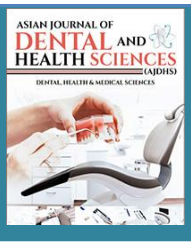

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Open Access Review Article

Computational Dissection of the Ovarian Cancer Genome: Integrative Analysis of Mutations and Signaling Pathways

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Abstract

Ovarian cancer remains one of the most lethal gynecologic malignancies, driven by profound genomic instability, molecular heterogeneity, and frequent therapeutic resistance. The rapid expansion of high-throughput sequencing technologies has generated large-scale genomic datasets that require advanced computational approaches for meaningful biological interpretation. This narrative review examines current bioinformatics strategies used to dissect the ovarian cancer genome, with a focus on integrative analyses of somatic mutations and dysregulated signaling pathways. We discuss computational methods for mutation profiling, copy number and structural variant analysis, pathway enrichment, and network-based modeling, as well as emerging multi-omics and machine learning frameworks. Particular emphasis is placed on key oncogenic pathways implicated in ovarian cancer pathogenesis, including DNA damage response, PI3K/AKT/mTOR, RAS/MAPK, and immune-related signaling networks. Finally, we highlight ongoing challenges related to tumor heterogeneity, clonal evolution, data integration, and clinical translation. Integrative computational dissection of ovarian cancer genomics provides a critical foundation for biomarker discovery, therapeutic stratification, and the advancement of precision oncology.

Keywords: Ovarian cancer genomics; Bioinformatics; Somatic mutations; Signaling pathways; Precision oncology

Introduction

Ovarian cancer represents a major global health burden and remains the most lethal gynecologic malignancy, largely due to its asymptomatic early course, late-stage presentation, and high rates of relapse following standard therapy [1]. Despite advances in cytoreductive surgery and platinum-based chemotherapy, long-term survival has improved only modestly over recent decades. The biological complexity of ovarian cancer, encompassing marked interpatient heterogeneity, extensive genomic instability, and adaptive therapeutic resistance, continues to undermine durable clinical responses. These challenges underscore the need for a deeper molecular understanding of ovarian tumorigenesis and progression to inform more precise and effective therapeutic strategies [2-3]. Molecular profiling studies have established ovarian cancer as a genomically complex disease characterized by pervasive somatic alterations, chromosomal instability, and widespread disruption of DNA repair mechanisms [4]. High-grade serous carcinoma, the most prevalent and aggressive subtype, exhibits near-universal TP53 mutations, frequent defects in homologous recombination repair involving BRCA1/2 and related genes, and extensive copy number aberrations. Other histological subtypes display distinct genomic landscapes, reflecting divergent oncogenic pathways and etiologic mechanisms. This molecular heterogeneity necessitates analytical frameworks capable of integrating diverse genomic alterations into coherent biological models that transcend single-gene interpretations [5-7].

The proliferation of next-generation sequencing and high-throughput omics technologies has enabled comprehensive characterization of the ovarian cancer genome, transcriptome, epigenome, and proteome. Large-scale consortia and institutional sequencing initiatives have generated vast, multidimensional datasets that capture the breadth of molecular alterations across ovarian cancer subtypes and disease stages. However, translating these data into actionable biological and clinical insights requires advanced computational methodologies for variant detection, data integration, functional annotation, and pathway-level interpretation. Bioinformatics has therefore emerged as an indispensable pillar of modern ovarian cancer research, providing the analytical infrastructure needed to distill complex genomic information into mechanistic understanding [8-9]. A critical limitation of gene-centric analyses is their inability to fully account for the systems-

level nature of oncogenesis. Tumor phenotypes arise not from isolated genetic lesions but from coordinated perturbations of signaling pathways and molecular networks that regulate cell cycle progression, DNA damage response, apoptosis, metabolism, angiogenesis, and immune surveillance. Consequently, pathway- and network-based computational approaches have gained prominence as frameworks for contextualizing genomic alterations within biologically meaningful circuits. By mapping mutations and copy number changes onto curated pathways and interaction networks, these approaches facilitate the identification of convergent oncogenic processes and potential therapeutic vulnerabilities [10-11].

