Reduction of excitation-source coupling artifacts in diffuse fluorescence tomography reconstructions

Chaincy Kuo, Ali Behrooz, Brad W. Rice, *PerkinElmer*

2013 World Molecular Imaging Congress

P 425

1 Introduction

Ill-posedness of diffuse fluorescence tomography inverse problems often leads to artifacts localized near the points where excitation light is injected into the subject. These artifacts are especially problematic in systems with high levels of non-specific dye, as is often encountered after intravenous injection of targeting agents in small animal models. Earlier efforts to remove these artifacts have utilized a priori structural information to guide the reconstruction on the location of inclusions. In this work for fluorescence tomography, an algorithm to reduce excitation source coupling artifacts near the air-tissue boundary using a least-squares method in the absence of user-imposed expectation is described. This method is based on a technique developed by Kempner, Ripoll and Yared (Poster P422, this conference) for the algebraic reconstruction technique.

2 Instrumentation

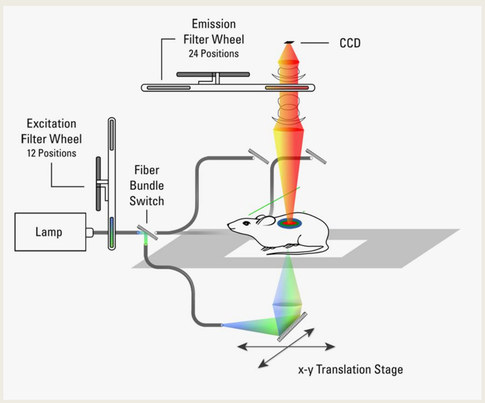
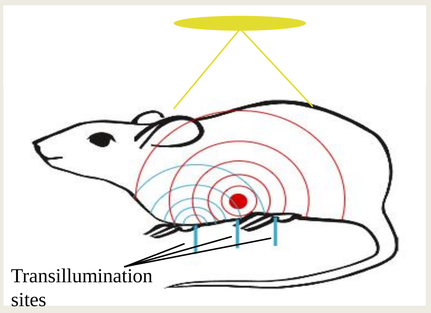


Figure 1. Fluorescence tomography instrumentation. The fluorescence tomography source-detector geometry in this work is such that excitation light is directed into the animal by a 2 mm diameter beam from underneath the animal bed (green/blue beam). The continuous wave fluorescence (red/yellow beam) is imaged through emission filters at the CCD.

Figure 2. A grid of excitation points is rastered, with a fluorescence emission image acquired from above the animal bed for each excitation point



3 Motivation

The fluorescence tomography problem is modeled as diffuse light propagation and homogeneous optical properties. The models compose the Green's function matrices mapping fluorescence inclusions to photon density data at the surface. The spatial sensitivity to the interior defined by Green's matrices is particularly high near the regions of the excitation source coupling to the volume. Due to the optical property errors and non-uniqueness, low order fluorescence background data measured at the surface can be fit by high intensity artifacts at these coupling regions.

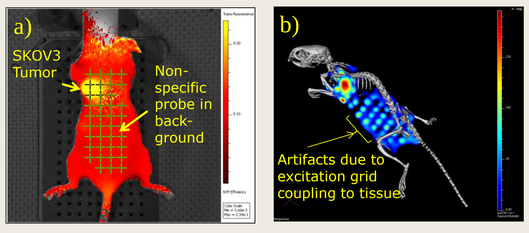


Figure 3. SKOV3 tumor on left shoulder
40 µg of Her2Sense injected IV. Imaged T=48 hours. a) Overview fluorescence image. b) Fluorescence tomography image.

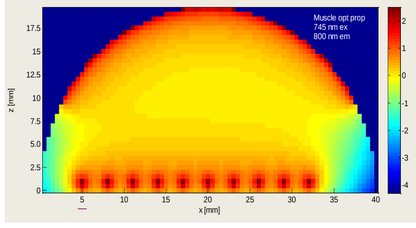
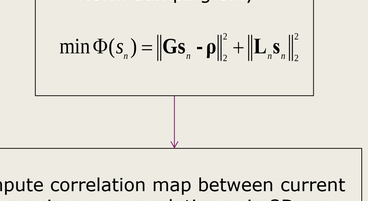


Figure 4. Normalized transmission fluorescence tomography model sensitivity to interior (Simulated animal cross section). Point beam excitation source coupling regions have high values of sensitivity, where injected light begins to diffuse.

