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ReadMax: A novel showcase approach for FISH biomarkers

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The recently published study demonstrates that novel approaches can overcome hidden issues in widely accepted FISH scoring approaches. The study dealt with EGFR-scoring in NSCLC, where the established Colorado scoring was found to blur actual aberrance and failed as predictor in pivotal trials. ReadMax represents a 'maximizing strategy', where the reader strives for recording of most aberrant cells. The reading results underwent a systematic analysis to identify different types of aberrance and to evaluate their predictive power for treatment with erlotinib. It was a surprising finding that scorings of polysomy and not amplification were the winners in predictiveness. Other areas may share hidden issues HER2, MET in different cancer types tend to rely mainly on the 'ratio' as quantification which is hazardous scientifically, as the role of polysomial aberrance is disregarded and is hazardous moneywise, as biomarker developments are based only on a narrow slice of the available aberrance information not a wise bet. The results of the ReadMax study are sketched and the methodological novelties are illustrated. The extension of this methodology to other areas of FISH biomarkers is discussed and real data results are presented.

Biography

Joachim Moecks holds a PhD in Applied Mathematics from the University of Heidelberg, Germany. He has worked in various fields of Bioscience and Medicine with contributions in biomath and biostats. He has published more than 70 peer review papers with subject-matter or methodological emphasis. Presently, he is a Science Head of Biomcon, focusing on biomath and biostats contribution for biomarkers in molecular pathology in collaboration with university pathology institutes and pharma companies.

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