Integrative multi-omics strategies further extend this systems perspective by linking genomic alterations to downstream functional consequences at the transcriptomic, epigenetic, and proteomic levels. Such integrative analyses enable the delineation of molecular subtypes, the identification of pathway activation states, and the discovery of biomarkers predictive of prognosis or therapeutic response. Machine learning and network inference methods augment these efforts by uncovering latent molecular patterns and constructing predictive models that support precision oncology initiatives. In parallel, advances in single-cell sequencing and spatial profiling are refining understanding of intratumoral heterogeneity, clonal evolution, and tumor–microenvironment interactions, revealing dynamic pathway reprogramming in response to therapeutic pressures [12-13]. Within this evolving landscape, the computational dissection of the ovarian cancer genome represents a critical translational interface between high-dimensional molecular data and clinical oncology. By integrating mutation profiling with pathway and network analyses, computational frameworks provide a systems-level view of ovarian cancer biology that informs biomarker discovery, therapeutic target identification, and rational combination therapy design. This narrative review synthesizes current computational approaches for integrative analysis of ovarian cancer genomics, highlighting methodological advances, biological insights, and translational implications, while also addressing persistent challenges related to data heterogeneity, model interpretability, and clinical implementation.

Aim

The primary aim of this review is to provide a comprehensive narrative overview of computational strategies for dissecting the ovarian cancer genome, with a focus on integrating somatic mutation profiling and pathway-level analysis. Specifically, the review seeks to:

1. **Summarize current bioinformatics approaches** for detecting and interpreting somatic mutations, copy number alterations, and structural variants in ovarian cancer.
2. **Highlight pathway- and network-based frameworks** that contextualize genomic alterations within biologically meaningful signaling circuits.
3. **Examine integrative multi-omics and systems biology methodologies** that link genomic changes to functional consequences at transcriptomic, proteomic, and epigenetic levels.
4. **Discuss the role of computational modeling in understanding tumor heterogeneity and clonal evolution** and its implications for therapeutic resistance.
5. **Explore translational applications** in precision oncology, including biomarker discovery, patient stratification, and rational design of targeted therapies.

Methods

This narrative review was conducted through a structured literature synthesis aimed at capturing the current state of computational genomics and systems biology in ovarian cancer research. Relevant studies were identified through comprehensive searches of electronic databases, including PubMed, Scopus and Web of Science using combinations of keywords such as *"ovarian cancer," "genomics," "somatic mutations," "copy number variation," "bioinformatics," "pathway analysis," "network modeling," "multi-omics integration,"* and *"precision oncology."* Additional sources were identified through reference lists of key publications and recent review articles. Selection criteria prioritized original research, computational and bioinformatics methodology studies, and integrative multi-omics analyses relevant to ovarian cancer genomics. Studies focusing on high-throughput sequencing, mutation profiling, pathway enrichment, network inference, and computational modeling of clonal evolution were included to ensure a comprehensive understanding of the field. Both preclinical and clinical studies were considered to contextualize computational findings in translational settings.

Data from the selected studies were extracted and synthesized narratively, emphasizing the following domains:

1. Somatic mutation profiling and variant detection pipelines in ovarian cancer.
2. Pathway-centric and network-based approaches for interpreting genomic alterations.
3. Integrative multi-omics and systems biology methodologies for functional annotation of tumors.
4. Computational modeling of tumor heterogeneity and clonal evolution.
5. Translational implications for biomarker discovery, precision therapy, and clinical trial design.

This narrative synthesis was organized thematically to provide a cohesive overview of computational strategies, biological insights, and clinical applications, highlighting both methodological advances and ongoing challenges in the field of ovarian cancer genomics.

