

PÁZMÁNY PÉTER CATHOLIC UNIVERSITY

Faculty of Information Technology and Bionics

ROSKA Tamás Doctoral School of Sciences and Technology



BÁNYAI Gréta Lilla

**Decoding cell migration – the impact of analytical choices
on biological interpretation**

Theses of the PhD Dissertation

Thesis Supervisor:

GARAY Tamás Márton, PhD

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INTRODUCTION

Cell migration is a fundamental biological process that plays a central role in embryonic development, tissue regeneration, immune surveillance, and pathological conditions such as cancer invasion and metastasis (Friedl and Gilmour, 2009; Shellard and Mayor, 2020). In malignant diseases, the migratory capacity of tumor cells critically determines their ability to disseminate from the primary tumor, invade surrounding tissues, and establish distant metastases, which are responsible for the majority of cancer-related deaths (Majidpoor and Mortezaee, 2022; Bergers & Fendt, 2021). Consequently, quantitative analysis of cell migration has become an essential component of experimental cancer research.

Cell migration emerges from the coordinated regulation of multiple molecular mechanisms, including cytoskeletal remodeling, dynamic regulation of cell-substrate adhesion, membrane receptor signaling, and force generation at the cell front and rear (Ridley et al., 2003). These molecular processes collectively determine two fundamental and partially independent components of migration: the speed of cell movement and the directional organization of cell trajectories (Shellard and Mayor, 2020). Importantly, these components are not necessarily regulated in parallel. Depending on the affected signaling pathways or pharmacological interventions, migration speed and directional persistence may change independently, resulting in complex and sometimes counterintuitive effects on cell migration (Weiger et al., 2013).

At the experimental level, cell migration can be investigated using a wide range of *in vitro* assay formats, each capturing different aspects of this multifaceted process.

Single-cell migration assays performed under low-density, two-dimensional conditions enable the analysis of autonomous cell movement. Despite the fact that this approach does not capture the structural and biochemical complexity of tissue environments encountered *in vivo*, its greatest advantage lies in the ability to investigate pure cell motility (along with the quantification of cell-intrinsic and morphological features) largely independent of confounding factors such as proliferation, cell-cell interactions, or mechanical constraints imposed by neighboring cells (Svensson et al., 2018).

Single-cell migration can be quantified using different tracking strategies, including manual, semi-automated, and fully automated approaches, each associated with specific advantages and limitations (Piccinini et al., 2016). While automated methods enable high-throughput analysis, they are sensitive to image quality, segmentation errors, and cell morphology, whereas manual tracking provides high accuracy at the expense of scalability. Once individual trajectories are obtained, a large number of quantitative migration parameters can be calculated. In the dissertation, these parameters were grouped into displacement-based, path-based, and directionality-related descriptors (Masuzzo et al., 2016; Svensson et al., 2018). Displacement-based parameters primarily capture long-range spreading capacity, path-based parameters reflect instantaneous movement characteristics such as velocity, and directionality-related metrics describe the organization and persistence of trajectories. As these parameter groups quantify distinct aspects of migration,

treatment-induced effects may manifest differently depending on which descriptors are selected. Consequently, analysis based on a limited parameter set may provide only a partial and potentially misleading view of migratory behavior.

Collective migration assays assess coordinated cell movement within a population context (Hohmann et al., 2022). Among these, gap-closure assays are widely used due to their technical simplicity. In the classical scratch assay, a confluent cell monolayer is mechanically disrupted, and migration is inferred from the dynamics of wound closure (Liang et al., 2007). However, this approach introduces several confounding factors, including cell damage, release of intracellular molecules, and exposure of matrix-bound proteins, all of which may influence migratory behavior independently of the applied treatment (Pijuan et al., 2019). In zone-exclusion assays cell-free areas are generated using physical barriers, such as silicone inserts, without damaging the cells. This approach yields more reproducible gap geometries and avoids injury-associated artifacts (Shiode et al., 2017). Nevertheless, in both gap-closure assays, closure dynamics are influenced not only by migration but also by proliferation and cell size. Importantly, cell size is rarely accounted for during data analysis, despite its direct impact on apparent closure rates (Pijuan et al., 2019).

