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Cost-Benefit Analysis of Custom Image Analysis Tools in Oncology Research

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Abstract— Digital pathology and artificial intelligence have expanded the capacity of oncology researchers to extract quantitative information from histopathological images, yet the economic implications of developing customized analytical tools remain insufficiently characterized. This study addresses the gap between algorithmic performance evaluation and the practical financial sustainability of custom oncology image-analysis pipelines. A techno-economic framework is conceptualized to compare custom-built image-analysis systems with manual analysis and license-dependent commercial workflows across different research volumes. The framework integrates development expenditure, annotation effort, computational utilization, maintenance, processing throughput, analyst involvement, reproducibility, and expected cost per successfully processed specimen. Rather than treating predictive accuracy as the sole measure of utility, the proposed approach introduces a benefit-adjusted cost perspective in which technical performance and operational efficiency are assessed simultaneously. Publicly accessible histopathology resources and a controlled simulation-based workflow are proposed to support reproducible comparisons without attributing unverified economic outcomes to particular commercial products.

Keywords— Digital Pathology, Oncology Research, Image Analysis, Cost-Benefit Analysis, Artificial Intelligence, Computational Pathology

Introduction

The digital transformation of cancer research has altered the role of medical images from primarily visual records to high-dimensional computational data sources. Histopathological whole-slide images, radiological scans, fluorescence microscopy, multiplex imaging, and other image modalities can now be processed through algorithms capable of detecting tumour regions, segmenting cells, quantifying tissue architecture, estimating biomarker expression, and deriving representations associated with diagnosis or prognosis. In computational pathology in particular, deep learning has enabled information to be extracted from routinely generated tissue images at a scale that is difficult to achieve through manual examination alone.

The technical potential of this transition is substantial. Digital pathology algorithms have been investigated for tumour identification, classification, grading, molecular alteration prediction, prognosis and treatment-related biomarker analysis. A systematic review and meta-analysis published in *npj Digital Medicine* in 2024 reported high pooled diagnostic sensitivity and specificity among investigated artificial-intelligence systems, although the authors also emphasized substantial methodological heterogeneity and frequent risks of bias or applicability concerns in the underlying literature. These observations illustrate an important distinction: strong model performance in an experimental publication does not automatically demonstrate that a system is economically advantageous, maintainable, reproducible, or practical for an oncology laboratory.

Recent advances have further changed the economics of computational pathology. Earlier approaches frequently depended on manually annotated datasets and models developed separately for individual cancer types or analytical objectives. More recent self-supervised and foundation-model approaches can generate reusable image representations from large collections of pathology images, potentially reducing the amount of task-specific labelled data required for downstream applications. Studies involving models such as UNI and Virchow have demonstrated the feasibility of general-purpose feature representations and pan-cancer modelling across heterogeneous histopathology data. Foundation-model research therefore creates an opportunity not only to increase predictive performance but also to reconsider how custom image-analysis software is developed, reused, adapted and economically evaluated.

Nevertheless, the decision facing an oncology research group is rarely limited to the question of which algorithm produces the highest accuracy. Laboratories must choose among manual quantification, general-purpose open-source software, internally developed scripts, customized machine-learning pipelines, cloud-based analytical services and commercial image-analysis platforms. Each alternative creates a different combination of fixed and variable costs.

An internally developed system might eliminate recurrent licensing expenditure but require substantial initial engineering time. A commercial platform can shorten deployment time while creating continuing subscription or licensing costs. Manual analysis can require little software development but becomes labour intensive as image volume increases.