Computational Profiling of Somatic Mutations in Ovarian Cancer

The systematic characterization of somatic mutations is foundational to understanding the molecular architecture of ovarian cancer. High-throughput sequencing technologies have enabled comprehensive detection of single-nucleotide variants, small insertions and deletions, copy number alterations, and structural rearrangements across diverse ovarian cancer subtypes. However, the biological interpretation of these complex genomic data is inherently dependent on robust computational pipelines that ensure analytical accuracy, reproducibility, and biological relevance. Contemporary bioinformatics workflows encompass sequential steps of sequence alignment, variant calling, quality control, and functional annotation, forming the backbone of mutation profiling in ovarian cancer research [14-15]. A central challenge in somatic mutation analysis is the discrimination of driver mutations, which confer selective growth advantages, from passenger alterations that accumulate stochastically during tumor evolution. Computational frameworks address this challenge through statistical modeling of background mutation rates, recurrence analysis across cohorts, and functional impact prediction. In ovarian cancer, such approaches have consistently identified recurrent alterations in TP53, BRCA1, BRCA2, NF1, RB1, and genes involved in chromatin remodeling and DNA repair. Beyond individual genes, mutational signature analysis has provided insights into the underlying mutagenic processes shaping the ovarian cancer genome, including defective homologous recombination repair and exposure to endogenous DNA-damaging mechanisms. These computationally derived signatures not only refine etiological understanding but also have prognostic and therapeutic implications, particularly in the context of DNA damage response–targeted therapies [16-17].

Copy number alterations and large-scale chromosomal rearrangements constitute defining features of high-grade serous ovarian carcinoma, reflecting profound genomic instability. Computational segmentation algorithms and allele-specific copy number inference methods enable the delineation of complex aneuploidy patterns and focal genomic events affecting oncogenes and tumor suppressors. Integrative analysis of copy number changes with mutation data reveals coordinated genomic programs that drive oncogenic signaling and therapy resistance. For example, focal amplifications in growth factor signaling components or deletions in DNA repair regulators can potentiate pathway activation states that are not readily apparent from point mutation analysis alone [18-19]. The increasing adoption of longitudinal and multi-region sequencing has further necessitated computational methods capable of modeling clonal architecture and evolutionary dynamics. Phylogenetic reconstruction algorithms infer the temporal ordering of somatic events, elucidating early driver mutations that initiate tumorigenesis versus late-emerging alterations associated with progression or therapeutic resistance. In ovarian cancer, these models have illuminated patterns of branched evolution and clonal diversification, highlighting how selective pressures imposed by chemotherapy can reshape the mutational landscape and promote the expansion of resistant subclones. Such insights underscore the importance of integrating evolutionary modeling into mutation profiling to capture the dynamic nature of ovarian cancer genomics [20-21] (Table 1).

Table 1: Computational Profiling of Somatic Mutations in Ovarian Cancer

Analytical Component	Purpose / Description	Key Computational Tools / Algorithms	Insights in Ovarian Cancer
Variant Calling	Identification of somatic single-nucleotide variants (SNVs) and small insertions/deletions (indels) from sequencing data	GATK, MuTect2, VarScan2	Detects recurrent driver mutations (e.g., TP53, BRCA1/2, NF1) and rare variants
Copy Number Alteration Analysis	Detection of genomic amplifications and deletions	CNVkit, FACETS, ASCAT	Reveals focal and broad copy number changes affecting oncogenes and tumor suppressors; highlights chromosomal instability
Structural Variant Detection	Identification of large genomic rearrangements, translocations, and inversions	Manta, Delly, GRIDSS	Characterizes complex genomic rearrangements common in high-grade serous ovarian carcinoma
Mutational Signature Analysis	Infers underlying mutagenic processes from SNV patterns	SigProfiler, MutationalPatterns	Identifies homologous recombination deficiency, aging-related mutations, and APOBEC activity
Functional Annotation	Predicts biological impact of identified variants	ANNOVAR, VEP, OncoKB	Differentiates driver mutations from passenger events; links mutations to known cancer pathways
Clonal and Phylogenetic Analysis	Reconstructs tumor subclonal architecture and evolutionary history	PyClone, SciClone, PhyloWGS	Reveals early truncal mutations vs. late subclonal events; informs understanding of therapeutic resistance
Integrative Genomic Analysis	Combines SNVs, CNVs, and structural variants for holistic profiling	cBioPortal, Integrative Genomics Viewer (IGV)	Provides comprehensive genomic landscape; identifies co-occurring alterations and pathway-level effects

