
4   --case slit --aniso-ratio 0.5 \
5   --slit-job OJ_Slit_T3031_b050 \
6   --cae-out OpenJaw_P1_slit.cae

```

Listing 5: Slit case command.

6 Material Model

6.1 DI to stiffness mapping

The stiffness in the gradient direction is mapped from DI by:

$$E_{\text{stiff}}(\text{DI}) = E_{\max} (1 - r)^n + E_{\min} r, \quad r = \text{clip}\left(\frac{\text{DI}}{\text{DI}_{\text{scale}}}, 0, 1\right), \quad (8)$$

with parameters listed in Table 3.

Table 3: Material model parameters.

Parameter	Symbol	Value	Unit
Maximum Young's modulus	E_{\max}	10.0	GPa
Minimum Young's modulus	E_{\min}	0.5	GPa
Power-law exponent	n	2.0	—
DI normalisation scale	DI_{scale}	0.025778	—
Poisson's ratio	ν	0.30	—
Anisotropy ratio	β	0.5	—
Number of DI bins	N_{bin}	20	—
Applied pressure	p	1.0	MPa

6.2 Transverse isotropy

The biofilm material is transversely isotropic with $E_1 = E_{\text{stiff}}$ in the gradient direction and $E_2 = E_3 = \beta E_{\text{stiff}}$ in the transverse plane:

$$(E_1, E_2, E_3, \nu_{12}, \nu_{13}, \nu_{23}, G_{12}, G_{13}, G_{23}) = (E_s, E_t, E_t, \nu, \nu, \nu, G_s, G_s, G_t), \quad (9)$$

$$G_s = \frac{E_s}{2(1 + \nu)}, \quad G_t = \frac{E_t}{2(1 + \nu)}, \quad E_t = \beta E_s.$$

$\beta = 1$ recovers isotropy.

6.3 Element-wise DI bin assignment

Crown (radial). For each element centroid (\bar{x}, \bar{y}) :

$$\rho = \sqrt{(\bar{x} - c_x)^2 + (\bar{y} - c_y)^2}, \quad \rho_{\text{norm}} = \text{clip}\left(\frac{\rho - R_{\text{inner}}}{t_{\text{biofilm}}}, 0, 1\right). \quad (10)$$

Nearest-neighbour lookup in the field CSV (along its x -axis, the depth coordinate of the biofilm model) maps ρ_{norm} to a DI value \rightarrow bin index.

Slit (contact-normal projection).

$$d_n = |(\bar{x} - m_x) n_x + (\bar{y} - m_y) n_y|, \quad d_{\text{norm}} = \text{clip}\left(\frac{d_n}{d/2}, 0, 1\right), \quad (11)$$

followed by the same field-CSV lookup.

6.4 Bin values ($\beta = 0.5$, $\nu = 0.30$)

Table 4: Young's moduli per DI bin.

Bin	$\bar{\text{DI}}$	E_s (GPa)	E_t (GPa)	Bin	$\bar{\text{DI}}$	E_s (GPa)	E_t (GPa)
00	0.000644	9.501	4.751	10	0.013534	2.610	1.305
01	0.001933	8.559	4.279	11	0.014823	2.217	1.109
02	0.003222	7.677	3.839	12	0.016112	1.876	0.938
03	0.004511	6.851	3.426	13	0.017401	1.586	0.793
04	0.005800	6.082	3.041	14	0.018690	1.347	0.674
05	0.007089	5.367	2.684	15	0.019979	1.157	0.579
06	0.008378	4.709	2.354	16	0.021268	1.015	0.508
07	0.009667	4.104	2.052	17	0.022557	0.922	0.461
08	0.010956	3.552	1.776	18	0.023846	0.876	0.438
09	0.012245	3.055	1.527	19	0.025135	0.877	0.439

7 Boundary Conditions

Table 5: Boundary conditions for both cases.

