Poornachandra G.

Lead Scientist - Clinical Translation · Precision Medicine in Oncology · NGS & ML for Clinical Genomics
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PROFESSIONAL SUMMARY

Bioinformatics Lead Scientist with **10+** years of experience in precision medicine in oncology. Expert in designing, building and productionizing end-to-end NGS and multi-omics pipelines for clinical workflows. Conceived and built the company's cross-functional Bioinformatics stack from scratch, delivering reproducible, scalable, and regulatory-ready solutions that integrate NGS analysis, clinical variant interpretation, and data-driven insights.

SELECTED HIGHLIGHTS & IMPACT

- Built and productionized end-to-end NGS pipelines (WGS/WES/TES, RNA-seq, CNV, SV) used in clinical and research workflows; reduced sample turnaround time through automated QC and reporting.
- Architected variant annotation and prioritization workflows (ACMG/AMP/ASCO/CAP) integrating multiple public and proprietary annotations to enable clinical decision support.
- Led ML initiatives for biomarker discovery and patient stratification: feature engineering from multi-omics inputs, model validation, and deployment in production environments.
- Mentored and grew a bioinformatics team; led technical hiring, performance reviews and cross-functional training.
- Delivered internal web applications and dashboards (Streamlit, Gradio) to deploy the AI based applications.

CORE COMPETENCIES

- **Clinical Genomics:** WGS/WES/Targeted Panels - Variant Interpretation (ACMG/AMP/ASCO/CAP) - Pharmacogenomics - Liquid Biopsy - Companion Diagnostics
- **Pipeline Engineering:** GATK Best Practices - Sentieon - DRAGEN - Parabricks - Nextflow Orchestration - QC Automation - Reproducibility & Performance Tuning
- **Machine Learning:** Supervised & Unsupervised Learning - Feature Engineering - Model Validation - Biomarker Discovery - Ensemble Methods
- **Leadership & Management:** Team Building - Project Management - Regulatory Compliance (HIPAA) - Risk Management - Stakeholder Communication

Technical Skills

🧬 NGS Analysis Tools

GATK • Sentieon • DRAGEN • Parabricks • FreeBayes • DeepVariant • DeepSomatic • PureCN • CNVKit • VEP • ANNOVAR

🧬 RNA-Seq & Single-Cell Analysis

Kallisto • Salmon • DESeq2 • edgeR • Seurat • Scanpy • GSEA

☁️ Cloud Platforms & Pipelines

DNAnexus • AWS (EC2, S3, Batch, HealthOmics) **• BaseSpace • Galaxy GenePattern • Terra / FireCloud • Illumina Connected Analytics**

🤖 ML / AI Stack

Hugging Face • LangChain • Ollama • LiteLLM • OpenAI / Anthropic / Gemini APIs • LightGBM • XGBoost • PyTorch • scikit-learn • AutoML • PyCaret • Scispacy • BioBERT

⚙️ Workflow & DevOps

Docker • Jupyter • Conda / Mamba • Nextflow • Git • HPC Concepts

📊 Visualization & Web Tools

Streamlit • Gradio • Matplotlib • Plotly • Seaborn

PROFESSIONAL EXPERIENCE

Cellworks — Lead Bioinformatician · 2024 – Present

- Lead the Bioinformatics R&D team — Defined the technical roadmap, recruited and mentored scientists, and drove project prioritization and delivery.
- Introduced structured upskilling sessions leveraging supplemental projects beyond core deliverables, improving engagement, critical thinking, and problem-solving.
- Designed and implemented input-consumption, monitoring, and reporting frameworks that reduced manual review time by 20%.
- Built multi-stage annotation and prioritization pipelines applying AMP/ASCO/CAP guidelines across public and proprietary annotation sources.
- Partnered with executive leadership to align strategy and communicate progress, while providing team members with the broader context needed to execute effectively.
- Established risk management practices for bioinformatics pipelines — Identified potential failure points, data-quality risks, and downstream repercussions, and implemented mitigation strategies to ensure robustness and continuity.

Cellworks — Senior Scientist, Reporting Manager 2022-2024

- Developed workflows for microsatellite instability (MSI), homologous recombination deficiency (HRD), mutation signatures, tumor mutational burden (TMB), and indel burden.
- Developed the **high-throughput variant calling stacks** on **AWS** following **GATK best practices**, including mutation and CNV calling, as well as biomarker extraction.
- **Built and led the bioinformatics team**: recruited, trained, mentored, and reviewed the work of 4 members; created custom training protocols that accelerated onboarding and competency development.
- Designed **input-agnostic workflows** supporting multiple formats (FASTQ, BAM, VCF, structured reports) across diverse vendors (4BC, Tempus, Caris, Foundation Medicine, Alacris, etc.), enhancing pipeline flexibility.
- Built **cancer driver and CNV vs. mRNA databases** for **30+** cancer types using public datasets/tools, enabling effective driver mutation identification amidst thousands of passenger mutations.
- Developed automated **multi-omics interpretation pipelines** for high-impact clinical trial datasets from **Takeda** and **Genentech**.
- Created an **in-house VUS reclassification pipeline** using an Ensembl-based approach, improving classification accuracy by **>40%** .