Another commonly used migration assay is the transwell system, which introduces a directional component by allowing cells to migrate through porous membranes toward a chemoattractant and is therefore often considered a confined, semi-three-dimensional assay (Justus et al., 2014). This assay captures an additional aspect of migration that is not addressed by two-dimensional surface-based methods. At the same time, transwell assays are strongly influenced by cell size, deformability, and mechanical properties, making it difficult to disentangle true motility changes from altered physical constraints (Zaki et al., 2019). Moreover, transwell assays typically provide endpoint measurements, in contrast to the time-resolved information obtained from videomicroscopy-based approaches. As a result, changes in migration dynamics over time cannot be directly assessed.

Beyond these methods, three-dimensional migration models aim to approximate *in vivo*-like conditions by incorporating extracellular matrix components and spatial conditions; however, such systems were not the focus of this dissertation.

Finally, the increasing methodological diversity of migration assays and analytical frameworks poses a challenge for data interpretation and cross-study comparison. As different assays generate distinct and often non-overlapping sets of quantitative descriptors, direct comparison of results across experimental systems is frequently not feasible (Masuzzo et al., 2016). In this context, machine learning approaches offer promising tools for integrating heterogeneous datasets and identifying patterns that may not be apparent through conventional parameter-based analyses (Way et al., 2021).

OBJECTIVES

Cell migration can be analyzed through a wide range of experimental and computational approaches, each capturing distinct aspects of motility and reflecting specific biological mechanisms. This methodological diversity is both an advantage and a challenge: while it enables the investigation of migration from multiple perspectives, it also introduces substantial variability in data acquisition and interpretation. Beyond assay design, the analytical framework, particularly the selection and computation of migration parameters, has a profound influence on the observed outcomes. This is especially evident in single-cell tracking experiments, where numerous quantitative descriptors can be calculated, each sensitive to different aspects of cell behavior such as velocity, persistence, or morphological plasticity.

The overarching aim of this dissertation was to obtain a comprehensive understanding of how methodological and analytical choices influence the quantitative and biological interpretation of cell migration. Thus, the following research were performed:

- Evaluate the sensitivity, repeatability, and robustness of common migration descriptors using large-scale videomicroscopic datasets analyzed through multiple tracking strategies (manual, semi-automatic, and noise-filtered semi-automatic).
- Dissect the determinants of parameter variability through a two-dimensional random-walk simulation framework, systematically testing how controlled alterations in speed and directionality affect quantitative metrics.
- Investigate the relationship between intrinsic cell morphology and motility, by correlating cell line-specific morphological and behavioral descriptors to reveal how cell-specific features shape both migratory behavior and tracking performance.
- Compare the behavior and interpretational scope of different migration assays, including single-cell, scratch/zone-exclusion, and transwell assays, under pharmacological modulation with nintedanib in melanoma cells.
- Integrate findings across analytical levels to formulate methodological recommendations for the standardized and biologically meaningful evaluation of cell migration.

Rather than seeking a single optimal assay or descriptor, this work aims to establish an integrative framework illustrating how diverse experimental and computational perspectives collectively contribute to a more nuanced, context-aware understanding of cell motility in cancer research.

METHODS

This dissertation is based on the analysis of two complementary data collections addressing cell migration from distinct but interrelated perspectives.

The first dataset comprised a large collection of two-dimensional single-cell migration recordings, including multiple cell lines derived from different tumor types and subjected to a wide range of pharmacological treatments. This dataset was used to systematically investigate how commonly applied single-cell migration parameters relate to one another and how analytical choices influence quantitative outcomes. Single-cell trajectories were obtained from time-lapse videomicroscopy and analyzed using displacement-based, path-based, and directionality-related migration descriptors. For each parameter group, three representative metrics were calculated, including mean squared displacement, net displacement, and maximal displacement (displacement-based); total traveled distance, velocity, and average velocity (path-based); as well as directionality ratio, average turning angle, and turning vector zero crossing (directionality-based).

