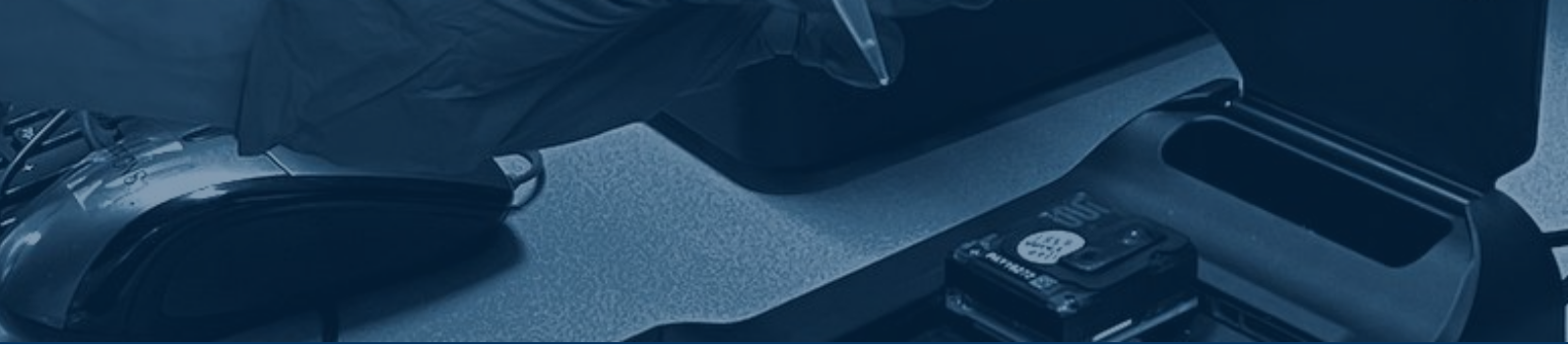
Epinn: tumour molecular analysis by anyone

Methylation and Copy number analysis for tumour molecular classification

Research use only

Cyclomics



Epinn in a nutshell

Epinn is a software suite for molecular characterization of several tumour types. It offers copy number variation analysis and precise tumour type classification from genomic methylation data using advanced AI models. The key characteristics of our software are:

Complete analysis

- Highly accurate **molecular classification powered by AI**
- **Copy number variation** analysis with genes of interest
- Regular updates with the latest models and biomarkers

Multi-platform support

- Use your sequencing technology of choice
- **Our AI models are sequencing platform agnostic**
- Up-to-date with the latest technologies

Comprehensive results

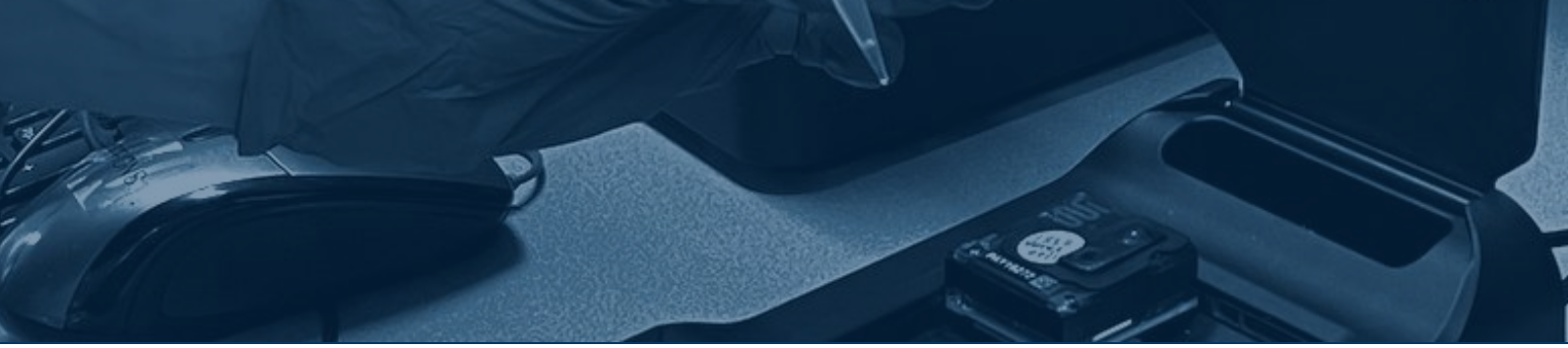
- Generate comprehensive **reports with a single click**
- **Real-time** updated results during sequencing analysis
- Easily re-run, view, and export past analysis

