

What's in your OpenMSK results

Everything OpenMSK produced for your scan, and where each number lives.

This document ships inside every results zip. It describes every file the pipeline can emit — your zip may not contain all of them, and §7 explains why that is normal rather than a failure.

Start here

Two facts are worth knowing before you open anything, because neither is guessable from the file listing and both cost people real time:

Cartilage thickness is stored on the *bone* meshes, not the cartilage meshes. `femur_mesh.vtk`, `tibia_mesh.vtk` and `patella_mesh.vtk` each carry a per-vertex thickness (mm) array. Thickness is measured outward from the bone surface, which is why it lives there. The cartilage meshes are geometry only and carry no point data at all.

BScore is not a file. It is the `Bscore` key inside `NSM_recon_params.json` and `NSM_bone_only_recon_params.json`. Searching filenames for "bscore" finds nothing, which looks like the feature is missing. It is not.

Filenames beginning `<scan>` below use the name of the file you uploaded.

1. Segmentation label maps

`<scan>_all-labels.nrrd` and `<scan>_all-labels.nii.gz` — the same data in two formats, so you can open it in whatever you already use. Integer labels on the same voxel grid as your input:

Value	Structure
1	Patellar cartilage
2	Femoral cartilage (whole)
3	Medial tibial cartilage
4	Lateral tibial cartilage
5	Medial meniscus
6	Lateral meniscus
7	Femur
8	Tibia

9	Patella
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<scan>_subregions-labels.nrrd / .nii.gz — the same map with the femoral cartilage split into the five regions the thickness numbers are reported over. Label 2 does not appear here; it is replaced by 11–15:

Value	Structure
1, 3, 4	Patellar and tibial cartilages (unchanged)
5, 6	Menisci (unchanged)
7, 8, 9	Femur, tibia, patella (unchanged)
11	Anterior femoral cartilage (trochlea)
12	Medial weight-bearing femoral cartilage
13	Lateral weight-bearing femoral cartilage
14	Medial posterior femoral cartilage
15	Lateral posterior femoral cartilage

These values are the segmentation model's native labels. If you are comparing against another tool's label conventions, map explicitly rather than assuming they agree.

2. Surface meshes

VTK PolyData, one file per structure, in the same physical coordinate space as your input image.

Bone meshes — these carry the measurements:

File	Point-data arrays
femur_mesh.vtk	thickness (mm), labels
tibia_mesh.vtk	thickness (mm), labels
patella_mesh.vtk	thickness (mm), labels

thickness (mm) is the cartilage thickness at each bone-surface vertex, in millimetres, and is 0 where there is no cartilage over that point. labels gives the cartilage region each vertex belongs to, using the subregion values from §1 — so you can reproduce the per-region summaries yourself, or plot any subset.

Cartilage meshes — geometry only, no arrays: femur_cart_0_mesh.vtk, tibia_cart_0_mesh.vtk, tibia_cart_1_mesh.vtk, patella_cart_0_mesh.vtk.

To render a thickness map: open a **bone** mesh and colour by thickness (mm).

```
import pyvista as pv
femur = pv.read("femur_mesh.vtk")
print(femur.point_data.keys())          # ['thickness (mm)', 'labels']
femur.plot(scalars="thickness (mm)", cmap="viridis")
```

In 3D Slicer, load the mesh as a Model and set Scalars to thickness (mm) in the Models module. In ParaView, open it and pick the array in the colouring dropdown.

3. Cartilage thickness measurements

<scan>_results.json and <scan>_results.csv — the same numbers, one flat record per scan.

Keys are <region>_mm_<statistic>, where statistic is mean, std or median, and thickness is in millimetres. The eight regions are:

pat_cart, ant_fem_cart, med_wb_fem_cart, lat_wb_fem_cart, med_post_fem_cart, lat_post_fem_cart, med_tib_cart, lat_tib_cart

So med_wb_fem_cart_mm_mean is the mean thickness of the medial weight-bearing femoral cartilage. That is 24 thickness values in total.

Statistics are computed over the bone-surface vertices belonging to each region — the same values in the thickness (mm) mesh array — so the mesh and the table always agree.

4. T2 relaxation maps

Only produced when the input is a qDESS DICOM series. If your zip has no _t2map files, see §7.