To disentangle biological effects from analytical artifacts, a random-walk simulation framework was implemented. This model provided a controlled, perturbation-free environment in which migration speed and directional persistence could be independently modulated, enabling a mechanistic interpretation of experimentally observed parameter behavior.

To assess the impact of tracking methodology on migration outcomes, the same single-cell datasets were analyzed using both manual and semi-automated tracking approaches. As semi-automated tracking is inherently affected by noise arising from intensity fluctuations and segmentation uncertainty, an additional noise-filtering step was applied to remove small, non-biological displacements. Migration parameters derived from manual, semi-automated, and noise-filtered semi-automated tracking were compared to evaluate parameter robustness and repeatability across methods. In addition, correlations between migration parameters and intrinsic cell line-specific features were examined, including cell size, cell number, coverage, and colonization-related descriptors, as well as multiple morphological features.

The second dataset consisted of experimental migration assays performed on human melanoma cell lines, designed to compare different *in vitro* migration assay formats under identical pharmacological conditions. In this dataset, the multikinase inhibitor nintedanib was applied as a model anti-migratory compound. Migration was assessed using complementary assay types, including 2D single-cell tracking, scratch assays generated by mechanical disruption of confluent monolayers, zone-exclusion assays using silicone inserts to create uniform cell-free gaps without cell damage, and transwell migration assays providing directional, endpoint-based readouts. Quantitative migration outcomes derived from these assays were directly compared to evaluate how assay format influences the apparent magnitude and interpretation of migration inhibition. In addition, machine learning-based classification approaches were applied to assay-derived feature sets to assess their ability to discriminate between treated and control conditions across experimental platforms.

NEW SCIENTIFIC RESULTS

I. THESES ON THE INVESTIGATION OF SINGLE-CELL MIGRATION PARAMETERS

- 1) I quantified how displacement- and path-based migration parameters respond to the same pharmacological perturbations and showed that they can exhibit opposite trends. I further demonstrated that, despite being derived from identical trajectories, these parameters may align more closely with other migration assay readouts than with each other, indicating that they capture mechanistically distinct facets of motility.

Across all tracking strategies applied in this work, we identified treatment conditions in which displacement-based and path-based migration parameters shifted in opposite directions relative to control (Figure 1). Importantly, these discordant responses were observed independently of the tracking method used, indicating that they do not arise from methodological noise but reflect underlying biological effects. Specifically, these patterns emerge when pharmacological perturbations differentially affect migration speed and directional persistence, two partially independent components of cell motility. Because path-based parameters primarily report changes in instantaneous movement intensity, whereas displacement-based parameters depend strongly on trajectory organization and directional persistence, treatments that slow cells while simultaneously stabilizing directionality can reduce path length yet increase net displacement. This decoupling has important biological implications. Under such conditions, cells may appear less motile when evaluated using path-based descriptors, while in fact retaining or even enhancing their ability to reach distant locations through straighter trajectories. In a physiological context, this could translate into more efficient access to vascular structures and increased dissemination potential, despite an apparent reduction in migration speed. These findings demonstrate that partial parameter reporting yields an incomplete and potentially misleading picture of migratory behavior and highlight the necessity of integrated parameter evaluation (Bányai et al., 2026).

Furthermore, we observed that the apparent magnitude and direction of migration changes inferred from individual single-cell parameters often showed closer agreement with outcomes obtained from other migration assay formats than with alternative descriptors derived from the same trajectories. This observation further underscores that migration parameters capture distinct facets of motility and that analytical choices critically shape biological interpretation (Bányai et al., 2026; Németh et al., 2025).