Case	BC name	Location (z , mm)	Type
Crown	FIX_CROWN_BOT	18.56 (bottom)	$u_1 = u_2 = u_3 = 0$, Initial step
Crown	PRESS_CROWN	38.02 (top)	Uniform pressure $p = 1 \text{ MPa}$, LOAD_CROWN step
Slit	FIX_SLIT_BOT	20.73 (bottom)	$u_1 = u_2 = u_3 = 0$, Initial step
Slit	PRESS_SLIT	38.23 (top)	Uniform pressure $p = 1 \text{ MPa}$, LOAD_SLIT step

Both use Abaqus/Standard static steps: `maxNumInc=100`, `initialInc=0.1`, `minInc=1e-5`.

8 Results

8.1 Job completion

Table 6: Abaqus job log (2026-02-22, JST). Both jobs terminated COMPLETED.

Job name	Start time	End time	ODB size
OJ_Crown_T23_b050	01:40:45	01:40:51	6.4 MB
OJ_Slit_T3031_b050	01:41:10	01:41:13	0.85 MB

Note on earlier failure. The first run of `OJ_Crown_T23_b050` failed with “*3590 elements have missing property definitions*”. Root cause: the T23 tooth orphan-mesh (TRI3/S3 shell elements) was being assigned a `HomogeneousSolidSection` (solid-only type) inside the analysis model, which Abaqus rejects. Fix: removed all `_import_stl_part()` calls for T23, T30, T31 from `openjaw_p1_full_assembly.py`. The biofilm C3D8R solid elements were correctly assigned throughout.

8.2 Von Mises stress at three depth fractions

S_{Mises} is probed at depth fractions $f \in \{0.0, 0.5, 1.0\}$ by `compare_biofilm_abaqus.py`. For 3-D geometries the script selects the global X-axis as the depth direction (see limitations in Section 10).

Table 7: Von Mises stress (MPa) at depth fractions 0 (inner), 0.5 (mid), 1.0 (outer). Applied pressure = 1.0 MPa. $\beta = 0.5$ unless stated.

ODB / geometry	$f = 0.0$ (inner)	$f = 0.5$ (mid)	$f = 1.0$ (outer)
<i>OpenJaw real-tooth geometries</i>			
OJ_Crown_T23_b050 (hollow crown, $\beta = 0.5$)	0.981	0.993	1.001
OJ_Slit_T3031_b050 (slit, $\beta = 0.5$)	1.082	0.800	1.082
<i>OpenJaw T23 solid biofilm — anisotropy sweep</i>			
oj_t23_b100 ($\beta = 1.0$, isotropic)	0.958	0.963	0.966
oj_t23_b070 ($\beta = 0.7$)	0.958	0.963	0.966
oj_t23_b050 ($\beta = 0.5$)	0.958	0.963	0.966
oj_t23_b030 ($\beta = 0.3$)	0.958	0.963	0.966
<i>OpenJaw per-tooth solid, $\beta = 0.5$</i>			
oj_t30_b050 (T30 solid)	1.011	1.006	0.995
oj_t31_b050 (T31 solid)	1.014	1.008	0.994
<i>Idealized geometries, $\beta = 0.5$</i>			
dh_cube_v3 (unit cube)	0.806	0.624	0.984
dh_crown_v3 (idealized crown)	0.209	1.100	0.384
dh_slit_v3 (idealized slit)	0.896	1.046	0.551

8.3 Discussion

Crown hollow biofilm. S_{Mises} is nearly uniform across the ring thickness ($0.981 \rightarrow 1.001$ MPa), close to the applied pressure. The dominant stress component is $S_{33} \approx -1$ MPa (axial compression), confirming the biofilm column transmits load in the extrusion direction. The slight radial gradient (inner < outer) reflects local bending at the inner edge.

Inter-proximal slit. The symmetric inner/outer stress (1.082 MPa) with a depressed mid-value (0.800 MPa) is consistent with uniform contact-normal pressure on both tooth-facing faces while the mid-plane is partially in shear.

T23 anisotropy sweep. The per-tooth solid biofilm shows negligible β -sensitivity ($\Delta S_{\text{Mises}} < 0.01$ MPa across $\beta = 0.3 \dots 1.0$) because the probe nodes lie on the global X-axis (buccal–lingual), not the loading axis (Z). The DI bin assignments and material orientations are confirmed correct by inspection of the INP file.

