

Short thesis for the degree of doctor of philosophy (PhD)

**Robust Time-Lapse Microscopy Automation: Detection,
Tracking, Annotation Transfer, and Reinforcement
Learning for Complex Biomedical Systems**

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Contents

1	Introduction	1
2	Theses	4
	2.1 Three-Stage Annotation Methodology	4
	2.2 Cell Detection Framework	7
	2.3 Robust Tracking via Enhanced DeepSORT .	9
	2.4 Domain Adaptation for Annotation Transfer	12
3	Conclusion of the dissertation	15
	Own publications	16
	References	19

1 Introduction

Phase-contrast microscopy remains a cornerstone technique in biomedical research and biotechnology because it enables direct, non-invasive observation of cellular morphology, motility, and division dynamics in living systems [1, 2]. Unlike fluorescence microscopy, which often requires genetic modification or chemical staining, phase-contrast imaging leverages optical principles to visualize transparent specimens, making it well suited for long-term studies without phototoxicity or perturbation of normal biological processes [3]. Quantitative analysis of time-lapse microscopy supports many high-impact applications, including cancer biology (e.g., proliferation and migration phenotypes) [4], drug discovery and toxicity screening (e.g., phenotype-based assays) [5, 6], regenerative medicine (e.g., monitoring cell-cycle progression and differentiation trajectories) [7], and fundamental studies of mitotic behavior and population dynamics [8].

Rapid advancements in modern laboratory workflows due to enhanced and automated microscope systems, and the implementation of multi-well scans with high temporal resolution capabilities are causing an unprecedented increase in imaging throughput [9]. A typical contemporary experiment generates thousands of frames throughout multiple fields-of-view and experimental conditions, leading to a critical analytical bottleneck that substantially minimises the value of the data obtained. Although manual inspection and annotation yield accurate results, the time taken to complete this process is considerable; additionally, there is significant inter-observer variability in the interpretation of the same data [10, 11]. These two factors create difficulties when trying to reproduce similar results across different analysts or laboratories. Issues associated with the quality of images obtained from phase-contrast microscopy (overlapping cells in confluent cell cultures and unclear borders due to optical artefacts such as halos and shading gradients) exacerbate the above-mentioned problems [12]. The identification of cells through frame-wise detection is limited when trying to track

individual cell activity over time, since missed detections can result in fragmented cell movements or incomplete histories, rendering downstream assessment of proliferation and cell division dynamics unreliable [13].

Deep learning has become the dominant paradigm for object detection and has been increasingly adopted for biomedical imaging [14, 15, 16, 17]. However, microscopy introduces domain-specific challenges that limit direct transfer of computer-vision pipelines trained on natural images. First, phase-contrast microscopy exhibits characteristic appearance phenomena absent from natural images, including low contrast between cellular structures and background and halo artifacts surrounding cell bodies, which can confuse detectors and degrade localization [3]. Second, cellular appearance varies markedly across the cell cycle and across imaging setups, and division events are rare and transient, creating strong class imbalance that complicates model training and evaluation [18]. Third, time-lapse sequences impose temporal consistency requirements: detectors with strong average performance may still fail transiently under occlusion, overlap, or rapid morphology transitions, producing gaps that undermine trajectory-level inference [19]. Fourth, domain shift across laboratories and acquisition conditions (optics, illumination, cell lines, culture protocols, and preprocessing pipelines) often leads to substantial performance degradation when deploying models trained on one dataset to a new target domain [20, 21].