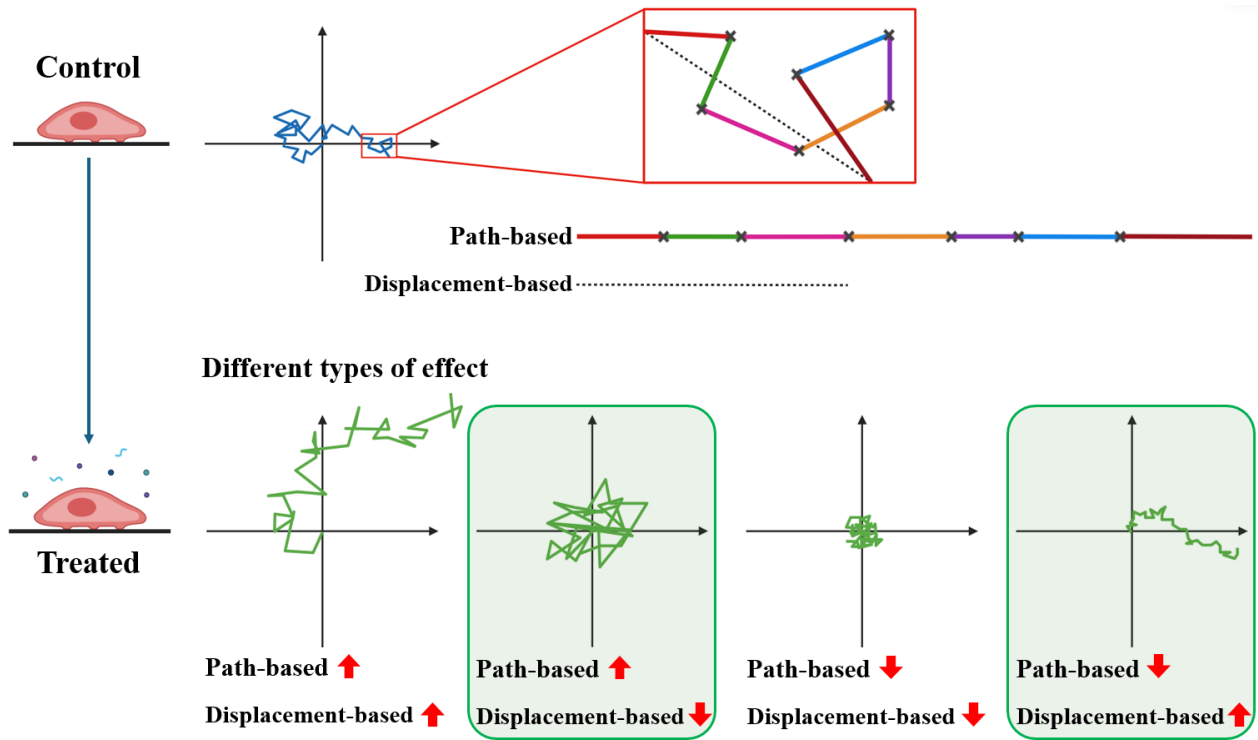


Figure 1. Conceptual illustration of migration parameter responses to differential regulation of speed and directional persistence, highlighting discordant cases

2) I systematically benchmarked the three major classes of migration parameters and identified a clear trade-off between sensitivity and robustness across all parameter groups.

Systematic comparison of displacement-based, path-based, and directionality-related migration parameters revealed clear trade-offs between sensitivity and robustness. Path-based metrics were the most responsive to treatment-induced changes and, therefore, well-suited for detecting subtle effects, but this sensitivity was accompanied by pronounced susceptibility to tracking noise and evaluation strategy. Displacement-based parameters showed the highest robustness; among these, maximal displacement exhibited intermediate behavior, being less affected by semi-automated tracking noise than path-based metrics while remaining sensitive enough to detect even modest treatment-induced effects compared to other displacement-based descriptors. In contrast, directionality-related parameters showed limited reliability under non-directed migration conditions, with the directionality ratio retaining the highest explanatory value within this group.