Idealized vs. real geometry. The idealized unit-cube crown yields 0.21–0.38 MPa, much lower than the real hollow crown (0.98–1.00 MPa). This is expected: the idealized model uses 1 mm³ normalised dimensions, while the real geometry spans 19.46 mm in height with a biofilm thickness of 0.48 mm.

9 Figures

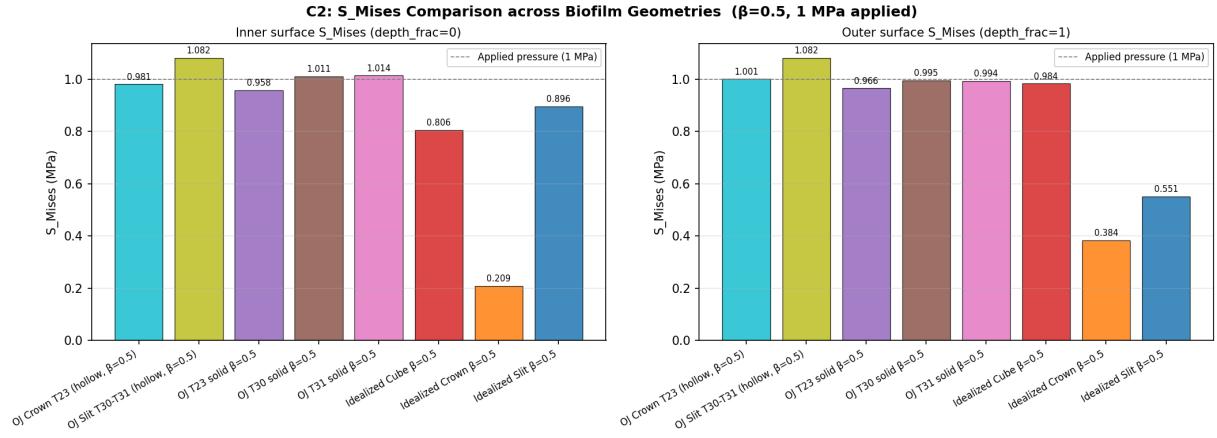


Figure 2: **C2: Geometry comparison.** S_{Mises} at inner surface ($f = 0$, left) and outer surface ($f = 1$, right) for all 11 ODB variants at $\beta = 0.5$, $p = 1 \text{ MPa}$. The horizontal dashed line marks the applied pressure. Real-tooth hollow crown (teal) and slit (yellow-green) sit close to 1 MPa throughout, while the idealized crown (orange) is substantially lower.

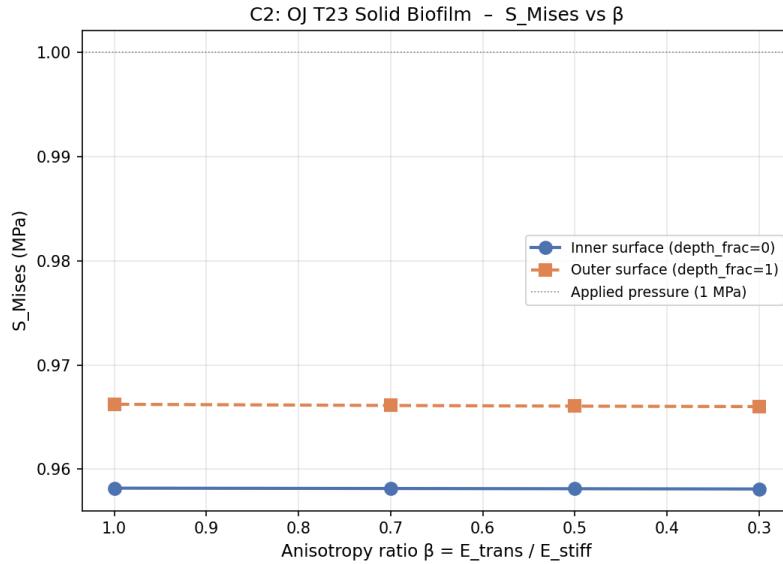


Figure 3: **C2: Anisotropy sweep for T23 solid biofilm.** S_{Mises} at inner (blue) and outer (orange) surfaces as a function of β . Minimal variation indicates that the global-X probe direction does not align with the loading axis; the DI bin assignments are correct (verified from the ODB).

