

differences among provenances, sites, and provenance-by-site interactions for all measured growth and medicinal traits. The same study reported broad phenotypic and genotypic variation, high repeatability for many traits, and positive associations between growth characteristics and key medicinal components, indicating strong potential for selection and breeding. Geo-climatic analyses further suggested that metabolite accumulation is not random: saponin content increased with altitude and temperature, whereas flavonoid accumulation was promoted under drier conditions (Cheng et al., 2026). Such findings underscore a central problem for medicinal plant research in Zhejiang: growth traits, environmental adaptation, and active compound accumulation are tightly coupled, but their relationships are multidimensional and difficult to resolve using conventional descriptive methods alone.

Advances in computational approaches now provide a practical framework for addressing this complexity. Reviews of medicinal plant informatics show that computational research has expanded from molecular docking and molecular dynamics simulation to artificial intelligence, including artificial neural networks, deep neural networks, and related machine-learning tools that reduce the time and cost of conventional screening. More recent work emphasizes that machine learning is particularly valuable when medicinal plant quality must be inferred from multi-source data, because single analytical techniques often fail to capture the multi-component nature of medicinal materials and their environmental responsiveness. Parallel advances in sequencing and analytical chemistry have also widened the computational toolbox: RNA-seq and related technologies can identify genes involved in biosynthetic pathways, while spectroscopy and chromatography generate the metabolite-level data needed for integrated modeling (Singh et al., 2022). At a higher systems level, emerging approaches such as AI-driven multi-omics integration and digital twin modeling seek to connect real-time or high-dimensional data with predictive models of growth dynamics and metabolite yield, although challenges remain in causal inference, interpretability, and cross-species generalization (Chen et al., 2026).

Against this background, this review aims to synthesize current knowledge on how computational analysis can be used to characterize growth characteristics and active compound accumulation in Zhejiang medicinal plants, with particular attention to the integration of ecological, phenotypic, phytochemical, and multi-omics information. The conceptual framework adopted here treats medicinal plant quality as an emergent property of interacting biological and environmental layers, rather than as a single trait measured in isolation (Chen et al., 2026). Accordingly, the review is organized around three connected objectives: first, to summarize the sources of variation in growth performance and secondary metabolite accumulation in Zhejiang-relevant medicinal plants; second, to examine computational methods capable of modeling these variations across scales, from trait statistics to network and AI-based prediction; and third, to identify how such methods can support germplasm evaluation, cultivation optimization, quality control, and sustainable resource use (Cheng et al., 2026). By combining regional cultivation evidence with advances in computational biology, this review positions Zhejiang medicinal plants as a model system for data-driven modernization of medicinal plant research and industry.

2 Biological Characteristics and Growth Dynamics of Zhejiang Medicinal Plants

2.1 Diversity, distribution, and habitat adaptation

Zhejiang medicinal plants should be understood within the broader biogeographic pattern of Chinese medicinal flora, in which richness is concentrated in central and southern China and shaped by fine-scale environmental heterogeneity. High-resolution national mapping showed that a small fraction of grid cells contains most medicinal plant diversity, while endemic medicinal plant richness is positively associated with contemporary precipitation and altitudinal range, both of which are highly relevant to Zhejiang's humid subtropical and topographically varied landscapes. This pattern suggests that Zhejiang's mountainous terrain, dissected watersheds, and strong local climatic gradients likely promote species coexistence, ecological specialization, and habitat partitioning among medicinal taxa rather than supporting a uniform regional flora.

Habitat adaptation in Zhejiang also depends on how populations respond to fragmentation, geographic isolation, and local environmental filters. A Zhejiang-focused population genomic study of *Coptis chinensis* var. *brevisepala* identified Zhejiang as the core distribution area of the species and found strong population differentiation largely driven by geographic isolation, with ultraviolet radiation and low temperature contributing to fine-scale