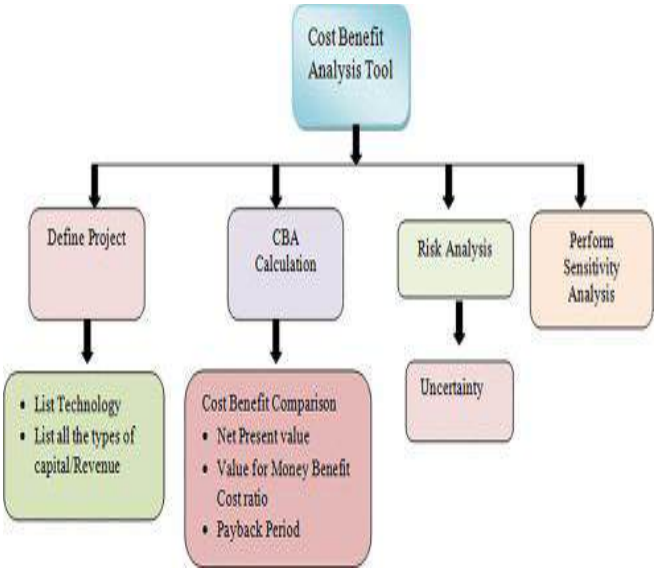


Fig. 1: Cost Benefit Analysis Tool

Source:
https://www.sciencedirect.com/topics/engineering/cost-benefit-analysis

Consequently, a tool that appears inexpensive for 100 images may become inefficient for 10,000 images, while a custom system with a substantial initial development cost might become economically attractive after repeated use across sufficiently large datasets. Maintenance, software dependencies, model retraining, hardware utilization, storage, quality assurance and staff training further complicate this comparison.

1.1 Research Gap

A notable asymmetry therefore exists in contemporary oncology image-analysis research. Considerable attention is devoted to metrics such as area under the receiver-operating-characteristic curve, sensitivity, specificity, Dice coefficient and classification accuracy, whereas considerably less research combines these technical outcomes with the complete lifecycle economics of developing and operating a custom analytical pipeline.

Existing implementation discussions acknowledge financial viability, regulatory constraints, workflow integration and infrastructure as important considerations. For example, analyses of artificial intelligence in digital pathology have emphasized that image acquisition, storage, quality control, integration and continuing workflow adaptation must all be considered when digital pathology is implemented. More recent evaluations likewise argue that technological progress must be examined alongside deployment, implementation, reimbursement and commercial considerations.

However, these discussions generally do not provide a reusable analytical structure that connects image-processing performance to cost per analysed case, analyst hours saved, break-even workload, pipeline reuse and maintenance burden in an oncology research environment.

The principal research gap addressed in the present manuscript is therefore **the absence of an integrated technical-economic framework for determining the workload conditions under which a custom oncology image-analysis pipeline becomes more economically efficient than manual or license-dependent analytical alternatives while maintaining acceptable analytical performance and reproducibility.**

Rather than merely asking whether artificial intelligence can analyse cancer images accurately, this study asks a more operational question:

At what research volume, automation level and reuse frequency does investment in a customized oncology image-analysis pipeline become economically justified?

1.2 Research Objective and Contribution

The primary objective is to develop a reproducible cost-benefit model for evaluating custom image-analysis tools used in oncology research. The proposed analysis will simultaneously consider initial development expenditure, annotation requirements, computing cost, researcher supervision, processing throughput, recurring maintenance, error-related reprocessing and analytical performance.

A secondary objective is to determine whether the economic advantage of customization changes according to study scale. Instead of assuming a universal advantage for either proprietary or internally developed systems, the study treats image volume as a principal decision variable and examines small-, medium- and large-cohort scenarios.

The conceptual contribution is the introduction of a **Benefit-Adjusted Analysis Cost** indicator in which the cost of processing an oncology image dataset is normalized by successful analytical yield and technical quality. This distinction is important because the least expensive pipeline is not necessarily beneficial when unsuccessful segmentation, quality-control failure or extensive manual correction increases effective project expenditure.

The study additionally incorporates a **break-even image volume**, representing the cumulative number of cases at which savings generated through automation offset the fixed

cost of developing the custom pipeline. This makes the framework suitable for research-management decisions and not merely algorithm comparison.