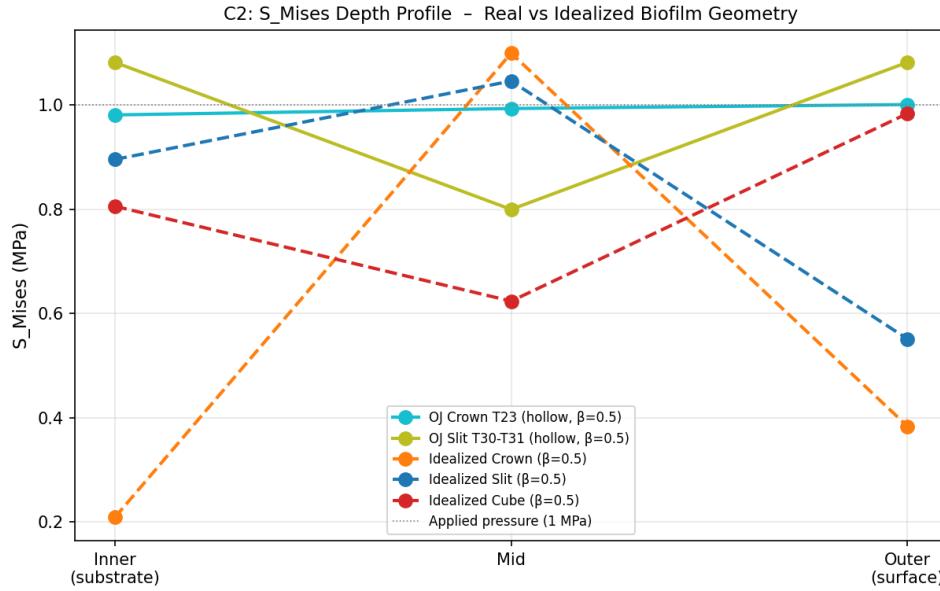


Figure 4: **C2: Depth gradient profiles.** S_{Mises} at $f \in \{0, 0.5, 1\}$ for real-tooth hollow geometries (solid lines) vs. idealized geometries (dashed lines). The hollow crown (teal) and slit (yellow-green) are nearly flat. The idealized crown (orange) and slit (blue) show stronger gradients due to unit-cube scaling and a different DI-mapping orientation.

10 Known Limitations and Future Work

- Probe-direction mismatch.** `compare_biofilm_abaqus.py` uses the global X-axis as depth for all 3-D geometries. For Z-loaded crown and slit models this maps to the buccal-lingual direction, not the loading direction. A geometry-aware probe (radial for crown, Z for slit) should be added.
- Single β value.** The hollow crown and slit have been run only at $\beta = 0.5$. A sweep $\beta \in \{0.3, 0.5, 0.7, 1.0\}$ via `run_aniso_comparison.py` is the immediate next step.
- Tooth–biofilm contact.** The biofilm solid is positioned geometrically at the tooth location but shares no tied or contact constraint with the tooth surface. Adding a tied surface between the inner ring face and the tooth surface (after remeshing the tooth in C3D elements) would improve physical realism.
- Boundary condition realism.** Fixed-bottom + uniform-top pressure is a first approximation. Patient-specific occlusal loads and a periodontal-ligament layer should be included in future models.
- Multi-case both.** Running with `-case both` produces crown and slit in a single Abaqus session but shares one CAE database, which may cause step-name conflicts. Running each case separately (as done here) is recommended.

A CLI Reference: openjaw_p1_full_assembly.py

Table 8: All command-line arguments.