Easy to use

- **No coding** or command-line skills required
- **Intuitive user interface** tailored for medical professionals
- Clear and easy-to-understand quality control metrics

Secure & Private

- Runs entirely **offline**—no internet connection required
- **Your data** stays local—ensuring full privacy and compliance
- Installed and managed on your preferred computer system

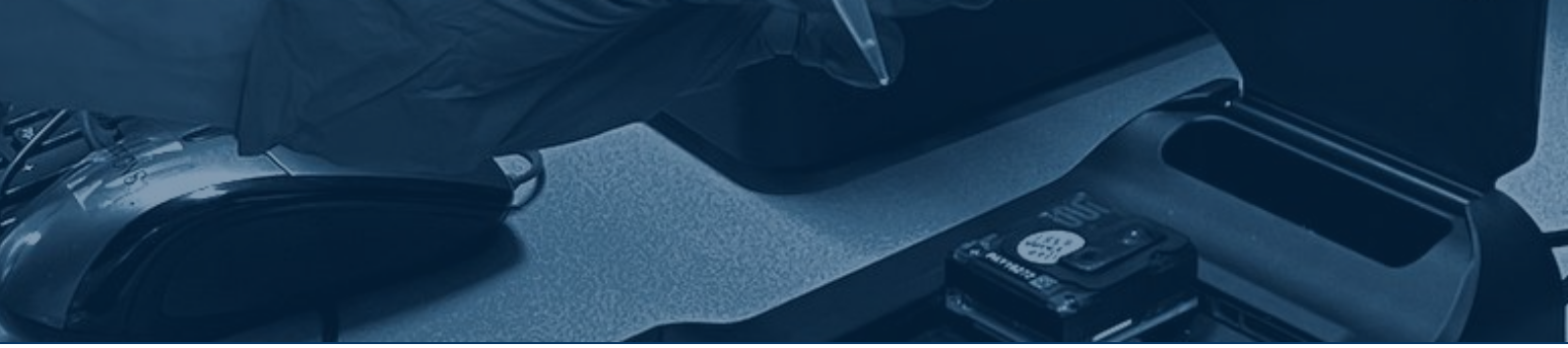


Any platform, complete results

Epinn is compatible with any platform capable of measuring genome-wide methylation data. It currently supports Oxford Nanopore Technologies sequencing, Illumina Infinium microarrays and whole genome bisulfite sequencing. All our methylation AI models are platform agnostic, you can change sequencing technologies without having to worry about model performance.

	Nanopore Sequencing	Illumina Microarray	Bisulfite Sequencing[3]
Platform	MinION PromethION	450k EPIC v1 and v2	WGS
Copy Number Variation analysis	Yes 10kb-1Mb bin size[1]	Yes 50kb bin size	Yes 10kb-1Mb bin size[1]
Methylation based tumour classification	Central Nervous System (CNS) tumours by Epinn-AI Oral Squamous Cell Carcinoma (OSCC) by Epinn-AI Sarcoma tumours by Epinn-AI[3] Your custom private model		
Real-time analysis	Yes	No	No
Analysis Runtime	3 minutes from pileup modkit	5 minutes from idat file	5 minutes from BigWig file

1. Bin size depends on sequencing depth and coverage
2. Vermeulen, C., Pagès-Gallego, M., Kester, L. *et al.* Ultra-fast deep-learned CNS tumour classification during surgery. *Nature* 622, 842–849 (2023).
3. Coming soon



Our offerings

Collaborative implementation service

Would you like to implement Epinn in your routine diagnostics workflow? Would you like to develop custom classification models using your own data? Let us know, our team of specialists will be happy to accommodate your requests.

