

# Testing the MitProfiler tool for detecting and counting dividing cells in stained tissue samples

<b>Submission date</b> 13/08/2025	<b>Recruitment status</b> No longer recruiting	<input type="checkbox"/> Prospectively registered <input checked="" type="checkbox"/> Protocol
<b>Registration date</b> 19/09/2025	<b>Overall study status</b> Ongoing	<input type="checkbox"/> Statistical analysis plan <input type="checkbox"/> Results
<b>Last Edited</b> 19/09/2025	<b>Condition category</b> Cancer	<input type="checkbox"/> Individual participant data <input checked="" type="checkbox"/> Record updated in last year

## Plain English summary of protocol

### Background and study aims

MitProfiler is a computer algorithm which uses machine learning, a form of artificial intelligence, to train computers to recognise mitotic figures in pathology samples (that is, samples of human or animal tissue prepared for microscopic examination). Mitotic figures are seen in cells which are dividing. They are the chromosomes in the cells which can be seen preparing to divide and separating into the daughter cells as the cells divide. They are an important feature of normal tissue biology (e.g. in growing regenerating tissue) and diseases such as cancer (where cells grow and divide in an uncontrolled manner). Pathologists see and count mitotic figures routinely in their work. Having the computer do this task saves time, reduces fatigue in pathologists and should deliver more consistent results as observations between individual human pathologists vary to some extent. By getting human pathologists and the MitProfiler algorithm to count mitoses in the same samples, this study aims to measure how the MitProfiler algorithm performs in comparison to human pathologists.

### Who can participate?

Patients with haematoxylin and eosin-stained tissue sections from various tumour types

### What does the study involve?

This study involves comparing the human pathologists' counts of mitotic figures in stained tissue sections with an automated mitotic counting algorithm.

### What are the possible benefits and risks of participating?

If the results are as good or better than human pathologists, the data derived will be used to support the regulatory approval of the device through the Medicines and Healthcare Regulatory Authority.

### Where is the study run from?

Histofy Ltd (UK)

### When is the study starting and how long is it expected to run for?

February 2025 to September 2025

Who is funding the study?

Innovate UK

Who is the main contact?

Prof. David Snead, david.snead@uhcw.nhs.uk

**Study website**

<https://histofy.ai>

## Contact information

**Type(s)**

Public, Scientific, Principal Investigator

**Contact name**

Prof David Snead

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**Contact details**

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## Additional identifiers

**EudraCT/CTIS number**

Nil known

**IRAS number**

342246

**ClinicalTrials.gov number**

Nil known

**Secondary identifying numbers**

MitPro Study Protocol 2.4

## Study information

**Scientific Title**

Validation of the MitProfiler algorithm for the detection and quantification of mitotic figures in haematoxylin and eosin-stained tissue sections

**Acronym**

MitPro validation study

**Study objectives**

MitProfiler is a computer algorithm which uses machine learning, a form of artificial intelligence, to train computers to recognise mitotic figures in pathology samples (that is, samples of human or animal tissue prepared for microscopic examination). Mitotic figures are seen in cells which are dividing. They are the chromosomes in the cells which can be seen preparing to divide and separating into the daughter cells as the cells actually divide. They are an important feature of normal tissue biology (e.g. in growing regenerating tissue) and diseases such as cancer (where cells grow and divide in an uncontrolled manner). Pathologists see and count mitotic figures routinely in their work. Having the computer do this task saves time, reduces fatigue in pathologists and should deliver more consistent results as observations between individual human pathologists vary to some extent. By getting human pathologists and the MitProfiler algorithm to count mitoses in the same samples, this study aims to measure how closely the MitProfiler algorithm performs in comparison to human pathologists. If the results are as good or better than human pathologists, the data derived will be used to support the regulatory approval of the device through the Medicines and Healthcare Regulatory Authority.

**Ethics approval required**

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**Ethics approval(s)**

Approved 20/02/2025, London - Fulham Research Ethics Committee (2 Redman Place, Stratford, London, E20 1JQ, United Kingdom; +44 (0)207 104 8084, (0)207 104 8286, (0)207 104 8109; fulham.rec@hra.nhs.uk), ref: 25/LO/0158

**Study design**

Observational cohort study

**Primary study design**

Observational

**Secondary study design**

Cohort study

**Study setting(s)**

Laboratory

**Study type(s)**

Diagnostic

**Participant information sheet**

Not applicable

**Health condition(s) or problem(s) studied**

Sarcoma, melanoma, carcinoma, carcinoid

**Interventions**

This observational study involves comparing the blinded counts of mitotic figures in archived hematoxylin and eosin (H&E) sections with an automated mitotic counting algorithm.

**Intervention Type**

Device

**Pharmaceutical study type(s)**

Not Applicable

**Phase**

Not Applicable

**Drug/device/biological/vaccine name(s)**

MitPro

**Primary outcome measure**

Interobserver variation of mitotic counts measured using data generated by the MitProfiler algorithm and human pathologists at one timepoint

**Secondary outcome measures**

Time taken to produce mitotic counts measured using data generated by the MitProfiler algorithm and human pathologists at one timepoint

**Overall study start date**

20/02/2025

**Completion date**

30/09/2025

## Eligibility

**Key inclusion criteria**

Patients with haematoxylin and eosin-stained tissue sections from tumour types:

1. Breast cancer
2. Neuroendocrine tumour
3. Melanoma (including uveal melanoma)
4. Soft tissue sarcoma
5. Leiomyoma
6. Lung cancer
7. Glioblastoma
8. Meningioma
9. Thyroid cancer
10. Retinoblastoma

**Participant type(s)**

Patient

**Age group**

Mixed

**Lower age limit**

1 Years

**Upper age limit**

100 Years

**Sex**

Both

**Target number of participants**

500

**Key exclusion criteria**

Haematoxylin and eosin-stained tissue section slides are unavailable

**Date of first enrolment**

13/08/2025

**Date of final enrolment**

20/09/2025

**Locations****Countries of recruitment**

England

United Kingdom

**Study participating centre**

**North Tees and Hartlepool NHS Foundation Trust**

University Hospital of Hartlepool

Holdforth Road

Hartlepool

United Kingdom

TS24 9AH

**Sponsor information****Organisation**

Histofy Ltd

**Sponsor details**

The Venture Centre

Sir William Lyons Road

Coventry

England  
United Kingdom  
CV4 7EZ

**Sponsor type**  
Industry

**Website**  
<https://histofy.ai/>

## **Funder(s)**

**Funder type**  
Government

**Funder Name**  
Innovate UK

**Alternative Name(s)**  
innovateuk

**Funding Body Type**  
Government organisation

**Funding Body Subtype**  
National government

**Location**  
United Kingdom

## **Results and Publications**

**Publication and dissemination plan**  
Planned publication in a peer-reviewed journal

**Intention to publish date**  
31/10/2025

**Individual participant data (IPD) sharing plan**  
The data sharing plans for the current study are unknown and will be made available at a later date

**IPD sharing plan summary**  
Data sharing statement to be made available at a later date

**Study outputs**

Output type	Details	Date created	Date added	Peer reviewed?	Patient-facing?
<a href="#">Protocol file</a>	version 2.4		21/08/2025	No	No