Cellworks — Senior Scientist, Bioinformatics 2018–2021

- Developed and benchmarked secondary analysis pipelines (Illumina DRAGEN, NVIDIA Parabricks, Psomagen), optimized for both accuracy and turnaround time.
- Led in custom panel design for liquid-biopsy samples, selecting targeted regions and collaborating with Cleveland Clinic Florida to build a machine learning pipeline using longitudinal genomic data to predict early relapse in Melanoma.
- Built a framework to process pediatric cancer cases, accommodating distinct omics profiles and disease mechanisms; served as the primary owner for pediatric hematological cancers.
- Designed and implemented a Panel of Normals (PoN) workflow for CNV and mutation calling using ~100 cases, improving support for tumor-only analyses.
- Created multiple tertiary analysis workflows (GSEA, pathway enrichment, PCA, statistical models, ML pipelines) leveraging multi-omics data for biomarker discovery and treatment-response characterization.
- Developed multi-omics interpretation pipelines for the Foundation Medicine dataset (18,000+ cases), enabling large-scale biomarker and outcome analysis.
- Compiled a comprehensive assay/test inventory across 88 cancers, based on NCCN, FDA, and other clinical guidelines, to inform disease modeling and therapy design.
- Designed a workflow to evaluate targeted panels for their coverage of critical genes linked to disease biology and therapeutic outcomes.

Cellworks — Scientist, Clinical Translation 2017–2018

- Curated rationale libraries to support therapy predictions, reducing turnaround time for live case analyses by >40%.
- Analyzed 200+ cancer cases, gaining deep expertise in target selection using cancer and drug networks in precision oncology.
- Conducted benchmarking of sequencing pipelines (DNAnexus, BeOne, MedGenome) to establish confidence and reproducibility in upstream bioinformatics inputs.
- Developed an in-house variant annotation and filtering pipeline, lowering processing costs and enabling greater customization for diverse project needs.
- Implemented a custom variant-tier classification system to improve prioritization and enhance the interpretability of genomic reports.

Cellworks — Associate Scientist 2015–2017

- Processed, interpreted, and harmonized multi-omics outputs (karyotyping, aCGH, IHC, mutations) for **> 500 cases**, building deep expertise in data variability and translating insights into automated data-harmonization and ETL pipelines that became core components of the company's ingestion framework.
- Curated and automated retrospective in-house dataset creation by integrating patient and cell-line data from **> 10,000** GDSC, TCGA, and published studies
- Standardized genomic data interpretation from external partners (Columbia University, University of Florida, Cedars-Sinai, Mayo Clinic, Washington University, MMRF-Michigan), enabling effective integration
- Automated report-generation workflows using reproducible pipelines and templates, reducing preparation time from **~15 hours to just minutes per week**.

EDUCATION

- **B.Tech, Biotechnology — JNTUA CEP, 2015**

SELECTED AI PROJECTS

- **Evaline:** Led design and prototype of a interactive chatbot combining a fine-tuned open sourced LLM with a RAG pipeline to deliver guideline-based treatment recommendations and patient-friendly explanations
- **PathoParse, Pathology Mining:** Built LLM-assisted and rule-based pipelines to extract structured clinical metadata from pathology reports for downstream analysis.
- **SQL Chat:** Created a multi-agent Streamlit demo that translates natural language clinical queries to SQL, runs statistical tests and returns interpretable Markdown summaries for non-technical users.
- **VarEffex:** Developed a multi-agent framework that mines literature to extract variant–function associations.

PUBLICATIONS

Castro M, Pampana A, Alam A, Parashar R, Rajagopalan S, Lala DA, et al. Combination chemotherapy versus temozolomide for patients with methylated MGMT glioblastoma: computational biological modeling predictions. Journal of Neuro-Oncology. 2021;153(3):393-402.

Ahluwalia MS, Watson D, Kapoor S, Parashar R, Ghosh Roy KG, Alam A, et al. Superior therapy response predictions for patients with low-grade glioma using Cellworks Singula: MyCare-009-04. Journal of Clinical Oncology. 2020;38(15_suppl):2569.

Marcucci G, Kumar A, Castro M, Grover H, Patil V, Alam A, et al. Biosimulation using the Cellworks Computational Omics Biology Model identifies novel biomarkers to inform MEC-based combination therapy. Blood. 2021;138(Suppl 1):1299.

Howard SC, Nair PR, Grover H, Tyagi A, Kumari P, Prasad SA, Mitra U, Alam A, et al. Predicting resistance to ATO and ATRA in APL patients with PML-RARA fusions using computational biology modeling: MyCare-021-01. Blood. 2020;136:31-32.

Castro M, Iwamoto F, Ahluwalia M, Usmani S, Kumar A, Kapoor S, Alam A, et al. Impact of mismatch repair deficiency on survival of temozolomide-treated glioblastoma patients with MGMT methylation: a Cellworks CBM study. Neuro-Oncology. 2022;24(Suppl 7):vii116-vii117.