Together, these findings demonstrate that parameter choice inherently incorporates a balancing between responsiveness and robustness and must be aligned with both the biological question and the analytical context rather than applied in a one-size-fits-all manner (Bányai et al., 2026).

- 3) I analyzed the impact of intrinsic cellular properties, including morphology, confluency, local cell density, and coverage, and showed that these factors substantially influence both the magnitude and variability of migration parameters. I further demonstrated that they differentially affect manual and semi-automatic tracking outputs.

Correlation analysis revealed that cell-intrinsic morphological features are major biological sources of variability in migration quantification. Larger and more elongated cells consistently exhibited higher net displacement and more effective movement, whereas round, highly solid, and colony-forming phenotypes displayed reduced motility and lower directional persistence. These relationships reflect established links between cell shape, cytoskeletal organization, and migration mode (e.g.: amoeboid, epithelial) and indicate that migration parameters inherently encode morphological state rather than pure movement alone (Bányai et al., 2026).

Beyond their biological impact, intrinsic cell features also shaped tracking precision and reproducibility. Round, low-motility cells generated larger discrepancies between manual and semi-automatic tracking due to segmentation-related jitter, whereas elongated cells provided clearer morphological landmarks and yielded more robust trajectories across methods. Importantly, noise filtering largely eliminated these morphology-dependent discrepancies. Under treatment conditions, cell number and coverage emerged as dominant contributors to residual variability, highlighting that tracking robustness depends on both cellular phenotype and experimental protocol (Bányai et al., 2026).

II. THESES ON THE CROSS-ASSAY BENCHMARKING OF MIGRATION

- 4) I compared gap-closure assay formats and showed that their outcomes are strongly influenced by assay type and intrinsic cellular properties. I further demonstrated that migration-related readouts are particularly sensitive to cell size and that scratch and zone-exclusion assays exhibit distinct closure dynamics.

Benchmarking of gap-closure assays revealed that apparent differences in collective migration often arise from assay-specific geometric and mechanical constraints rather than intrinsic motility. In scratch assays, irregular wound geometry and mechanically induced cellular damage resulted in substantial variability and accelerated closure dynamics, along with pronounced sensitivity to cell size and morphology. In contrast, zone-exclusion assays provided a more standardized collective migration readout, in which normalization to cell size only minimally alter the relative ranking of cell lines based on their migration speed. These findings demonstrate that gap-closure assays differ fundamentally in what aspect of migration they emphasize and that assay choice critically determines whether collective mechanics or intrinsic migratory behavior dominates the readout (Németh et al., 2025).

- 5) I evaluated transwell assays across multiple cell lines and showed that they produce the largest divergence in apparent migratory behavior among assay formats. I further demonstrated that pharmacological treatments can, under certain conditions, increase apparent migration through treatment-induced changes in cell size and morphology.

Comparison with surface-based migration assays showed that transwell measurements diverged most strongly from other formats, reflecting their unique dependence on cell size, shape, and mechanical adaptability during pore traversal. Under pharmacological inhibition, apparent increases in transwell migration could arise despite reduced motility, indicating that treatment-induced morphological changes can facilitate membrane passage independently of migratory capacity. As transwell assays integrate motility with confinement-dependent mechanical filtering and provide only endpoint information, their readouts represent a composite migration pattern rather than a direct measure of migration speed or persistence (Németh et al., 2025).

- 6) I demonstrated that single-cell tracking provides the most informative and mechanistically interpretable assessment of drug effects by capturing both motility parameters and cell-intrinsic morphological features. When combined with machine-learning analysis (performed in collaboration with Dr. Csaba Köllöd), this approach achieved the highest discriminatory power among all investigated assay formats.

Among all evaluated assay formats, single-cell tracking yielded the most interpretable representation of treatment-induced migration changes by enabling simultaneous quantification of motility and cell-line specific features. Because cells migrate in isolation, these assays preserve shape- and size-related information that is distorted or lost in collective or confined formats. Integration of single-cell-derived features into machine-learning classifiers resulted in the highest accuracy for distinguishing treated and control conditions, highlighting that assay sensitivity

depends not on a single migration metric, but on the ability to capture multidimensional phenotypic changes (Németh et al., 2025).