The dissertation is organized as follows: Chapter 1 introduces the dissertation by summarizing its context and motivation, defining the thesis’ problem statement, outlining its research objectives, summarizing its contributions, and describing how the entire thesis is structured. Chapter 2 examines prior research in microscopy detection, multi-object tracking, and domain adaptation, and discusses the methodological shortcomings of previous research that this dissertation addresses [J5]. Chapter 3 describes the two datasets used in this research, as well as the annotation process, labeling protocols, preprocessing, and reproducible splits of these

datasets [J3]. Chapter 4 benchmarks current state-of-the-art detection architectures used for detecting cells and cell divisions and compares their performance with respect to accuracy, class-specific performance, and efficiency/cost trade-offs [J3]. Chapter 5 presents the integrated detection-tracking pipeline and enhanced DeepSORT framework, inclusive of changes made to motion and appearance modelling, and presents quantitative evaluation [J2]. Chapter 6 introduces the unsupervised annotation transfer framework using CycleGAN reverse mapping and describes evaluation using proxy reliability measures on unlabeled target-domain data [J4]. Chapter 7 presents a complex-systems perspective on biomedical and biotechnological AI pipelines and summarizes reinforcement-learning concepts relevant to closed-loop decision-making built on top of reliable perception modules [J1]. Finally, Chapter 8 concludes the dissertation by summarizing the main findings and contributions, discussing limitations, and outlining future research directions.

The booklet focuses specifically on the four experimentally validated theses (dataset and annotation methodology, detection benchmarking, an integrated detection-tracking pipeline, and annotation transfer), while the reinforcement learning perspective is presented in the full dissertation.

2 Theses

2.1 Three-Stage Annotation Methodology

For datasets obtained through time-lapse microscopy, annotation is typically generated manually, resulting in significant time consumption and human effort. In order to alleviate this challenge, an annotation pipeline has been intentionally built for the purpose of accurately creating ground-truth labels at scale across all frames of a data set collected from time-lapse microscopy. This pipeline utilizes a three-phase annotation system based on data-focused approaches used in large-scale visual cognition tasks [22]. This approach combines both expert review and automatically generated pseudo-labels along with an advanced multi-mode object tracking system to enhance the quality of the annotations while reducing the amount of manual supervision necessary for generating quality annotations, as shown in (Figure 2.1). The design of this three-stage workflow was developed iteratively and is empirically motivated by the detection–tracking experiments in Chapter 5/Section2.3, which quantify how model-assisted labeling and temporal association improve annotation coverage while maintaining feasible human effort.

1. **Stage 1: Manual Annotation:** In the first step of the annotation methodology, a carefully selected subset of images from the B16BL6 database was manually annotated. This included training on 204 frames from the data set and validation on 134 frames resulting in a total of 342 frames for this first phase of study (19% of the total data set). The expert annotators worked alongside domain experts to ensure accurate bounding box measurements around relevant cell locations as well as correct class labels assigned to each annotation.
2. **Stage 2: Semi-Automatic Annotation:** As mentioned in the first stage, where 19% of the dataset was annotated manually, this stage aimed to extend the annotation to the entire

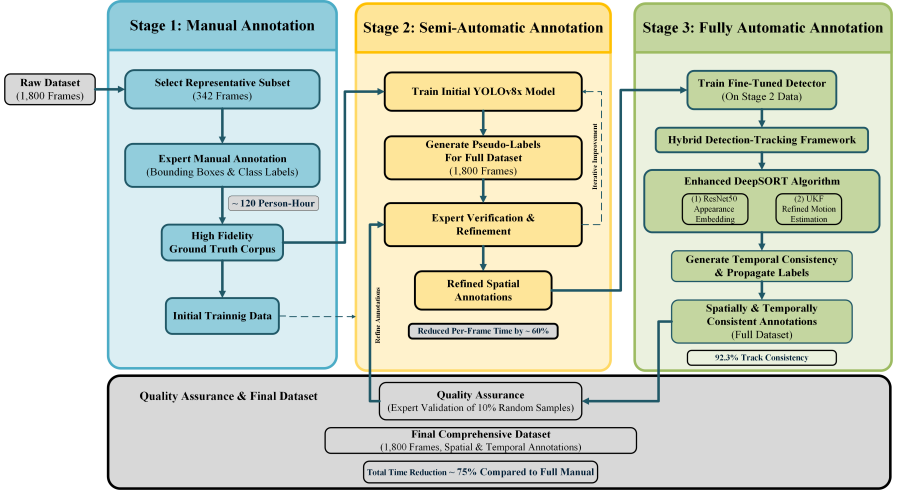


Figure 2.1: Flowchart of three-stage annotation methodology

dataset while maintaining quality. The YOLOv8x model was trained on the manually labeled data and then utilized to generate pseudo-labels for the entire 1800-frame dataset. This phase achieved a Modified-Recall score of 85.95 on the validation subset, thereby establishing its capacity as a trustworthy mechanism for pseudo-labeling. The pseudo-labels generated by the model underwent meticulous verification and rectification by expert reviewers.