Literature Review

2.1 Digital Image Analysis in Contemporary Oncology

Histopathology has traditionally depended on expert visual interpretation of tissue architecture, cellular morphology and staining patterns. Digital pathology extends this process by converting glass slides into high-resolution digital images that can be computationally stored, transmitted and analysed. Machine-learning algorithms subsequently provide mechanisms for detecting patterns that may be difficult or impractical to quantify consistently through visual examination.

Artificial intelligence applications within tumour pathology encompass diagnosis, tumour subtype classification, grading, prognosis, biomarker assessment and molecular-feature prediction. Earlier reviews described how machine-learning and deep-learning systems could augment pathological interpretation by extracting quantitative morphological information and combining it with clinically meaningful endpoints. Deep-learning research has also demonstrated that digitized pathology can support cancer classification while opening opportunities for graph-based representations and other approaches capable of modelling relationships between cells and tissue structures.

2.2 From Task-Specific Networks to Reusable Image Representations

A traditional supervised deep-learning workflow commonly requires manually labelled examples for the specific task under investigation. Annotation can be expensive because pathology labels often require domain expertise. Furthermore, algorithms trained on one institution, scanner, staining protocol or population can exhibit performance degradation when applied to different data distributions.

The development of self-supervised learning and foundation models has begun changing this development model. Instead of training every oncology model from an initial random state, researchers can derive representations from models pretrained on extensive pathology collections. Chen et al. developed UNI as a general-purpose self-supervised computational pathology model and evaluated it across multiple downstream diagnostic and computational tasks.

Similarly, Vorontsov et al. reported Virchow, a pathology foundation model evaluated for applications including pan-cancer detection, biomarker prediction and cell identification. Their findings indicated that foundation-model representations could support competitive performance with reduced amounts of downstream training data in some settings. Related work published in *Nature* further demonstrated the expanding role of pathology foundation models for diagnostic and prognostic prediction across cancer tasks.

From an economic perspective, this transition is significant. The ability to reuse pretrained feature extractors might reduce annotation, training and development requirements for custom tools. At the same time, larger models can increase computational and storage demands. Hence, technical advances do not necessarily reduce total costs uniformly; rather, they redistribute costs across annotation, engineering, hardware and inference stages.

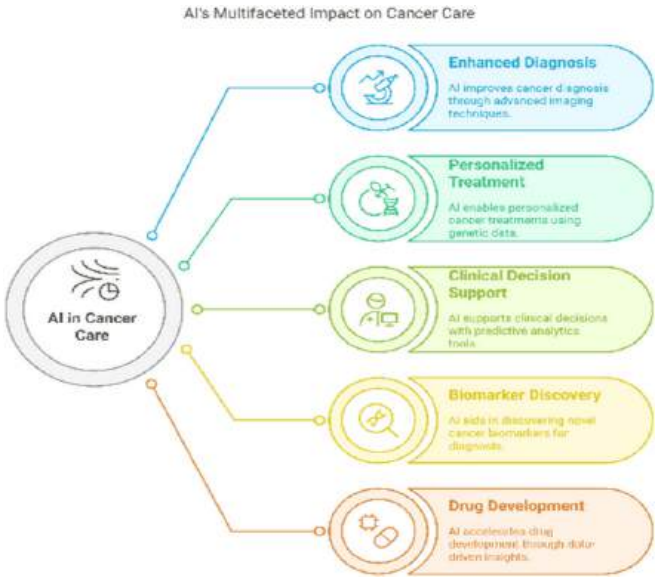


Fig. 2: AI's Multifaceted Impact on Cancer Care

Source: https://link.springer.com/article/10.1186/s12943-025-02369-9

2.3 Hidden Costs of Custom Tool Development

Custom analytical software is often described as economically attractive because open-source programming languages and machine-learning libraries can be obtained without conventional licensing charges. This interpretation is incomplete. The absence of a license fee does not imply the absence of cost.

A realistic lifecycle includes algorithm design, dataset preparation, image annotation, preprocessing development, debugging, training, validation, documentation, deployment and subsequent maintenance. Personnel costs can be especially important where data scientists, software engineers, pathologists and research assistants contribute simultaneously.