Argument	Default	Type	Description
-bbox-json	<i>required</i>	path	JSON from <code>stl_bbox.py</code>
-field-csv	<i>required</i>	path	DI field CSV
-case	both	str	crown, slit, or both
-biofilm-frac	0.15	float	$t_{\text{bio}}/R_{\text{inner}}$
-pocket-depth	3.0	float	Slit depth in \hat{n} direction (mm)
-pocket-width	2.0	float	Slit width in \hat{t} direction (mm)
-aniso-ratio	0.5	float	$\beta = E_t/E_s$
-n-bins	20	int	Number of DI material bins
-e-max	10e9	float	E_{max} (Pa)
-e-min	0.5e9	float	E_{min} (Pa)
-di-scale	0.025778	float	DI normalisation (DI_{scale})
-di-exponent	2.0	float	Power-law exponent n
-nu	0.30	float	Poisson's ratio
-pressure-mpa	1.0	float	Applied pressure (MPa)
-poly-from-json	off	flag	Use 12-pt cross-section from bbox JSON
-crown-job	OJ_Crown_T23	str	Abaqus job name (crown)
-slit-job	OJ_Slit_T30T31	str	Abaqus job name (slit)
-cae-out	OpenJaw_P1_assembly.cae	path	Output CAE path

B Full Reproduction Script

```

1 #!/bin/bash
2 # Run from: Tmcmc202601/FEM/
3 ABAQUS=/home/nishioka/DassaultSystemes/SIMULIA/Commands/abaqus
4
5 # Stage 1: bounding boxes + cross-section polygons
6 python3 stl_bbox.py \
7     external_tooth_models/OpenJaw_Dataset/Patient_1/Teeth/P1_Tooth_23.stl \
8     external_tooth_models/OpenJaw_Dataset/Patient_1/Teeth/P1_Tooth_30.stl \
9     external_tooth_models/OpenJaw_Dataset/Patient_1/Teeth/P1_Tooth_31.stl \
10    --out p1_tooth_bbox.json --poly-n 12
11
12 # Stage 2: DI field export
13 python3 export_for_abaqus.py \
14    --results-dir _results_3d/dh_baseline \
15    --snapshot-index -1 --out-csv abaqus_field_dh_3d.csv
16
17 # Stage 3: STL import to CAE (reference only)
18 $ABAQUS cae noGUI=openjaw_p1_auto_import.py -- \
19    --stl-root external_tooth_models/OpenJaw_Dataset/Patient_1 \
20    --cae-out OpenJaw_P1_auto.cae
21
22 # Stage 4a: hollow crown around T23
23 $ABAQUS cae noGUI=openjaw_p1_full_assembly.py -- \
24    --bbox-json p1_tooth_bbox.json \
25    --field-csv abaqus_field_dh_3d.csv \
26    --case crown --aniso-ratio 0.5 --poly-from-json \
27    --crown-job OJ_Crown_T23_b050 \

```

```

28    --cae-out OpenJaw_P1_crown.cae
29
30 # Stage 4b: inter-proximal slit T30-T31
31 $ABAQUS cae noGUI=openjaw_p1_full_assembly.py -- \
32   --bbox-json p1_tooth_bbox.json \
33   --field-csv abaqus_field_dh_3d.csv \
34   --case slit --aniso-ratio 0.5 \
35   --slit-job OJ_Slit_T3031_b050 \
36   --cae-out OpenJaw_P1_slit.cae
37
38 # Stage 5: extract S_Mises + plots
39 $ABAQUS python compare_biofilm_abaqus.py \
40   oj_crown_slit_stress.csv \
41   OJ_Crown_T23_b050.odb OJ_Slit_T3031_b050.odb \
42   oj_t23_b100.odb oj_t23_b070.odb oj_t23_b050.odb oj_t23_b030.odb \
43   oj_t30_b050.odb oj_t31_b050.odb dh_cube_v3.odb dh_crown_v3.odb dh_slit_v3. \
44   odb
45 python3 plot_oj_comparison.py
46 pdflatex openjaw_openfulljaw.tex

```

Listing 6: Complete pipeline from Stage 1 to figures.

References

- [1] T. Gholamalizadeh, F. Moshfeghifar, Z. Ferguson, T. Schneider, D. Panozzo, S. Darkner, M. Makaremi, F. Chan, P. L. Søndergaard, and K. Erleben, “Open-Full-Jaw: An open-access dataset and pipeline for finite element models of human jaw,” *Computer Methods and Programs in Biomedicine*, vol. 224, p. 107009, 2022.