Pathway-Centric Interpretation of Genomic Alterations

The interpretation of ovarian cancer genomics has progressively shifted from a gene-centric paradigm toward a pathway-centric framework that more accurately reflects the systems biology of oncogenesis. Individual tumors often harbor numerous, heterogeneous genetic alterations, many of which are rare or context-dependent. Evaluating these alterations in isolation provides limited insight into tumor behavior, as phenotypic consequences typically arise from the coordinated dysregulation of signaling pathways and molecular networks. Pathway-centric interpretation addresses this limitation by contextualizing genomic alterations within structured biological circuits that govern fundamental cellular processes, including proliferation, DNA repair, apoptosis, metabolism, angiogenesis, and immune modulation [22-23]. Computational pathway analysis integrates somatic mutations, copy number changes, and gene expression profiles with curated biological knowledge bases to identify recurrently perturbed signaling cascades. In ovarian cancer, such analyses consistently implicate DNA damage response and homologous recombination repair pathways, reflecting the central role of genomic instability in disease pathogenesis. Parallel perturbations in growth factor–mediated signaling, notably the PI3K/AKT/mTOR and RAS/MAPK axes, further underscore the convergence of diverse genomic events on common proliferative and survival circuits. Importantly, pathway-level aggregation of alterations enables the detection of functional dysregulation even when individual genes are infrequently mutated, thereby enhancing sensitivity for identifying clinically relevant molecular vulnerabilities [24-25].

Beyond canonical pathways, network-based computational models reconstruct interaction maps that capture cross-talk and feedback regulation among signaling modules. These network representations reveal emergent properties of ovarian cancer biology, such as pathway redundancy and compensatory signaling, which can underlie intrinsic or acquired resistance to targeted therapies. For example, inhibition of a single oncogenic node may be circumvented through activation of parallel pathways or feedback loops, a phenomenon that becomes apparent only through network-level analysis. Consequently, pathway-centric and network-informed interpretations provide a rational basis for designing combination therapies that simultaneously target multiple nodes within interconnected signaling circuits [26-27]. Pathway-centric frameworks also facilitate functional stratification of tumors into molecular subtypes with distinct biological behaviors and therapeutic susceptibilities. By integrating genomic alterations with pathway activation states inferred from transcriptomic or proteomic data, computational models enable the classification of ovarian cancers according to dominant signaling dependencies. This stratification supports precision oncology initiatives by aligning patients with therapies targeting pathway-level vulnerabilities rather than single-gene aberrations. Moreover, pathway-centric biomarkers may offer greater robustness and clinical utility than isolated genomic markers, as they reflect the integrated functional state of oncogenic networks [28-29] (Table 2).

Table 2: Pathway-Centric Interpretation of Genomic Alterations in Ovarian Cancer

Pathway / Network	Commonly Altered Genes	Functional Consequences	Computational Approaches / Tools	Clinical / Biological Insights
DNA Damage Response & Homologous Recombination	BRCA1, BRCA2, RAD51, PALB2	Impaired DNA repair, genomic instability	Gene set enrichment analysis (GSEA), Pathway Commons, Reactome	Predicts sensitivity to PARP inhibitors; identifies tumors with HR deficiency
PI3K/AKT/mTOR Signaling	PIK3CA, PTEN, AKT1/2, MTOR	Enhanced proliferation, survival, metabolic reprogramming	KEGG pathway mapping, Cytoscape, Ingenuity Pathway Analysis	Supports targeting of PI3K/AKT/mTOR axis in selected patients
RAS/MAPK Signaling	KRAS, BRAF, NF1, MEK1/2	Increased proliferation, invasion, and therapy resistance	Reactome, Pathway Enrichment Analysis, NetworkAnalyst	Highlights combinatorial inhibition strategies to overcome compensatory signaling
Notch Signaling	NOTCH1-4, FBXW7	Dysregulated differentiation, stemness, tumor progression	Pathway enrichment, STRING, Cytoscape	May contribute to chemoresistance and cancer stem cell maintenance
Wnt/β-Catenin Pathway	CTNNB1, APC, AXIN1	Altered cell adhesion, proliferation, and metastasis	KEGG/WikiPathways, GSEA, Network modeling	Implicated in aggressive phenotypes and immune evasion

Immune Signaling & Checkpoints	PD-L1 (CD274), CTLA4, JAK/STAT pathway genes	Immune suppression, evasion of anti-tumor immunity	ImmPort, Reactome, Network inference	Supports immunotherapy stratification and identification of immune-active subtypes
Cell Cycle Regulation	TP53, RB1, CDKN2A, CCNE1	Loss of cell cycle control, enhanced proliferation	GSEA, Pathway Commons, Cytoscape	Truncal mutations like TP53 drive genomic instability; CCNE1 amplification associated with poor prognosis