These assay- and parameter-dependent differences are summarized in Figure 2, which illustrates how the relative migratory ranking of melanoma cell lines varies across experimental formats and single-cell descriptors.

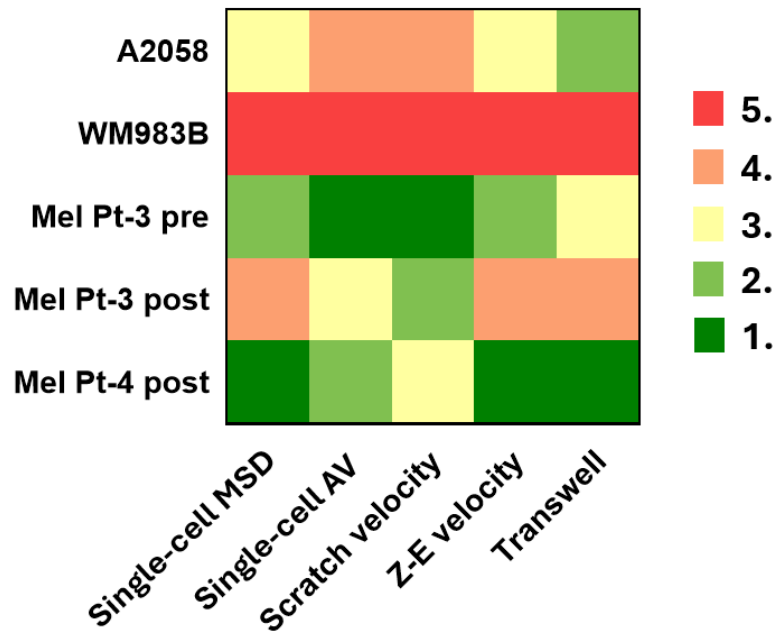


Figure 2. Divergent migration rankings across assays and single-cell parameter choices

METHODOLOGICAL IMPLICATIONS AND PRACTICAL CONSIDERATIONS

The primary aim of this work was to systematically evaluate how different migration assays and quantification strategies influence the interpretation of cell motility under identical biological perturbations. Beyond direct performance comparison, we sought to provide a practical framework for the field by clarifying assay-specific strengths, limitations, and sources of bias. The summary below condenses the core experimental and computational findings of this dissertation into guidance intended to support informed assay selection, parameter choice, and result interpretation.

Migration assay		Key strengths	Key limitations	Recommended use
Single-cell migration		Captures pure motility and cell-intrinsic features, enabling robust and interpretable separation of treatment effects when analyzed integratively	Labor- and data-intensive; limited scalability	Precise dissection of drug effects at the single-cell level
Parameter class (single-cell migration)	Displacement-based	Robust across tracking methods; low sensitivity to noise	Insensitive to subtle effects; morphology-dependent	Cross-experimental comparison: assessing net migratory capacity
	Path-based	Highly sensitive to perturbations; captures the dynamics of motility	Noise-sensitive; strongly tracking-dependent	Detecting weak treatment effects; analyzing motility dynamics
	Directionality-based	Explains trajectory organization and discordant readouts	Low sensitivity; difficult to interpret alone	Mechanistic interpretation of treatment effects
Scratch assay		Simple, rapid setup; high apparent closure dynamics	High variability in gap geometry; wounding-induced paracrine effects; strong cell-size dependence	Preliminary screening and high-throughput applications, with careful interpretation and cell-size normalization
Zone-exclusion assay		Uniform, reproducible gaps; minimal cell damage	Slower closure; cell-line-dependent sensitivity	Controlled collective migration studies with critical reproducibility
Transwell assay		Captures chemotaxis and migration under confinement	Strongly morphology- and size-dependent; endpoint readout	Chemotaxis- or invasion-focused studies, interpreted alongside morphological data