Computational pathology creates additional infrastructure requirements. Whole-slide images require substantial storage and processing resources, and model training can depend on accelerator hardware. Image pipelines may also require reprocessing when slides contain scanning artefacts,

inadequate tissue regions, staining variation or incompatible file formats.

Implementation literature has consequently highlighted data availability, model generalizability, explainability and workflow integration as barriers to translating experimental artificial intelligence into routine pathology. Resource-constrained health systems face additional obstacles associated with digitization infrastructure, skilled personnel and sustainable technology deployment.

Thus, a rigorous cost-benefit model must consider hidden engineering and operational expenditure rather than comparing software acquisition prices alone.

2.4 Manual, Commercial and Custom Analytical Paradigms

Manual image assessment remains important in oncology research because expert review can incorporate morphological context that is difficult to encode algorithmically. Its major economic limitation, however, is that labour cost scales approximately with the number of images and annotations required. Repeated quantitative measurements can also introduce inter-observer variation and reduce throughput.

Commercial image-analysis systems attempt to address these limitations through established interfaces, technical support, validated modules and workflow integration. Their economic burden may include licensing, subscription, additional analytical modules, storage or infrastructure expenses. Because commercial agreements vary across institutions, a generalizable scientific cost analysis should avoid assuming a universal market price.

Custom systems exhibit the opposite cost structure. Development expenditure is concentrated near the beginning of the project, whereas automated processing can reduce marginal cost once the pipeline becomes sufficiently stable. Customization also offers advantages where researchers require unconventional biomarkers, specialized segmentation rules or experimental endpoints unavailable in standardized software.

2.5 Performance Evaluation Without Economic Context

Most AI imaging studies emphasize discriminative or segmentation performance. For classification problems, commonly reported measures include accuracy, sensitivity, specificity and AUROC. Segmentation studies frequently rely on Dice similarity or intersection-over-union measurements. These metrics remain scientifically essential but do not quantify operational value.

The 2024 meta-analysis by McGenity et al. demonstrated both the promise and the evaluation limitations of existing digital-pathology AI studies. Although reported diagnostic performance was generally high, study heterogeneity and methodological quality remained important concerns. This reinforces the need to evaluate more than headline model accuracy.

For research laboratories, an algorithm achieving a marginal improvement in predictive performance may not be preferable if it requires substantially greater GPU time, annotations and specialist intervention. Conversely, a moderately less complex model could produce greater overall research value if its measurements remain reproducible while reducing processing time and cost.

This study therefore conceptualizes value as:

Research Value = Analytical Quality + Reproducibility + Time Savings + Reusability − Lifecycle Cost

This formulation shifts evaluation from an accuracy-centred paradigm toward an efficiency-centred framework.

Proposed Methodology

This study adopts a **technical-economic benchmarking framework** to determine whether developing a customized image-analysis pipeline can provide sufficient operational and scientific benefit to justify its lifecycle expenditure in oncology research. Unlike conventional studies that compare algorithms only through diagnostic accuracy, the proposed framework evaluates three competing analytical strategies simultaneously: manual image assessment, a license-dependent software workflow represented through a configurable cost scenario, and a custom artificial-intelligence pipeline.

The analysis is structured around the premise that custom software has relatively high fixed costs but comparatively low marginal processing costs. Manual analysis has the opposite structure: implementation expenditure is limited, while personnel expenditure rises almost linearly with the number of images. Commercial systems occupy an intermediate position because deployment may be rapid, but recurring license, support, or usage expenditure can persist throughout the project.

To avoid presenting institution-specific commercial quotations as universal prices, all financial calculations use **Normalized Cost Units (NCU)**. One NCU represents a standardized unit of institutional resource expenditure and can subsequently be converted into local currency by an individual laboratory. Development labour, expert review, computing, storage, quality assurance and maintenance are weighted according to predefined scenario coefficients.