3. **Stage 3: Fully Automatic Annotation:** The final stage of our integrated pipeline included both a fine-tuned version of the YOLOv8x model from Stage 2 and a modified version of the DeepSORT tracking algorithm, which included two new enhancements to improve tracking results: better estimates of motion and better estimates of appearance. Therefore, this integrated detection-tracking approach enabled temporal consistency of label propagation across successive frames, thereby mitigating false positives, restoring missed detections by leveraging trajectory continuity, and reducing identity switch problems frequently encountered in dense cell pop-

ulations. Track consistency was evaluated by computing the fraction of tracks extending over at least 10 consecutive frames without identity switches, yielding a 92.3% consistency score (modified recall) on manually validated sequences.

Thesis 1: Three-stage annotation methodology.

I developed and operationalized a scalable three-stage annotation methodology for dense time-lapse microscopy that balances label fidelity with practical annotation cost. I first established a carefully curated expert-labeled subset to define consistent class semantics for *Cell* and *Division* and to provide high-quality supervision for initial model training. I then implemented a model-assisted pseudo-labeling stage to expand annotation coverage across the dataset, followed by a temporal refinement stage in which detection–tracking consistency was exploited to recover missed instances and reduce frame-to-frame label discontinuities. Through this pipeline, I demonstrated that accurate detection supervision can be constructed at scale while maintaining reproducibility, enabling subsequent benchmarking and system integration experiments in a controlled and consistent data regime.

For details on Thesis 1, see Chapter 3 of the dissertation.

Related papers: [J2] and [J3].

2.2 Cell Detection Framework

A comprehensive comparative analysis of state-of-the-art object detection architectures for automated cell detection and division recognition in microscopy images. Multiple detector families, including YOLO variants, SSD, Faster R-CNN and its extensions, and RT-DETR, are evaluated on the B16BL6 dataset described in Section 2.1 using standardized metrics, such as mean average precision, inference speed, and model complexity. The results offer practical guidance for appropriate detection architecture selection in microscopic cellular image analysis.

Table 2.1 and 2.2 display the overall performance for each of the model architectures tested based on various metrics (i.e., accuracy), robustness, and inference speed. It also illustrates the results from both the baseline and fine-tuned models. Thus, models can perform differently even among all of the evaluated models. The performance levels exhibited across models guided the selection process for microscopy applications.

Table 2.1: Performance comparison of one-stage detectors on the B16BL6 dataset.

Model	mAP@0.50	mAP@0.50:0.95	AP@0.50 (Cell)	AP@0.50 (Division)	Best F1 / Conf	Prec. (Peak)	Rec. (Peak)
YOLOv8x (Baseline)	0.837	0.627	0.870	0.805	0.77 / 0.21	1.000	0.910
YOLOv8x (FT, Pat=5)	0.824	0.607	0.855	0.794	0.77 / 0.17	1.000	0.900
YOLOv8x (FT, Pat=15)	0.815	0.605	0.864	0.767	0.76 / 0.27	1.000	0.900
YOLOv11-L (Baseline)	0.811	0.607	0.861	0.761	0.75 / 0.23	1.000	0.910
YOLOv11-L (FT, Pat=5)	0.794	0.589	0.853	0.768	0.75 / 0.44	1.000	0.930
YOLOv11-L (FT, Pat=15)	0.798	0.589	0.859	0.737	0.76 / 0.34	1.000	0.900
RT-DETR-L (Baseline)	0.786	0.586	0.868	0.705	0.75 / 0.63	1.000	0.920
RT-DETR-L (FT, Pat=5)	0.776	0.578	0.819	0.734	0.72 / 0.49	1.000	0.740
RT-DETR-L (FT, Pat=15)	0.785	0.579	0.859	0.710	0.74 / 0.49	1.000	0.830
SSD300 (Baseline)	0.562	0.317	0.591	0.534	0.66 / 0.03	0.967	0.668
SSD300 (Pat=5)	0.669	0.408	0.691	0.647	0.70 / 0.16	1.000	0.849
SSD300/512 (Pat=5)	0.687	0.404	0.671	0.703	0.69 / 0.15	0.999	0.836