Table 1. Practical considerations for migration assays and parameter selection

LIST OF PUBLICATIONS

Journal publications of the thesis:

- 1) Bányai, G. L., Naszlady, M. B., Juhász, J., Horváth, A., Hegedűs, B. & Garay, T. (2026). Revisiting single-cell migration parameters from 2D video microscopic measurements. *European Journal of Cell Biology*, 105, 151524.
- 2) Németh, A., Bányai, G. L.*, Andrászek, M., Dobos, N. K., Köllöd, C., Garay, T. (2025). Comparison of in vitro migration assays evaluating nintedanib's migration inhibitory effects on melanoma cells. *Scientific Reports*, 15, 42599.

Further journal publications:

- 1) Németh, A., Ekström, K., Crescitelli, R., Bagge, R. O., Bányai, G. L., Rák, Á., Cserey, G., Bölükbas, S., Visnovitz, T., Hegedűs, B., Garay, T. Machine learning-enhanced analysis of extracellular vesicle profiles in pleural effusions for cancer diagnosis. *MedComm – Under revision*.
- 2) Németh, A., Bányai, G. L., Dobos, N. K., Kós, T., Gaál, A., Varga, Z., Buzás, E. I., Khamari, D., Dank, M., Takács, I., Szász, A. M., Garay, T. (2024). Extracellular vesicles promote migration despite BRAF inhibitor treatment in malignant melanoma cells. *Cell Communication and Signaling*, 22(1), 282. <https://doi.org/10.1186/s12964-024-01660-4>
- 3) Jász, B., Balogh, T., Ambrus, S., Schmidt, P., Bányai, G. L., Körmendi, S., Jász, M. (2024). Pure rotation in the temporomandibular joint during jaw opening? A digital motion analysis. *BDJ Open*, 10(1), 32. <https://doi.org/10.1038/s41405-024-00213-8>

Proceedings papers:

- 1) Bányai, G. L. (2025). Exploring diffusion-driven variations in extracellular vesicles from cancer patients using microfluidic systems. *PhD Proceedings – Annual Issues of the Doctoral School, Faculty of Information Technology and Bionics*, 20, 23–26.
- 2) Bányai, G. L. (2024). Exploring the correlation between migration parameters and cell characteristics. *PhD Proceedings – Annual Issues of the Doctoral School, Faculty of Information Technology and Bionics*, 19, 23–26.
- 3) Bányai, G. L. (2023). Comparison of commonly used single-cell migration parameters. *PhD Proceedings – Annual Issues of the Doctoral School, Faculty of Information Technology and Bionics*.
- 4) Bányai, G. L. (2022). Quantitative analysis of single-cell trajectories. *PhD Proceedings – Annual Issues of the Doctoral School, Faculty of Information Technology and Bionics*, 17, 17.

Conference posters:

