

Curing-protocol-dependent macroscopic shape errors in PDMS replication

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PDMS is an elastomer increasingly used in tribology to prepare rubbing samples, the roughness of which replicates that of a rigid mold. While the replication of the small scales is usually faithful, very few information exists about the agreement on large, centimetric scales. Here, we show that the free surface of molded PDMS blocks deviate from their expected planicity. The amplitude of the deviation depends on the crosslinking protocol. We identified a suitable such protocol which eliminates large scale replication errors.

Keywords: PDMS, molding, cross-linking protocol, rough samples

1. Introduction

PolyDiMethylSiloxane (PDMS) is a widely used elastomeric material, in particular for molding purposes, for instance in microfluidics or mechanics. In tribology, it is increasingly used to prepare rubbing samples with a desired surface roughness, replicating that of a rigid mold [1,2]. While the faithfulness of the replication has been investigated on the small scale features (μm and below [3]), that on the large scale (mm to cm) remains largely unexplored. In this work, we have discovered that the free surface of a molded parallelepiped exhibits an unwanted curvature, the amplitude of which depends on the crosslinking protocol. As a practical response, we identify a protocol which avoids such a replication error.

2. Methods

We prepare PDMS samples made of Sylgard 184, mixed in a Base / Curing ratio of 10: 1. Different crosslinking times and temperatures have been applied and the replicated PDMS samples were submitted to the various following tests.

The final hardness was measured with a classical Shore A durometer, on samples cured inside a Petri dish. The Young's modulus was extracted from an indentation test between a smooth glass plate and a smooth PDMS spherical probed molded in a concave optical glass lens (radius of curvature 9.42mm).



Fig. 1: Picture of the mold (rectangular base of horizontal size 26mm).

The topography of the free surface of various samples molded in a centimetric parallelepipedic aluminum mold (Fig.1) was measured using an optical interferometric profilometer (Bruker Contour GT K1). The topographies were analyzed using the Mountains Map software (Fig.2). A method has been defined in order to identify the best-fitting ellipsoid to the PDMS surface, and to determine the maximum amplitude of the shape error ($\Delta_z \text{ max}$).

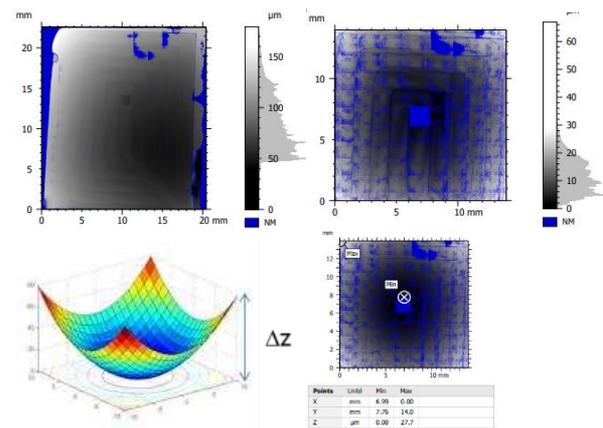


Fig. 2: Illustration of some steps used for the determination of the best-fitting ellipsoid and the error amplitude. From left to right and from top to bottom: raw topography (blue points are non measurable); cropped and tilt-corrected topography (blue points are deemed aberrant); illustration of the type of ellipsoid fitted to the topography, and of its amplitude, $\Delta_z \text{ max}$; automatically determined value of $\Delta_z \text{ max}$ (see bottom table), between highest corner and fitted ellipsoid summit.

3. Discussion

The final crosslinking protocol involves two steps. First a room temperature curing to reach the gel point. Second, a hot step to complete the crosslinking and reach a hardness of at least 43 Shore A. The moment at which demolding is performed is also of importance. All those results will prove helpful to optimize the manufacturing process of samples in Sylgard 184, in order to perform reproducible tribological tests on well-defined topographies, including their large scale features.

4. References

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