File	What it is
<scan>_t2map.nrrd, <scan>_t2map.nii.gz	Voxelwise T2 in milliseconds, on the input grid
<scan>_depth_seg.nrrd	Cartilage split into deep and superficial layers

When T2 is computed, <scan>_results.json gains up to 72 further keys:

- <region>_t2_ms_<statistic> — whole-thickness T2 (24 values)
- <region>_deep_t2_ms_<statistic> — deep layer, nearest bone (24 values)
- <region>_superficial_t2_ms_<statistic> — superficial layer, nearest the joint space (24 values)

using the same eight regions and three statistics as §3. T2 is in milliseconds. A full run therefore has 96 measurement keys; a run without T2 has 24.

5. Shape model and BScore

OpenMSK fits a neural shape model (NSM) to the femur and reports **BScore**, a research measure of osteoarthritis-related shape.

File	What it is
NSM_recon_params.json	Bone + cartilage fit: Bscore, latent, assd_bone_mm, assd_cartilage_mm
NSM_bone_only_recon_params.json	Bone-only fit: Bscore, latent, assd_bone_mm
NSM_recon*_mesh_NSM_orig.vtk	The reconstructed surfaces the model fitted
femur_mesh_NSM_orig.vtk, fem_cart_mesh_NSM_orig.vtk	Your surfaces in the model's coordinate frame

- **BScore** — the shape score. Higher generally indicates shape more characteristic of osteoarthritis. It is a research number, not a validated clinical measure, and should not be interpreted for an individual patient.
- **latent** — the shape model's latent vector for your scan, useful if you want to do your own analysis in the model's shape space.
- **assd_bone_mm / assd_cartilage_mm** — average symmetric surface distance between your surface and the model's reconstruction, in millimetres. This is a **fit-quality** number: large values mean the model reconstructed your anatomy poorly, so treat that scan's BScore with caution.

Which of the two files you get depends on the shape-model options you chose.

6. Run records

File	What it is
job_manifest.json	Settings used: model, options, pipeline_version, and the Terms of Use version you accepted
_step_log.json	Per-step status, so you can see exactly which stages completed
openmsk-terms-v<version>.pdf	The Terms of Use in force for this job

job_manifest.json is what makes a run reproducible — it records which segmentation model and which pipeline version produced these files.

7. Missing files are usually expected

OpenMSK completes what it can rather than failing outright, so a partial result is a normal outcome and not an error.

- **No `_t2map` files.** T2 needs a qDESS DICOM series — two echoes plus the gradient-spoiling parameters held in the DICOM headers. A single-volume NIfTI or NRRD cannot carry that, so the step is skipped. Converting a qDESS series to a single volume before uploading also forecloses it.
- **No NSM or BScore files.** Either shape modelling was not enabled, or the fit did not succeed for this scan.
- **No mesh or thickness files.** Segmentation succeeded but mesh generation did not. The label maps are still valid.
- **Empty or partial `_results.json`.** The steps that produce those numbers did not complete.

`_step_log.json` tells you which of these applies. Segmentation is the only step whose failure stops the run.

8. Units and conventions, in one place

- Thickness: **millimetres**. T2: **milliseconds**.
- Meshes and label maps share your input image's coordinate space, so they overlay without registration.
- `mean` / `std` / `median` are computed across the bone-surface vertices in a region; `std` is the spread within the region, not a measurement uncertainty.
- A thickness of 0 on a mesh vertex means no cartilage there, not missing data.

Terms, reuse, and citation

Your results are yours to use and publish. Use of the service is governed by the Terms of Use — the version that applied to this job is included in this zip, and the current version is at <https://openmsk.com/terms>.

Research use only. Not a medical device, and not for clinical diagnosis, treatment planning, or any decision about a patient. Results are generated automatically, are not reviewed by a clinician, and may be wrong.

If OpenMSK contributes to your work, please cite:

Goyal A, Belibi F, Sahani V, Pedersen R, Vainberg Y, Williams A, Chu C, Haddock B, Gold G, Chaudhari A, Kogan F, Gatti A. *Automating Imaging Biomarker Analysis for Knee Osteoarthritis Using an Open-Source MRI-Based Deep Learning Pipeline*. medRxiv 2025. doi:10.1101/2025.02.21.25322094

Questions, or something here that doesn't match what you received: info@openmsk.com.