

# Leveraging Vision Reconstruction Pipelines for Satellite Imagery

## Supplemental Material

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In this document, we provide an analysis of the numerical stability of the proposed homography computation. Assume that  $\mathbf{P}_1$ ,  $\mathbf{P}_1^{-1}$ , and  $\mathbf{P}_2$  are pre-computed on the CPU with double precision, which is assumed to be sufficient for accurate representation of these quantities. Assume further that these matrices have also been scaled by the inverse of the largest magnitude of the matrix elements. First, it is easy to show that the numbers involved in Eq. 10 are typically on the order of  $10^3 - 10^4$ , improving numeric stability. Second, COLMAP MVS attempts to assign a slanted plane hypothesis  $(\mathbf{n}, m)$  at each pixel of the reference view, and hence the homography must be evaluated separately for each pixel.

Now, consider the case where  $\mathbf{P}_1$ ,  $\mathbf{P}_1^{-1}$ , and  $\mathbf{P}_2$  are transferred to GPU for parallel homography application. This transfer requires conversion from double to single precision, introducing errors that can be modelled by perturbing the matrix elements by a small amount  $o(\epsilon)$ .<sup>1</sup> In Eq. 10, if we perturb  $\mathbf{P}_2$ ,  $\mathbf{P}_1^{-1}$ ,  $\mathbf{q}$ ,  $r$  by  $o(\epsilon)$ , then their multiplication is subject to an error at most  $o(\epsilon)$ :

$$a(1 + o(\epsilon)) \cdot b(1 + o(\epsilon)) = ab(1 + o(\epsilon) + o(\epsilon^2)). \quad (1)$$

Such a small  $o(\epsilon)$  error in  $\mathbf{H}$  leads to negligible error in  $\mathbf{u}_2$ , because the image size  $\mathbf{u}_1$  is bounded by thousands of pixels.

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<sup>1</sup>A real number  $a$  becomes  $a(1 + o(\epsilon))$  after perturbation.  $\epsilon = 10^{-7}$  since single precision has just 7 effective digits.