Table 2.2: Performance comparison of two-stage detectors on the B16BL6 dataset.

Model	mAP@0.50	mAP@0.50:0.95	AP@0.50 (Cell)	AP@0.50 (Division)	Best F1 / Conf	Prec. (Peak)	Rec. (Peak)	FPS (E2E)
Faster R-CNN (Baseline)	0.787	0.566	0.816	0.758	0.80 / 0.54	0.992	0.875	12.78
Faster R-CNN (FT, Pat=5)	0.770	0.551	0.810	0.731	0.79 / 0.71	0.988	0.872	11.74
Mask R-CNN (Baseline)	0.769	0.552	0.811	0.727	0.80 / 0.70	0.986	0.868	5.98
Mask R-CNN (FT, Pat=5)	0.744	0.535	0.817	0.672	0.79 / 0.49	0.996	0.871	6.85
Libra R-CNN (Baseline)	0.761	0.554	0.789	0.733	0.78 / 0.20	0.993	0.844	12.34
Libra R-CNN (FT, Pat=5)	0.767	0.539	0.826	0.709	0.78 / 0.45	0.997	0.911	11.10

The findings indicate that YOLOv8x is the best model for detection accuracy, whereas YOLOv11-L is the best model for real-time processing since it provides the best balance between accuracy and inference speed. When class imbalance is a significant issue, multi-stage detectors are the most robust but have the slowest inference times. Conversely, SSD-based models are for situations when speed of inference is more important than accuracy. Collectively, these guidelines will help with determination of which types of detection models may work well within automated microscopy applications.

Thesis 2: Unified deployment-oriented comparison of 7 detectors.

I performed a unified, deployment-oriented benchmark of seven representative modern object-detection architectures for cell and division detection under a standardized experimental protocol. I implemented consistent data splits, preprocessing, and training settings to ensure fair comparison across one-stage, two-stage, and transformer-based detector families. Beyond reporting accuracy, I evaluated practical deployment criteria, including inference throughput and computational complexity, to characterize accuracy–efficiency trade-offs relevant to real laboratory workflows. My findings show that detector selection in microscopy should be guided not only by peak performance metrics but also by the operational constraints of the intended application, and they provide empirically grounded evidence that can inform and support deployment decisions in real-time and high-throughput settings.

For details on Thesis 2, see Chapter 4 of the dissertation.

Related paper: [J3].

2.3 Robust Tracking via Enhanced DeepSORT

Despite achieving strong framework performance through modern detectors in Section 2.2, there are still instances where they fail to detect an object due to temporary disruptions such as occlusions, overlapping cells, ambiguities at cell boundaries, and rapid cellular morphological change. Detection failure in time-lapse sequences creates gaps (or missing frames) within an object’s trajectory, leading to incomplete temporal histories of individual cells and compromised downstream analyses like monitoring cellular proliferation and the dynamics of cell division. This section therefore presents an integrated detection-tracking pipeline to address these limitations. The proposed pipeline is constructed by fine-tuning the YOLOv8x object-detection model and using the DeepSORT multi-object tracking algorithm with two modifications (replacing the conventional Kalman Filter with an Unscented Kalman Filter (UKF) for modeling non-linear cell motion and the development of a multi-scale ResNet50-based visual descriptor to improve appearance-based data association and reduce identity switches) [J2].

Table 2.3: Performance metrics measured on the B16BL6 dataset.