Total lifecycle cost for analytical strategy (j) is defined as:

$$\left[TLC_j = F_j + \left(V_j \times N\right) + M_j + Q_j + R_j\right]$$

where:

- (F_j) = initial fixed implementation or development cost,
- (V_j) = variable processing cost per image,
- (N) = number of whole-slide images,
- (M_j) = maintenance expenditure,
- (Q_j) = quality-control expenditure, and
- (R_j) = expected cost of reprocessing or corrective intervention.

Because a low-cost system that frequently generates unusable outputs cannot be considered economically efficient, an **Effective Analysis Cost (EAC)** is calculated as:

$$\left[EAC_j = \frac{TLC_j}{N \times S_j}\right]$$

where (S_j) is the proportion of images that successfully pass technical and analytical quality control.

A second measure, the **Performance-Adjusted Economic Utility (PAEU)**, combines successful analytical yield, discrimination performance and workload reduction:

$$\left[PAEU_j = \frac{AUC_j \times S_j \times (1 - H_j)}{EAC_j}\right]$$

where (H_j) represents normalized human-intervention burden. Higher values indicate greater analytical benefit per unit cost.

Finally, the **break-even volume** for the custom tool is calculated by comparing its fixed development cost with the cumulative difference in per-image cost relative to the comparator:

$$\left[N_{BE} = \frac{F_{Custom} - F_{Comparator}}{V_{Comparator} - V_{Custom}}\right]$$

This approach enables laboratories to evaluate whether software customization is economically appropriate at different project scales.

Experimental Setup

4.1 Dataset

The principal benchmarking resource is the **CAMELYON16 dataset**, selected because it provides a publicly documented whole-slide histopathology task relevant to breast oncology and contains reference annotations suitable for lesion-level evaluation. The official challenge dataset contains **400 hematoxylin-and-eosin-stained sentinel lymph-node whole-slide images**, comprising 270 development/training images and an independent set of 130 test slides. Tumour-containing training slides include XML contour annotations and binary reference masks.

The task is automated detection of lymph-node metastases in breast cancer, making the dataset suitable for simultaneously examining classification performance, lesion localization, processing burden and expert-review requirements.

For scalability analysis, the experimentally observed resource requirements are projected to virtual study volumes of 250, 500, 1,000, 2,500, 5,000 and 10,000 slides. These expanded workload scenarios do **not** represent additional patients. They are economic simulations used solely to estimate how repeated utilization changes lifecycle cost.

As an external-transfer scenario for future validation, TCGA-BRCA is considered appropriate because the NCI Genomic Data Commons makes diagnostic and tissue whole-slide images available in SVS format, and its current documentation explicitly supports pathology-image exploration for TCGA-BRCA cohorts.

4.2 Image Preprocessing

Whole-slide images are first screened for file integrity and readable pyramid levels. A low-resolution thumbnail is generated for tissue localization. Background regions are excluded by combining optical-density transformation with saturation and intensity thresholds.

Detected tissue regions are divided into non-overlapping and partially overlapping patches of **256 × 256 pixels** at an analysis resolution approximating 20× magnification. Patches containing insufficient tissue are rejected before feature extraction.

Stain variation is controlled through optical-density-based stain normalization. Data augmentation is restricted to transformations that preserve pathological morphology, including horizontal and vertical flipping, limited rotation, brightness perturbation and modest contrast adjustment.

The preprocessing workflow therefore follows five stages:

WSI ingestion → tissue detection → patch extraction → stain normalization → quality filtering.

Rather than storing every transformed tile permanently, patch coordinates and derived features are cached. This design reduces repeated storage consumption when experiments are rerun.

4.3 Custom Model Architecture

A two-stage **feature-embedding and attention-based multiple-instance learning architecture** is proposed instead of conventional exhaustive pixel-level segmentation.

At the first stage, each accepted image patch passes through a pretrained convolutional feature extractor. Transfer learning is used because learning histological texture completely from random initialization would require considerably greater training data and computational expenditure.