Integrative Multi-Omics and Systems Biology Approaches

The complexity of ovarian cancer extends beyond genomic alterations alone, encompassing coordinated changes across multiple molecular layers that collectively shape tumor phenotype and clinical behavior. Integrative multi-omics and systems biology approaches have therefore emerged as essential frameworks for capturing the multidimensional nature of ovarian cancer biology. By computationally integrating genomic, transcriptomic, epigenomic, proteomic, and, increasingly, metabolomic data, these approaches enable a holistic reconstruction of the molecular networks that drive tumor initiation, progression, and therapeutic response [30-31]. At the core of multi-omics integration is the principle that genomic alterations exert their biological effects through downstream modulation of gene expression, protein activity, and cellular signaling states. Computational models that align somatic mutations and copy number changes with transcriptional programs and epigenetic regulation provide functional annotation of genomic events, distinguishing biologically consequential alterations from neutral background variation. In ovarian cancer, such integrative analyses have elucidated how defects in DNA repair pathways manifest as distinct transcriptional signatures of genomic instability, or how aberrant activation of growth factor signaling cascades is reflected in proteomic patterns of pathway activation. This functional layering enhances interpretability and strengthens causal inference in genomic studies [32-33].

Systems biology methodologies further extend multi-omics integration by constructing network-based representations of molecular interactions. These models capture the dynamic interplay between genes, proteins, regulatory elements, and signaling pathways, revealing emergent properties of tumor systems that are not apparent from single-layer analyses. In ovarian cancer, network inference approaches have identified critical regulatory hubs and bottlenecks within oncogenic circuits, highlighting potential points of therapeutic intervention. Importantly, systems-level models accommodate pathway cross-talk and feedback regulation, providing mechanistic explanations for phenotypes such as therapeutic resistance, adaptive signaling reprogramming, and phenotypic plasticity [34-35]. Machine learning and advanced statistical frameworks play an increasingly prominent role in multi-omics integration, enabling the extraction of latent molecular patterns from high-dimensional datasets. Unsupervised learning approaches facilitate the discovery of molecular subtypes defined by coordinated pathway activation states, while supervised models support the development of prognostic and predictive signatures linked to clinical outcomes. In ovarian cancer, integrative machine learning models have demonstrated potential for stratifying patients according to risk, therapeutic responsiveness, and likelihood of relapse, thereby supporting precision oncology paradigms. Nevertheless, the interpretability and clinical generalizability of these models remain active areas of methodological refinement [36-37].

The incorporation of temporal, spatial, and single-cell dimensions further enriches integrative systems biology frameworks. Longitudinal profiling captures dynamic molecular reprogramming in response to therapy, while spatially resolved and single-cell analyses reveal intratumoral heterogeneity and microenvironmental interactions that shape pathway activity. Computational integration of these data modalities provides insight into clonal evolution, niche-specific signaling states, and immune–tumor interactions, offering a more nuanced understanding of ovarian cancer as an evolving, ecosystem-level disease. Collectively, integrative multi-omics and systems biology approaches provide a comprehensive analytical paradigm that bridges molecular complexity with biological insight, advancing the translational impact of computational genomics in ovarian cancer research [38-39] (Figure 1).