Model Name	Modified Recall	Average IoU	Detected Cells	Missed Cells	Time per Frame (s)
YOLOv8x (Original Model)	53.47%	77.82%	662	576	0.055
YOLOv8x (Fine-tuned Version)	85.95%	76.77%	1064	174	0.047
YOLOv8x (Fine-tuned) + Standard DeepSORT	90.71%	76.00%	1123	115	0.26
YOLOv8x (Fine-tuned) + Enhanced DeepSORT (UKF + ResNet50)	93.21%	76.73%	1154	84	8.5

The results in Table 2.3 clarify the role of temporal tracking in the proposed pipeline. Standard DeepSORT already provides a substantial improvement over the fine-tuned detector alone, increasing Modified Recall from 85.95% to 90.71% and reducing the number of missed cells from 174 to 115. The proposed enhanced DeepSORT pipeline then provides a further measurable gain, increasing

Modified Recall to 93.21% and reducing the number of missed cells to 84. These results show that temporal association itself is an important source of recovery under incomplete annotations, while the proposed UKF-based motion modeling and multi-scale appearance representation provide additional benefit beyond the standard tracking baseline. Since Modified Recall does not penalize false positives, these gains should be interpreted primarily as improved recovery of annotated objects and stronger temporal continuity rather than as a complete characterization of overall tracking quality. To further support these results, frame-sequence samples were published in [23], which qualitatively demonstrate the improved continuity of the proposed solution.

The integrated pipeline also reveals a clear performance complexity trade-off. Standard DeepSORT provides a favorable intermediate solution, whereas the enhanced DeepSORT variant incurs substantially higher computational cost, reaching an average processing time of 8.5 s per frame. Accordingly, the proposed enhanced pipeline is best suited to settings in which maximizing temporal recovery is more important than near-real-time execution.

Thesis 3: Temporal robustness in dense time-lapse sequences.

I developed a temporally robust detection-tracking framework designed to reduce fragmentation in dense time-lapse microscopy sequences. I integrated a high-performing detector with a tracking-by-detection pipeline and introduced targeted enhancements to improve temporal association under occlusions, overlap, and rapid morphology changes. By explicitly leveraging motion continuity and appearance consistency across consecutive frames, I demonstrated that temporal integration can recover missed detections that occur in framewise inference and can improve continuity across evaluated time-lapse sequences. In addition, the proposed enhancements provide additional measurable gains beyond standard DeepSORT

on the evaluated datasets. My results support the conclusion that reliable downstream temporal analysis requires more than strong per-frame detection, and that temporal modeling is an important component for applications such as proliferation monitoring and division dynamics.

For details on Thesis 3, see Chapter 5 of the dissertation.

Related paper: [J2] and [C1].

2.4 Domain Adaptation for Annotation Transfer

Deep learning detectors trained on microscopy data frequently fail to generalize across laboratories and acquisition setups due to *domain shift* (e.g., illumination polarity, texture, contrast, and background statistics). In phase-contrast microscopy, this issue is especially pronounced because subtle photometric differences can trigger systematic false positives (over-detection) or suppress true detections (under-detection). Manual re-annotation of each new dataset remains expensive and often infeasible.

This section presents an *unsupervised annotation transfer* framework based on CycleGAN, designed to reuse existing bounding-box annotations from a labeled source dataset (B16BL6) while adapting the visual appearance to an unlabeled target dataset (HeLa). The key idea is a *reverse-mapping* formulation that translates annotated source images into the target style so that the original labels remain geometrically valid and can be used directly for target-style training without manual relabeling. The main contribution is the detection-focused use of reverse mapping for annotation transfer, rather than the use of CycleGAN. The proposed methodology preserves spatial annotations, eliminating the need for pseudo-label refinement by restricting transformations to photometric changes via cycle-consistency and identity losses. The introduced unsupervised proxy measures and a composite reliability score to evaluate detection performance without target-domain ground truth, addressing practical constraints in microscopy. The framework is validated on cross-domain datasets of B16BL6 and HeLa cells acquired under different imaging conditions, demonstrating substantial improvements in detection reliability and annotation transfer fidelity.