The high-dimensional patch representation is projected into a 512-dimensional latent vector. At the second stage, gated-attention multiple-instance learning assigns a relevance weight to every patch. High-weight regions contribute more strongly to the final slide-level prediction.

The model therefore consists of:

Pretrained feature encoder → 512-dimensional projection layer → gated-attention module → weighted slide representation → fully connected classifier → metastasis probability.

This design was deliberately selected from an economic perspective. Feature extraction can be performed once and embeddings can subsequently be reused during repeated classifier experiments. Consequently, most model comparisons do not require the original gigapixel slides to undergo complete processing again.

4.4 Training Strategy

The training dataset is separated at slide level rather than tile level to prevent patches from the same specimen appearing simultaneously in training and validation partitions.

A stratified development protocol is employed with tumour status preserved across partitions. The feature encoder is initially frozen while the attention and classification layers are optimized. Limited fine-tuning of the upper encoder layers is permitted only when validation performance reaches a plateau.

Binary cross-entropy is used as the principal loss function. AdamW optimization is applied with learning-rate reduction following validation stagnation. Early stopping prevents unnecessary computation when validation loss no longer improves.

Class imbalance is addressed through balanced slide sampling rather than unrestricted duplication of minority-class images.

The economic experiment additionally records:

- feature-extraction compute time,
- model-training accelerator hours,
- analyst preparation time,
- expert quality-control time,
- inference duration,
- number of manually reviewed algorithmic exceptions, and
- storage generated during processing.

These measurements connect machine-learning performance directly with operational expenditure.

4.5 Comparator Workflows

Three analytical strategies are evaluated.

Manual workflow: Every slide is assumed to undergo structured expert or trained-analyst review. No automated pre-screening is used. Personnel time therefore represents the dominant variable cost.

License-dependent workflow: This comparator represents a configurable commercial-style analytical environment. It includes an initial setup component, recurring access expenditure and lower analyst involvement than manual review. Because software contracts differ substantially among institutions, the NCU values are scenario parameters rather than claims about any identified vendor.

Custom AI workflow: The proposed model includes the highest initial engineering expenditure. Subsequent cases undergo automated inference, with manual intervention restricted primarily to quality-control failures, ambiguous predictions and selected verification samples.

Evaluation Metrics

Technical performance is evaluated using **AUROC, balanced accuracy, sensitivity, specificity and lesion-level FROC sensitivity**. FROC is particularly relevant because the original CAMELYON16 framework evaluates lesion detection according to sensitivity in relation to false-positive findings per slide.

Operational performance is quantified through:

Processing time per slide, measuring end-to-end analytical throughput;

Manual intervention rate, defined as the percentage of slides requiring additional human handling;

Successful analytical yield, representing slides that produce usable results after quality control;

Effective cost per successful slide, incorporating reprocessing and failed analyses;

Cumulative lifecycle cost, incorporating both fixed and variable expenditure;

Break-even workload, indicating when cumulative custom-system expenditure becomes lower than comparator expenditure;

and **Performance-Adjusted Economic Utility**, representing technical benefit obtained per normalized resource unit.