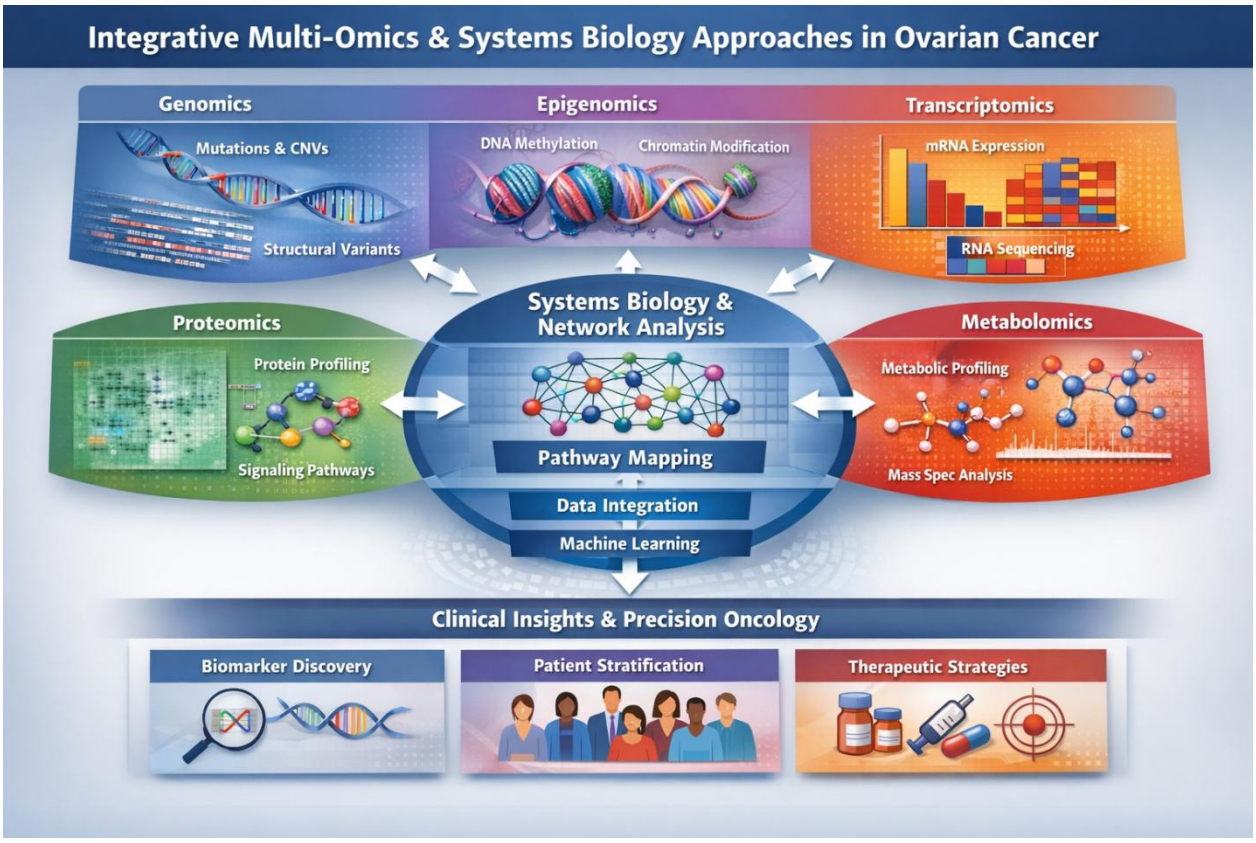

Figure 1: Integrative Multi-Omics and Systems Biology Approaches

Tumor Heterogeneity, Clonal Evolution, and Computational Modeling

Tumor heterogeneity is a defining feature of ovarian cancer and a principal driver of disease progression, therapeutic resistance, and relapse. At diagnosis, ovarian tumors often comprise multiple genetically and phenotypically distinct cell populations that differ in proliferative capacity, metastatic potential, and sensitivity to therapy. This intratumoral diversity reflects ongoing clonal evolution shaped by genomic instability and selective pressures imposed by the tumor microenvironment and therapeutic interventions. Understanding this dynamic heterogeneity requires computational models capable of reconstructing clonal architectures and evolutionary trajectories from complex genomic data [39-41]. Computational approaches to clonal inference leverage variant allele frequencies, copy number states, and phylogenetic algorithms to infer the number, composition, and evolutionary relationships of tumor subclones. In ovarian cancer, such analyses have revealed branched evolutionary patterns in which early, truncal driver events—such as TP53 mutation and defects in DNA repair pathways—are shared across all tumor cells, while later, subclonal alterations confer selective advantages in specific microenvironmental or therapeutic contexts. These models provide a temporal framework for distinguishing foundational oncogenic events from adaptive mutations associated with progression, metastasis, and chemoresistance [42-43].

