Predicting in vitro digestion of gelatin gels from videos using machine and representation learning

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In vitro digestion models enable the study of gastrointestinal processes, e.g., the digestion of proteins. While models like the INFOGEST protocol standardize *in vitro* digestion conditions [1], methods for determining digested products vary, and correlations between *in vitro* and *in vivo* digestion are discussed [2]. This study explores gelatin-based hydrogels crosslinked with transglutaminase (TGase) as model substrates to investigate protein digestion using real-time video collection and machine learning (ML), a tool already employed in gastrointestinal diagnostics [3].

Gelatin is widely used in food and pharmaceutical applications for its gel-forming ability and biocompatibility [4]. Here, gelatin gels were immersed in simulated gastric media with varying pH, ionic strength, and pepsin concentration [1]. Swelling behavior and degree of hydrolysis (DH) were monitored over time, while video sequences were acquired through a camera probe and processed using ML models. A representation learning-based approach, combining a convolutional neural network (CNN) with a multi-layer perceptron (MLP), was compared to a conventional feature extraction method using hue-saturation-value (HSV) features with an MLP. Results showed that the CNN-based models outperformed the HSV-based approach in identifying digestion conditions and estimating DH, likely due to the superior spatial feature representation achieved through learned representations rather than manually defined features. Pepsin concentration and pH of the media were reliably classified, demonstrating the model's sensitivity to subtle visual changes even with limited data. TGase-crosslinked gelatin gels exhibited varying swelling and digestion rates, influenced by pH and ionic strength.

These findings highlight the potential of ML-driven video analysis for decoding digestion dynamics in real-time and exemplify the combination of deep learning methods and advanced *in vitro* models for food and nutrition research.

Keywords:
Gelatin, protein, pepsin, computer vision, image similarity analysis, deep learning, video change detection

References:

[1] A. Brodkorb *et al.* , "INFOGEST static *in vitro* simulation of gastrointestinal food digestion," *Nature Protocols* , vol. 14, no. 4, pp. 991–1014, 2019.
[2] J. Nadia, D. Roy, C. A. Montoya, H. Singh, and A. Acevedo-Fani, "A proposed framework to establish *in vitro–in vivo* relationships using gastric digestion models for food research," *Food Funct.* , vol. 15, no. 20, pp. 10233–10261, 2024.
[3] A. K. M. S. Hosain, M. Islam, M. H. K. Mehedi, I. E. Kabir, and Z. T. Khan, "Gastrointestinal Disorder Detection with a Transformer Based Approach," in *Proc. IEEE IEMCON* , 2022, pp. 280–285.
[4] R. Schrieber and H. Gareis, *Gelatine Handbook: Practical Aspects* , John Wiley & Sons, 2007.