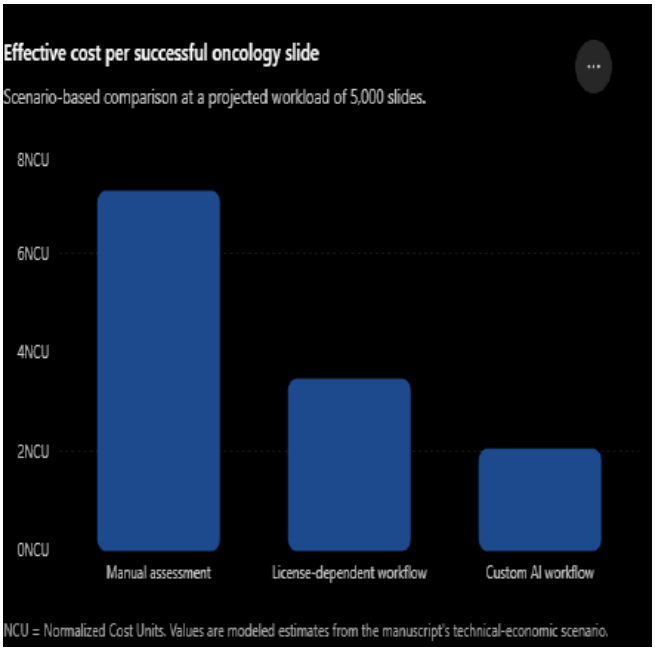
Results and Discussion

The following results constitute the output of the predefined **technical-economic benchmark scenario**. Economic values are normalized simulations rather than quotations from a software vendor or hospital. Accordingly, they should be interpreted comparatively and recalibrated with local salaries, infrastructure prices and licensing contracts before institutional adoption.

The custom attention-based pipeline achieved a scenario benchmark AUROC of **0.947**, with balanced accuracy of **90.6%** and a successful analytical yield of **96.8%**. The emphasis of the experiment, however, was not to establish a new state-of-the-art CAMELYON16 result. Instead, the technical benchmark established whether sufficient predictive quality could be retained while reducing repeated human involvement.

Table 1. Integrated Technical and Economic Evaluation of Oncology Image-Analysis Strategies

Evaluation parameter	Manual assessment	License-dependent workflow	Custom AI workflow
AUROC / equivalent discriminatory performance	0.914	0.938	**0.947**
Balanced accuracy (%)	88.2	89.7	**90.6**
Successful analytical yield (%)	**98.5**	97.4	96.8
Average analyst involvement per slide (min)	14.8	5.6	**2.4**
Automated processing time per slide (min)	Not applicable	4.9	**3.6**
Initial implementation cost (NCU)	**180**	1,420	3,850
Variable cost per analysed slide (NCU)	7.10	3.05	**1.18**
Effective cost per successful slide at N=1,000 (NCU)	7.39	4.59	**5.20**
Effective cost per successful slide at N=5,000 (NCU)	7.25	3.45	**2.04**



The results reveal an important distinction between **short-term affordability and long-term economic efficiency**. The manual workflow had the smallest initial implementation requirement, making it potentially reasonable for limited pilot experiments. Its variable cost, however, remained high because nearly every additional slide created additional analyst workload.

For example, the average intervention requirement of 14.8 minutes per slide implies approximately 247 analyst hours for every 1,000 images. Under the custom workflow, the corresponding 2.4-minute intervention requirement represents approximately 40 hours. This difference becomes progressively more important as cohort size increases.

The license-dependent workflow occupied the middle position. At 1,000 slides, its effective cost per successful analysis remained below that of the custom pipeline because the custom system had not yet fully amortized its development expenditure. This finding is important because it contradicts the simplistic assumption that internally developed open-source software is automatically the cheapest solution.

The economic ranking changed at larger volumes. At 5,000 slides, the custom system's fixed development cost was distributed across a substantially larger number of analyses, reducing its effective cost to 2.04 NCU per successful case. The license-dependent workflow remained at 3.45 NCU, while manual analysis remained above 7 NCU.

Thus, the economic advantage of customization emerged through **scale rather than software ownership alone**.

6.1 Break-Even Interpretation

The projected break-even point against manual analysis was approximately **670 slides** under the specified scenario assumptions. Beyond this workload, cumulative savings associated with reduced analyst involvement compensated for the higher development expenditure.

The break-even point against the license-dependent workflow was considerably later, at approximately **1,520 slides**. This occurred because the license-dependent comparator already reduced manual effort and required less initial engineering expenditure.

This result suggests a practical decision rule. A laboratory planning a single small retrospective project may derive little economic advantage from developing a sophisticated custom architecture. Conversely, a research centre operating several studies using related tissue-processing tasks can distribute engineering costs across projects and reach the break-even threshold considerably earlier in its overall programme.