Cyclomics Epinn Validation Program

We offer a comprehensive 16-week program to seamlessly integrate Epinn into your organization. Our structured approach ensures a smooth implementation process while aligning all stakeholders. The program is divided into four phases:

- Phase I - **Stakeholder Alignment & Requirement Setting** (4 weeks):

  Introduction to Epinn with key stakeholders at your organization, definition of implementation requirements and performance targets.

- Phase II - **User Training** (2 weeks)

  Hands-on training sessions for end users within your organization, ensuring operational readiness and competence.

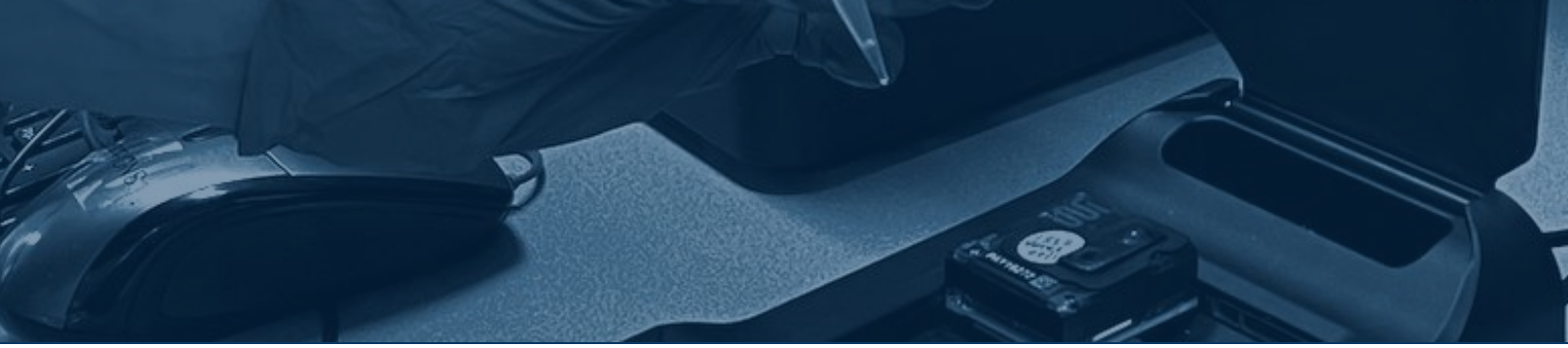
- Phase III - **Sample Validation & Observation Review** (8 weeks)

  Monitoring software performance within your organization, validating observations to meet organizational needs.

- Phase IV - **Workflow Integration Support** (2 weeks)

  Providing assistance in integrating Epinn into existing workflows and computational pipelines, ensuring a seamless transition and long-term success.

Interested? Please contact us at: info@cyclomics.com



CNS tumour classification with Epinn

Molecular diagnostics of central nervous system (CNS) tumors is currently based on genome-wide microarray methylation profiles[1]. Tumor type can be a major determinant in surgical strategy. Microarray analysis takes several days to be completed, making them unsuitable for intraoperative procedures. Methylation models have been shown to be capable of accurate CNS tumour classification from sparse methylation profiles[2].

In conjunction with Nanopore sequencing, this enables a fast molecular classification that can be done during surgery. This analysis can be done in just 90 minutes. Together with our Epinn software platform, it is possible to easily generate a complete report with quality control metrics, methylation-based classification, and copy number variation (CNV) profile.

Workflow at a glance

Sample type	Tumour resection or biopsy
Input type	Native DNA
Input DNA requirements	200 ng
Sample purity requirements	> 50%
Preparation time	25 minutes
Analysis time	30-60 minutes
Classification [2]	78 tumour types
Calibrated Accuracy [2]	95%
Reports CNV	Yes