Table 2.4: Performance metrics measured on the HeLa target dataset. Values are reported as mean $\pm$ SD. Higher *Composite* indicates better reliability.

Model	Mean Conf.	Median Conf.	Det. / Img.	Consensus	Box Area ($\times 10^{-3}$)	Composite
Bright B16BL6 (Baseline)	0.439 $\pm$ 0.18	0.41	85.7 $\pm$ 43.9	0.852	0.7 $\pm$ 0.4	0.726
Dark B16BL6 (Inverted)	0.577 $\pm$ 0.15	0.59	46.9 $\pm$ 12.4	0.485	0.8 $\pm$ 0.3	0.786
CycleGAN (B16BL6 $\rightarrow$ HeLa)	0.692 $\pm$ 0.12	0.77	46.4 $\pm$ 17.9	0.662	2.0 $\pm$ 0.6	0.933

Table 2.4 summarizes the performance of the proposed framework. The CycleGAN from B16BL6 to HeLa adaptation achieved the most realistic cell density (46.4 detections/image) and the highest confidence (0.69), resulting in a 28.5% higher composite score than the baseline (0.933 vs 0.726) and an 18.7% improvement over Dark B16BL6 (0.933 vs 0.786). A higher composite score indicates greater overall reliability by balancing over- and under-detection propensities. This achievement demonstrates that the proposed approach has successfully bridged the domain gap, enabling YOLOv8x to maintain high confidence, stable geometry, and realistic detection density on the unlabeled HeLa dataset.

Thesis 4: Cross-laboratory generalization with minimal labeling.

I proposed an unsupervised cross-domain generalization strategy that enables annotation transfer across laboratories and acquisition conditions without requiring target-domain ground truth. I implemented an annotation-preserving reverse-mapping approach in which labeled source-domain images are translated into target-domain appearance while maintaining geometric validity of bounding-box labels. I further designed proxy evaluation measures to assess target-domain detection reliability in unlabeled data, allowing principled comparison of adaptation configurations when standard supervised metrics are unavailable. My findings show that domain shift can be mitigated without costly manual re-annotation and provide practical evidence for annotation-efficient cross-domain deployment

in microscopy, as assessed through unsupervised proxy indicators and qualitative target-domain evaluation.

For details on Thesis 4, see Chapter 6 of the dissertation.

Related paper: [J4].

3 Conclusion of the dissertation

This dissertation presents an integrated approach to the conceptualization of scalable automation methods that are applicable to biomedical and biotechnological workflow processes dependent on time-lapse microscopy technologies. The mentioned theses centre on the development of one robust perception pipeline. The principal contributions of this dissertation are summarized as follows: (i) a standardized dataset preparation and annotation pipeline for dense microscopy analysis, including consistent class definitions, fixed splits, and a scalable three-stage labeling strategy suitable for detector training and evaluation; (ii) a unified evaluation of representative detector families under consistent protocols, reporting both accuracy and resource-oriented measures (speed and complexity) to support practical selection for microscopy applications; (iii) an enhanced DeepSORT-based tracking framework integrated with YOLOv8x, incorporating UKF motion modeling and multi-scale appearance embeddings to improve temporal continuity and reduce missed detections and identity drift; (iv) and finally a CycleGAN reverse-mapping strategy that preserves label geometry by translating annotated source images into target appearance, enabling target-style training without manual target-domain labeling.