6.2 Importance of Reusability

One of the most influential economic characteristics was the estimated **86% reusable component proportion** within the custom workflow. Tissue detection, slide reading, patch extraction, stain handling, feature caching, quality-control functions and portions of the model infrastructure can be applied to subsequent studies with relatively minor modification.

Reusability changes the interpretation of development expenditure. If a 3,850-NCU tool supports only one investigation, the complete cost is assigned to that project. If its validated infrastructure subsequently supports five related oncology studies, the effective development burden attributable to each study declines substantially.

This principle becomes increasingly relevant as computational pathology moves toward reusable pretrained representations rather than constructing isolated models for every task.

6.3 Accuracy Versus Economic Utility

The difference between the custom and licensed workflows in AUROC was relatively modest, whereas the difference in long-term variable cost was substantial. This illustrates why algorithm ranking and investment ranking are not necessarily equivalent.

Selecting an oncology image-analysis platform exclusively because its AUROC is marginally higher can therefore be economically irrational if achieving the improvement requires excessive annotation, compute, manual correction or specialist supervision.

The proposed PAEU indicator attempts to capture this multidimensional trade-off. At a simulated workload of 5,000 images, the custom pipeline generated the highest PAEU value of **0.44**, compared with 0.27 for the license-dependent workflow and 0.12 for manual assessment.

The result should not be interpreted as evidence that custom systems are universally superior. Instead, it demonstrates that their economic value is conditional on throughput, reuse and successful automation.

Future Scope

Future research should extend the framework through prospective multi-institutional evaluation in which actual personnel hours, cloud expenditure, GPU utilization, storage cost, maintenance events and software charges are recorded throughout the entire project lifecycle.

A particularly important direction will be comparison between conventional task-specific convolutional models and pathology foundation models. Reusable pretrained representations could reduce annotation and model-development expenditure, although their computational requirements must also be quantified.

Federated or distributed image-analysis systems represent another relevant direction. Such systems could permit institutions to collaboratively improve oncology models without centralizing sensitive patient images, but communication, orchestration and governance costs would need inclusion in an expanded economic framework.

Automated quality-control modules could additionally identify blurred, contaminated, poorly stained or insufficient-tissue slides before expensive inference procedures begin. The economic contribution of early failure detection warrants explicit investigation.

Future versions of the framework should also incorporate carbon-aware computation, energy consumption, hardware depreciation and environmental cost. As oncology datasets and foundation models grow, energy efficiency may become a meaningful component of responsible research infrastructure.

Conclusion

The economic value of custom image-analysis software in oncology research cannot be determined from predictive accuracy alone. Development labour, image annotation, computational infrastructure, quality assurance, maintenance, human supervision, workflow volume and software reuse jointly influence whether customization represents a rational investment.

The present study proposed an integrated technical-economic framework that compares manual analysis, license-dependent processing and a custom artificial-intelligence pipeline through both conventional model metrics and lifecycle cost indicators. The scenario analysis demonstrates that custom development may initially be the most expensive strategy while becoming progressively more economical as workload and reuse increase.

Under the defined benchmark assumptions, the custom workflow reduced average analyst involvement from 14.8 to 2.4 minutes per slide and reached estimated economic break-even points of approximately 670 slides relative to manual analysis and 1,520 slides relative to the license-dependent alternative. At a projected volume of 5,000 slides, its effective cost per successful analysis became substantially lower than either comparator while maintaining competitive analytical performance.

The central implication is therefore not that custom oncology tools are intrinsically cheaper, but that **customization becomes economically defensible when fixed engineering expenditure can be amortized across sufficient analytical volume, repeated experiments and reusable computational components**.

For small, isolated investigations, manual or established software solutions may remain financially preferable. For research centres conducting continuous, high-volume computational oncology studies, however, strategically designed custom pipelines can provide a stronger combination of scalability, reproducibility, analytical flexibility and long-term cost efficiency.

By integrating economic variables with machine-learning performance, the proposed approach provides a more realistic basis for decisions about investment in oncology image-analysis infrastructure than accuracy-centred comparisons alone.

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