The integration of longitudinal and multi-region sequencing further refines computational reconstructions of clonal evolution by capturing spatial and temporal heterogeneity. Computational modeling of paired primary and recurrent ovarian tumors has demonstrated how cytotoxic therapies impose selective bottlenecks that reshape clonal composition, often enriching for resistant subpopulations with altered signaling pathway dependencies. Such insights highlight the evolutionary cost of therapeutic pressure and underscore the need for adaptive treatment strategies that anticipate and constrain clonal escape. Computational simulations of evolutionary dynamics can be used to explore hypothetical treatment scenarios, providing a platform for in silico testing of combination or sequential therapeutic regimens [44-46]. Single-cell sequencing and spatial transcriptomics have introduced new dimensions to computational modeling of heterogeneity by resolving cellular diversity at unprecedented resolution. These data enable the identification of rare subclones, transient cell states, and microenvironmentally conditioned phenotypes that may be obscured in bulk analyses. Computational frameworks integrating single-cell and bulk genomic data provide multiscale models of tumor ecosystems, capturing both clonal structure and functional heterogeneity in pathway activation states. In ovarian cancer, such models have illuminated the coexistence of proliferative, mesenchymal-like, and immune-interacting tumor cell states, each associated with distinct signaling networks and clinical behaviors [47-49].

Clinical Translation and Precision Oncology Implications

The clinical translation of computational genomics in ovarian cancer represents a critical step in transforming

molecular insights into tangible improvements in patient care. Integrative analyses of somatic mutations and dysregulated signaling pathways have progressively reframed ovarian cancer as a biologically stratified disease, in which therapeutic vulnerabilities are determined not solely by histopathology but by the functional state of oncogenic networks. Precision oncology seeks to operationalize this paradigm by aligning individual patients with targeted therapies based on their molecular profiles, thereby improving therapeutic efficacy while minimizing unnecessary toxicity [50-52]. Pathway-informed biomarkers derived from computational analyses offer a robust framework for patient stratification and therapeutic decision-making. In contrast to single-gene biomarkers, pathway-level signatures capture the cumulative functional impact of multiple genomic alterations converging on shared signaling circuits. In ovarian cancer, computational models that integrate DNA damage response defects, growth factor signaling activation states, and immune pathway perturbations have demonstrated potential for predicting response to targeted agents, including DNA repair–directed therapies and pathway inhibitors. Such pathway-centric stratification enhances the clinical relevance of molecular profiling by aligning treatment selection with systems-level tumor biology [53-55].

Computational platforms also support rational therapeutic design by identifying network vulnerabilities and potential synergistic targets within interconnected signaling pathways. Network-based modeling can reveal compensatory pathways and feedback loops that mediate intrinsic or acquired resistance, informing the selection of combination therapies designed to suppress adaptive signaling reprogramming. In ovarian cancer, this approach is particularly relevant given the propensity for tumors to activate alternative survival pathways in response to targeted inhibition, underscoring the need for combinatorial strategies guided by computational network analysis rather than empirical trial-and-error approaches [56-58]. The integration of computational genomics into clinical workflows further facilitates biomarker-driven clinical trial design and patient enrichment strategies. Adaptive trial frameworks that incorporate real-time molecular profiling and computational interpretation enable dynamic treatment allocation based on evolving tumor biology. Moreover, predictive models trained on multi-omics datasets can inform prognostic assessment and risk stratification, supporting personalized surveillance and treatment planning. However, the clinical implementation of these computational tools requires rigorous validation, standardization of analytical pipelines, and the development of interoperable decision-support systems that can be seamlessly integrated into routine oncology practice [59-62].

Conclusion

The computational dissection of the ovarian cancer genome has fundamentally transformed the understanding of this complex and heterogeneous malignancy. By integrating somatic mutation profiling with pathway- and network-level analyses, researchers can move beyond isolated gene-centric views to systems-level models that capture the coordinated dysregulation of signaling pathways driving tumor initiation, progression, and therapeutic resistance. Multi-omics integration, evolutionary modeling of clonal dynamics, and network-based analyses further enhance mechanistic insight, revealing critical vulnerabilities and compensatory circuits that inform targeted interventions.

These computational frameworks have direct translational relevance, supporting precision oncology approaches that align patients with therapies based on pathway-level dependencies and molecular subtypes rather than histology alone. Despite ongoing challenges related to data heterogeneity, interpretability, and clinical implementation, integrative computational genomics offers a robust foundation for biomarker discovery, rational combination therapy design, and adaptive treatment strategies. Continued refinement and clinical validation of these approaches will be pivotal in realizing the full potential of precision oncology, ultimately improving outcomes for patients with ovarian cancer.

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