Own publications

List of Own Publications Referred in the Dissertation

- [J1] **Al-Hamadani, M. N. A.**; Fadhel, M. A.; Alzubaidi, L.; Harangi, B. Reinforcement Learning Algorithms and Applications in Healthcare and Robotics: A Comprehensive and Systematic Review. *Sensors*, 24(8), 2461, 2024. ISSN: 1424-8220. <https://doi.org/10.3390/s24082461>. (**Q1; CiteScore: 9.4; IF: 4**).
- [J2] **Al-Hamadani, M. N. A.**; Poroszlai, R.; Szeman-Nagy, G.; Hajdu, A.; Hadjidemetriou, S.; Ferrarini, L.; Harangi, B. Improving Cell Detection and Tracking in Microscopy Images Using YOLO and an Enhanced DeepSORT Algorithm. *Sensors*, 25(14), 4361, 2025. ISSN: 1424-8220. <https://doi.org/10.3390/s25144361>. (**Q1; CiteScore: 9.4; IF: 4**).
- [J3] **Al-Hamadani, M. N. A.**; Szilágyi, P.; Szeman-Nagy, G.; Hajdu, A.; Harangi, B. B16BL6: A Public Time-Lapse Microscopy Dataset and Data-Centric Annotation Pipeline for Cell and Division Detection. *Array*, 30, 100946, 2026. ISSN: 2590-0056. DOI: <https://doi.org/10.1016/j.array.2026.100946>. (**Q1; CiteScore: 10.1; IF: 5.3**).
- [J4] **Al-Hamadani, M. N. A.**; Hadjidemetriou, S.; Szeman-Nagy, G.; Skourides, P. A.; Hajdu, A.; Harangi, B. Unsupervised Annotation Transfer in Phase Contrast Microscopy using a CycleGAN. *Sensors*, Under Revision, ISSN: 2590-0056. DOI: (**Q1; CiteScore: 9.4; IF: 4**).
- [J5] **Al-Hamadani, M. N. A.**; Harang, B. Deep Learning for Cell Detection and Tracking in Microscopy: A Systematic Review of Architectures, Benchmarks, and Emerging Applications in Biomedical Research. In Preparation
- [C1] **Al-Hamadani, M. N. A.**, Szilágyi, P., AlBurai K. I., and Harangi, B. Integrating Motorized Microscopy and YOLO-Based Deep Learning for Automated Cell Detection. In: *Proceedings of the 13th International Conference on Applied Informatics*, Eger, Hungary, 2026.

List of Own Publications not Referred in the Dissertation

- [J6] Fadhel, M. A.; Duham, A. M.; Saihood, A.; Sewify, A.; **Al-Hamadani, M. N. A.**; Albahri, A. S.; Alzubaidi, L.; Gupta, A.; Mirjalili, S.; Gu, Y. Comprehensive systematic review of information fusion methods in smart cities and urban environments. *Information Fusion*, 107, 102317, 2024. ISSN: 1566-2535; eISSN: 1872-6305. <https://doi.org/10.1016/j.inffus.2024.102317>. (**Q1/D1; CiteScore: 26.7; IF: 17.4**).
- [J7] **Al-Hamadani, M. N. A.** Classification and analysis of the MNIST dataset using PCA and SVM algorithms. *Vojnotehnicki glasnik*, 71(2), 221–238, 2023. <https://doi.org/10.5937/vojtchg71-42689>
- [J8] Ahmed, A. H.; **Al-Hamadani, M. N. A.**; Satam, I. A. Prediction of COVID-19 disease severity using machine learning techniques. *Bulletin of Electrical Engineering and Informatics*, 11(2), 1069–1074, 2022. ISSN: 2089-3191; eISSN: 2302-9285. <https://doi.org/10.11591/eei.v11i2.3272>. (**Scopus; Q3; CiteScore: 4.2**).
- [J9] Ahmed, A. H.; **Al-Hamadani, M. N. A.** Designing a secure campus network and simulating it using Cisco Packet Tracer. *Indonesian Journal of Electrical Engineering and Computer Science*, 19(1), 466, 2020. pISSN: 2502-4752, eISSN: 2502-4760 <http://doi.org/10.11591/ijeecs.v23.i1.pp479-489>. (**Scopus; Q3**).
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Registry number:
Subject:

DEENK/479/2026.PL
PhD Publication List

Candidate: Mokhaled N. A. Al-Hamadani
Doctoral School: Doctoral School of Informatics
MTMT ID: 10084564

List of publications related to the dissertation

Foreign language scientific articles in international journals (4)