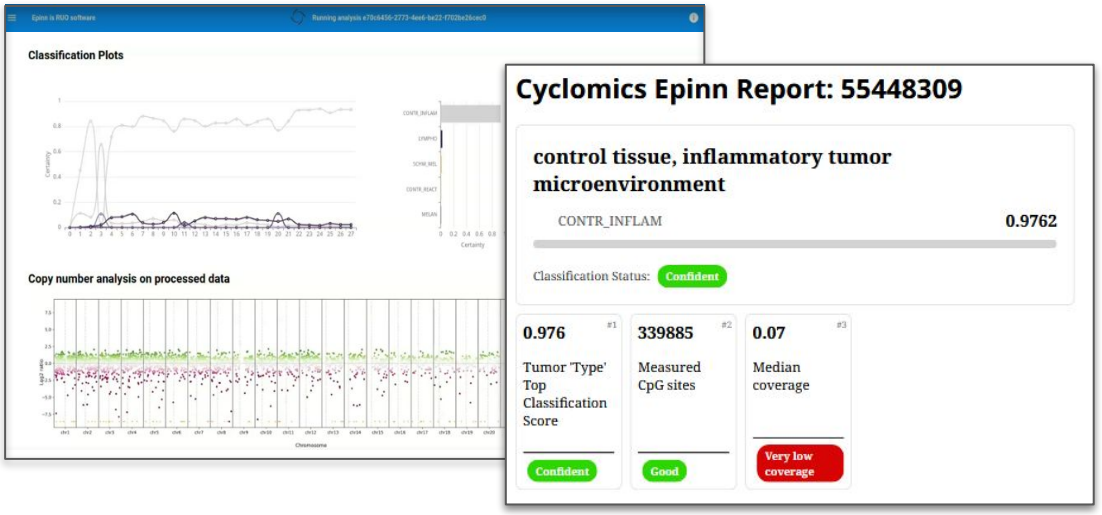
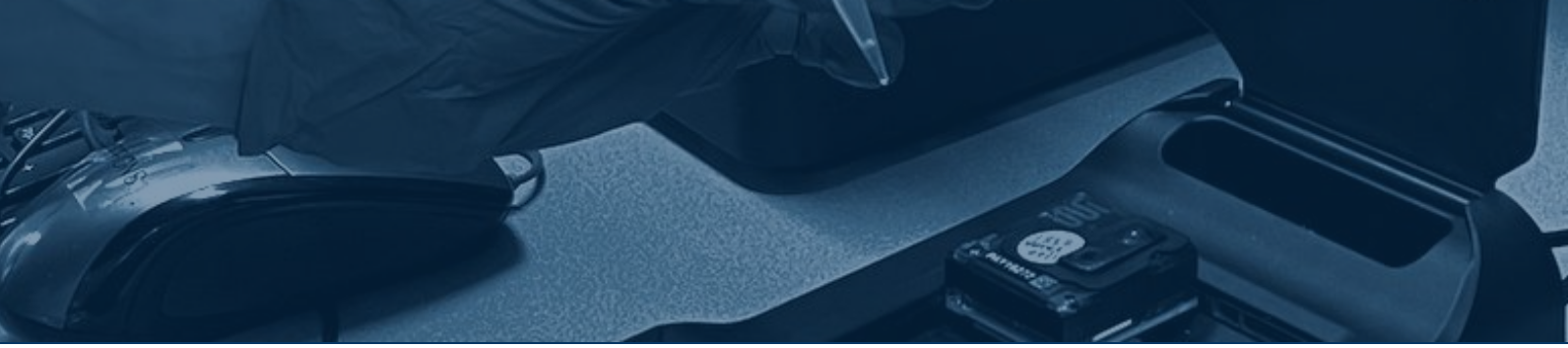


Figure: Epinn app running classification and CNV analysis Left, example screenshot of the Epinn app with the classification and CNV graphs updated real-time. Right, example of screenshot of the report generated by Epinn. These are partial screenshots, for a complete information on the app and report content please check our technical documentation.

1. Capper, D., Jones, D., Sill, M. *et al.* DNA methylation-based classification of central nervous system tumours. *Nature* 555, 469–474 (2018).
2. Vermeulen, C., Pagès-Gallego, M., Kester, L. *et al.* Ultra-fast deep-learned CNS tumour classification during surgery. *Nature* 622, 842–849 (2023).



Extensively validated

Methylation based models have shown to be highly effective in the clinic[2]. Their performance has been tested on both microarray and nanopore sequencing data, including samples from biobanks and tumor resections performed during live surgical procedures. Our Epinn-CNS model is meticulously calibrated to deliver accurate molecular classifications, and refraining from reporting results when uncertainty exists. This built-in robustness is critical for handling challenges such as low sample purity, uncommon tumor types or tumour heterogeneity. These validations ensure that the platform delivers robust and reproducible results across varied conditions. Furthermore, Independent researcher have implemented these models, with findings published in peer-reviewed journals[3].

