



Morphological analysis of SARS-CoV-2 cells from images applying a 3D recovery isomorphism



B. Cuevas Otahola^{1,2}, J. Arriaga Hernández³, M. Morin Castillo², J. Oliveros Oliveros³ and Y. Martínez Laguna⁴

Instituto de Radioastronomía y Astrofísica-Universidad Nacional Autónoma de México (UNAM)¹, 58089 Morelia, Michoacán, México
Facultad de Ciencias de la Electrónica-BUAP², Facultad de Ciencias Físico Matemáticas-BUAP³; Instituto de Ciencias (ICUAP)-BUAP⁴
Benemérita Universidad Autónoma de Puebla (BUAP), 72000 CU, Puebla centro, Puebla, México.

bolivia.cuevasotahola@viep.com.mx

We present a proposal for data analysis and recovery from medical images obtained by HIM (Helium Ion Microscopy). To this aim, we apply and modify an isomorphism for data recovery, which simulates object digitization techniques from gray tones according to base changes obtained in simple and binary structured pattern projections. Subsequently we interpret the isomorphism results in the recovered phase to integrate data from each image element, according to the intensity profile in gray tones and 3D reliefs in the data under analysis, in order to obtain the data from all the elements in an image without neglecting any of them.

I. Body

This work is based on an isomorphism developed by Arriaga et al. [1], as a mathematical model to interpret objects in micrographs obtained by TEM. Such micrographs should abide by certain parameters, highlighting the illumination type, which should be aerial. Moreover, the electron beams allowing the visualization by the TEM should have a suitable power and needs to be perpendicular to the mounting where the sample is deposited. For this work, we analyze objects (crystals with several depositions) observed by an SEM. To this aim, we modified the original isomorphism in the interpretation of micrographs gray tones to interpret the profiles since the image intensities are slightly modified. Furthermore, it is crucial to have images or objects without drifts induced by the SEM. In Arriaga [1], we show the isomorphism simulating the projection of the periodic pattern. In this work, we consider periodic patterns as well to simulate the projection, and then, we consider the proposal by Chuanwei et al. [2] with Moiré patterns and simulate the projection with the modified isomorphism.

II. Results

Analyzing the results obtained by the modified isomorphism, we obtain the 3D profiles [Fig. 1 (c)] of the objects in the micrography [Fig. 1 (a), if and only if the illumination and beam power requirements are met] for both the SEM and TEM.

We analyze micrographs of COVID infected cells compared with cells from healthy patients. Our 3D identification procedure is suitable for anomalies due to COVID, in addition to their filtering using their histograms or spectra. The analyzed results were obtained by Frese et al. [3], where they compare the effects in different patients and cellular tissue due to COVID. In Fig. 1, we show a part of our results, considering the isomorphism applications [1] for micrographs by TEM and SEM, in addition to the analysis in human cells diagnosed with COVID, identifying the anomaly in Fig. 1 (b), showing the isomorphism and applying several Fourier filters to visualize the modification in the histograms and spectra of the micrographs comparing healthy and infected cells.

$$\begin{cases} \hat{e}_1 & \text{pixel equal to 1} \\ \hat{e}_0 & \text{pixel equal to 0} \end{cases}, \quad \vec{K}_{i,j} = \gamma_{i,j}\hat{e}_1 + \eta_{i,j}\hat{e}_0, \quad \vec{P}_{i,j} = \alpha_{i,j}\hat{e}_1 + \beta_{i,j}\hat{e}_0,$$

$$\begin{cases} \|g_i\| = d(0, g_i) \\ \|g_i - g_k\| = d(g_k, g_i) \end{cases}, \quad \begin{cases} \|\vec{K}_{i,j}\| = d(0, \vec{K}_{i,j}) \\ \|\vec{K}_{i,j} - \vec{K}_{l,h}\| = d(\vec{K}_{l,h}, \vec{K}_{i,j}) \end{cases},$$

Isomorphism: Let V_{RM} be the vector space defined as the Ronchi Mask images and V_{FI} the vector space defining the Flat Images and the metric d (a real function). If for two vectors from different pixels and Gray Tones holds $d(K_{i,j}, K_{i,j})=0$, then for the pixels in which g reaches a minimum difference holds $T(K_{i,j})=P_{i,j}$ and $T(K_{l,h})=P_{l,h}$ simultaneously.

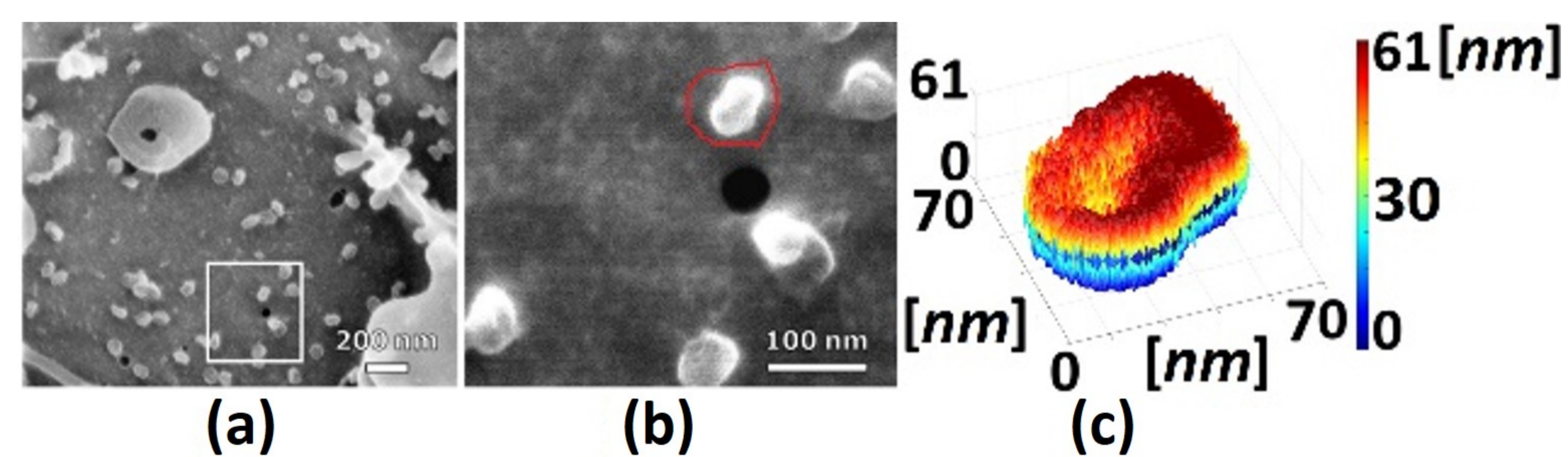


Figure 1. Main results applying isomorphism [1] in (c) and modified isomorphism in COVID cell (a) and (b).

References

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