1. **Al-Hamadani, M. N. A.**, Szilágyi, P., Szemán-Nagy, G., Hajdu, A., Harangi, B.: B16BL6: A public time-lapse microscopy dataset and data-centric annotation pipeline for cell and division detection.
Array. 30, 1-16, 2026. ISSN: 2590-0056.
DOI: <http://dx.doi.org/10.1016/j.array.2026.100946>
IF: 5.3 (2025)
2. **Al-Hamadani, M. N. A.**, Hadjidemetriou, S., Szemán-Nagy, G., Skourides, P. A., Hajdu, A., Harangi, B.: Unsupervised Annotation Transfer in Phase Contrast Microscopy using a CycleGAN.
Sensors. [Epub ahead of print], 1-12, 2026. ISSN: 1424-8220.
IF: 4 (2025)
3. **Al-Hamadani, M. N. A.**, Poroszlai, R., Szemán-Nagy, G., Hajdu, A., Hadjidemetriou, S., Ferrarini, L., Harangi, B.: Improving Cell Detection and Tracking in Microscopy Images Using YOLO and an Enhanced DeepSORT Algorithm.
Sensors. 25 (14), 1-15, 2025. ISSN: 1424-8220.
DOI: <http://dx.doi.org/https://doi.org/10.3390/s25144361>
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4. **Al-Hamadani, M. N. A.**, Fadhel, M. A., Alzubaidi, L., Harangi, B.: Reinforcement Learning Algorithms and Applications in Healthcare and Robotics: A Comprehensive and Systematic Review.
Sensors. 24 (8), 1-42, 2024. ISSN: 1424-8220.
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List of other publications

Foreign language scientific articles in international journals (9)

5. Fadhel, M. A., Duhaime, A. M., Saihood, A., Sewify, A., **Al-Hamadani, M. N. A.**, Albahri, A. S., Alzubaidi, L., Gupta, A., Mirjalili, S., Gu, Y.: Comprehensive systematic review of information fusion methods in smart cities and urban environments.
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6. **Al-Hamadani, M. N. A.**: Classification and analysis of the MNIST dataset using PCA and SVM algorithms.
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7. Ahmed, A. H., **Al-Hamadani, M. N. A.**, Satam, I. A.: Prediction of COVID-19 disease severity using machine learning techniques.
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8. Ahmed, A. H., **Al-Hamadani, M. N. A.**: Designing a secure campus network and simulating it using Cisco packet tracer.
IJECS. 23 (1), 479-489, 2021. ISSN: 2502-4752.
DOI: <http://dx.doi.org/10.11591/ijeecs.v23.i1.pp479-489>
9. Satam, I. A., Shahab, S. N., Kamel, H. A., **Al-Hamadani, M. N. A.**: Execution of a smart street lighting system for energy saving enhancement.
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10. **Al-Hamadani, M. N. A.**, Satam, I. A., Daoud, R. W., Shihab, S. N., Kamel, H. A.: Design and implement a self-managed computer network for electronic exams and sharing.
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11. Satam, I. A., **Al-Hamadani, M. N. A.**, Kamel, H. A.: Implementation of A Smart Neighborhood to Enhance Energy Consumption.
Solid State Technol. 63 (5), 7814-7823, 2020. ISSN: 0038-111X.
12. Satam, I. A., **Al-Hamadani, M. N. A.**, Ahmed, A. H.: Design and Implement Smart Blind Stick.
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13. Satam, I. A., **Al-Hamadani, M. N. A.**, Kamel, H. A.: A Review of Classification Production using Controlled Conveyor.

IJEEE. 5 (11), 9-11, 2018. EISSN: 2348-8379.

DOI: <http://dx.doi.org/10.14445/23488379/IJEEE-V5I11P102>

Total IF of journals (all publications): 32,3

Total IF of journals (publications related to the dissertation): 16,8

The Candidate's publication data submitted to the Tudóstér have been validated by DEENK on the basis of the Journal Citation Report (Impact Factor) database.

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