Minimal setup

Our workflow is designed for simplicity and speed, making it ideal for both established and emerging laboratories. Only a compact set of laboratory equipment is required (*see figure below*), a setup so portable, that all consumables fit in a backpack.

Beyond intra-operative classification

While optimized for rapid molecular classification, Methylation based models functionality extends well beyond intraoperative settings. In combination with Epinn, Our methylation based models can be applied to Illumina microarray data to analyze any available tissue sample or cell line to gain molecular insights. Methylation based models are suitable for retrospective analyses, exploratory studies, and a variety of other research scenarios.

Epinn in combination with Oxford Nanopore Technologies

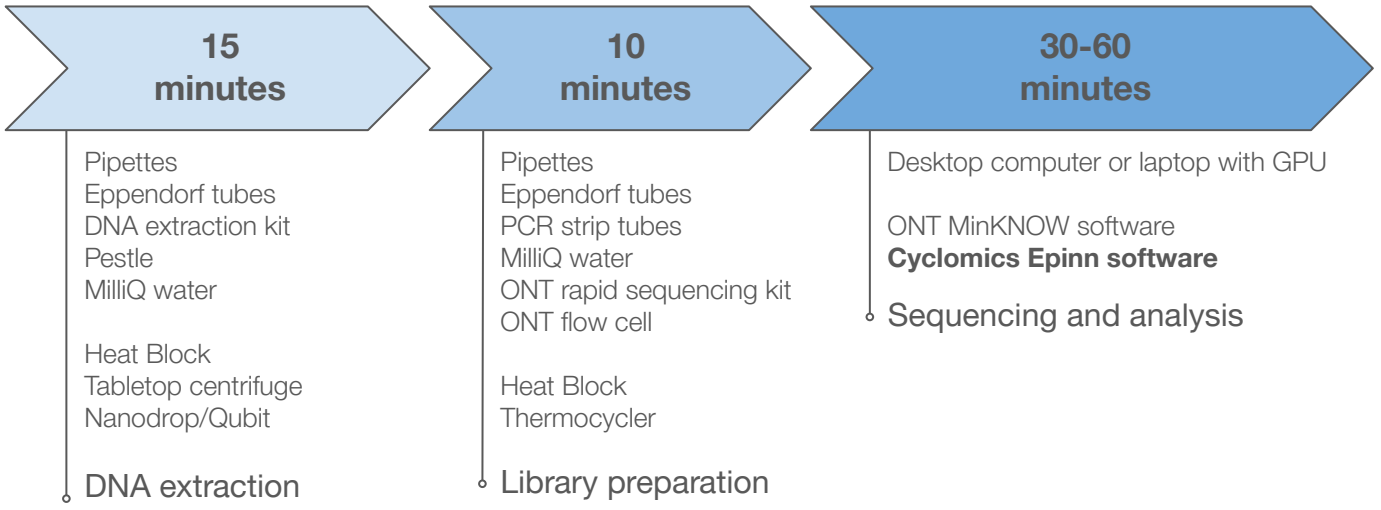


Figure: Workflow on brain tumor molecular classification
DNA extraction takes approximately 15 minutes from brain tumor biopsy material to DNA quality control suitable for library preparation. Library preparation is based on the ONT rapid sequencing kit. Once sequencing is started, analysis starts immediately and reports back results in real-time. Required sequencing time depends on sequencing throughput, sample purity, and tumour type.

2. Vermeulen, C., Pagès-Gallego, M., Kester, L. *et al.* Ultra-fast deep-learned CNS tumour classification during surgery. *Nature* 622, 842–849 (2023).
3. Afflerbach, AK., Albers, A., Appelt, A. *et al.* Nanopore sequencing from formalin-fixed paraffin-embedded specimens for copy-number profiling and methylation-based CNS tumor classification. *Acta Neuropathol* 147, 74 (2024)