- 1) Bányai, G. L., Merényi, A., Szabó, A., Németh, A., Gaál, A., Pongor, C., Garay, T. (2025). Utilizing microfluidic techniques to differentiate cancer patient samples based on extracellular vesicle profiles. ISEV2025, Vienna, Austria.
- 2) Németh, A., Ekström, K., Crescitelli, R., Bagge, R. O., Bányai, G. L., Rák, Á., Cserey, G., Bölükbas, S., Visnovitz, T., Hegedűs, B., Garay, T. (2025). Diagnostic potential of pleural fluid-derived extracellular vesicles in differentiating pleural-associated diseases using machine learning. ISEV2025, Vienna, Austria.
- 3) Németh, A., Kós, T., Bányai, G. L., Gaál, A., Varga, Z., Dank, M., Takács, I., Szász, A. M., Garay, T. (2022). Effects of extracellular vesicles on vemurafenib sensitivity in syngeneic melanoma cell lines. ISEV2022, Lyon, France.
- 4) Németh, A., Kós, T., Bányai, G. L., Gaál, A., Varga, Z., Dank, M., Takács, I., Szász, A. M., Garay, T. (2022). Can extracellular vesicles transmit vemurafenib resistance in melanoma cells in vitro? EACR Congress 2022, Seville, Spain.
- 5) Bányai, G. L., Dobos, N. K., Németh, A., Merényi, A., Szabó, A., Gaál, A., Pongor, C., Garay, T. (2025). Microfluidic profiling of extracellular vesicle fractions reveals systemic changes in cancer patients. HSEV2025, Budapest, Hungary.
- 6) Bányai, G. L., Merényi, A., Szabó, A., Gaál, A., Pongor, C., Garay, T. (2025). Identifying tumor-associated differences in extracellular vesicle populations using microfluidic techniques. Semmelweis Scientific Days 2025, Budapest, Hungary.
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- 9) Bányai, G. L., Szabó, A., Gaál, A., Pongor, C., Merényi, A. G., Garay, T. (2024). Advancing extracellular vesicle characterization: Microfluidic approaches for cancer diagnostics. UKEV2024, Newcastle upon Tyne, United Kingdom.
- 10) Bányai, G. L., Szabó, A., Gaál, A., Pongor, C., Kós, T., Garay, T. (2024). Microfluidic-based methods for the analysis of extracellular vesicles in liquid biopsies. HSEV, Budapest, Hungary.
- 11) Kvasznicza, J., Magyar, R., Bányai, G. L., Szőcs, L., Németh, A., Garay, T. (2024). Cyclodextrins affect extracellular vesicle production in melanoma cells in vitro. HSEV2024, Budapest, Hungary.

- 12) Németh, A., Bányai, G. L., Dobos, N. K., Kós, T., Gaál, A., Varga, Z., Buzás, E. I., Khamari, D., Dank, M., Takács, I., Szász, A. M., Garay, T. (2024). Extracellular vesicles promote migration despite BRAF inhibitor treatment. HSEV2024, Budapest, Hungary.
- 13) Bányai, G. L., Naszlady, M. B., Juhász, J., Garay, T. (2024). Analysis of migration parameter sensitivity. Applied Mathematics Conference (AMK), Szeged, Hungary.
- 14) Bányai, G. L., Szabó, A., Gaál, A., Pongor, C., Kós, T., Garay, T. (2023). Microfluidics as a tool for analyzing the size distribution of plasma-derived microsomal fractions. ASEV – Small New World 2.0, Graz, Austria.
- 15) Choi, J., Görög, D., Gaál, A., Khamari, D., Buzás, E. I., Németh, A., Garay, T., Bányai, G. L. (2023). Investigating the effects of extracellular vesicles on proliferation and migration in syngeneic colorectal cancer cell lines. ASEV – Small New World 2.0, Graz, Austria.
- 16) Németh, A., Bányai, G. L., Dobos, N. K., Kós, T., Gaál, A., Varga, Z., Szász, A. M., Garay, T. (2023). Extracellular vesicles can promote migration and transfer vemurafenib resistance among melanoma cells. ASEV – Small New World 2.0, Graz, Austria.
- 17) Kvasznicza, J., Magyar, R., Bányai, G. L., Rohan, Z., Szócs, L., Németh, A. (2023). Cyclodextrins affect extracellular vesicle production in melanoma cells in vitro. ASEV – Small New World 2.0, Graz, Austria.
- 18) Bányai, G. L., Naszlady, M. B., Németh, A., Molnár, E., Rittler, D., Hegedűs, B., Garay, T. (2022). Is an increase or decrease in cell migratory activity merely a consequence of parameter selection? Semmelweis Symposium 2022, Budapest, Hungary.
- 19) Németh, A., Bányai, G. L., Dobos, N. K., Kós, T., Gaál, A., Varga, Z., Buzás, E. I., Khamari, D., Dank, M., Takács, I., Szász, A. M., Garay, T. (2022). Extracellular vesicles in vemurafenib resistance in melanoma cells. Semmelweis Symposium 2022, Budapest, Hungary.

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