4 Ensemble Correlation Method

Multiple reconstructions are performed, each using a subset of unique excitation source patterns. Pearson's correlation spatial maps between solutions are utilized to guide the final reconstruction, where the entire excitation source grid pattern is incorporated. This scheme is naïve to any a priori expectation of fluorescence localization.

- After data on grid has been acquired,
- Vary excitation pattern on animal during analysis (done in algorithm).



- Excitation Pattern + tumor will show up on reconstructions
- Compute union between reconstructions

Figure 6. Algorithm flow chart, utilizing ensemble correlation map as a prior in a Bayesian framework in the final reconstruction with all excitation sources.

5 In vivo experimental results

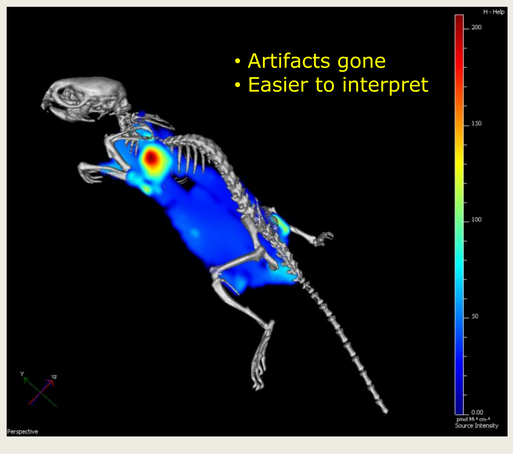


Figure 7. SKOV3 tumor model from Figure 3b), fluorescence reconstruction utilizing ensemble correlation method for prior.

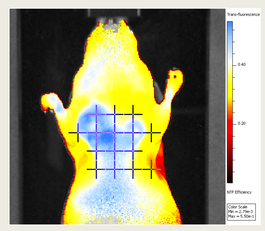


Figure 8. a) Normalized transmission fluorescence overview image of orthotopic, necrotic HT29 mammary fat pad tumors. Image was acquired 24 hours after injection of ProSense 750EX. Animal imaged with ventral side facing camera.

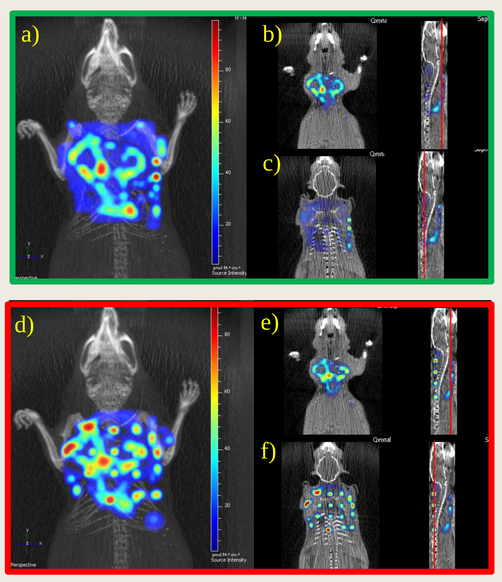


Figure 9. Recon with excitation source artifact treatment via **ensemble correlation method** (green) and without (red). a)&d) 3D perspective view of fluorescence tomography recon registered to CT. b)&e) Coronal slice near ventral side. c)&f) Coronal slice near dorsal side. Slice locations depicted by red line in sagittal view.

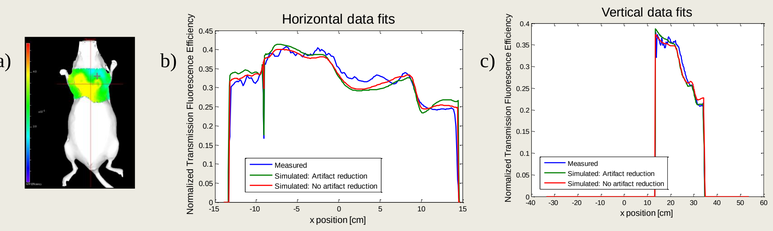


Figure 10. The artifact reduction via ensemble correlation algorithm does not adversely degrade the simulated data compared to the measured, demonstrating that it is a viable solution. a) Normalized fluorescence transillumination data for a single excitation point, denoted by the small crosshair. The white shaded area is the animal surface. Pseudocolor region is data mapped onto the surface. Red horizontal and vertical lines indicate the pixels for data profiles. b) Horizontal line profile data fits. c) Vertical line profile data fits.

6 Summary

This work utilizes multiple reconstructions, each using a subset of unique excitation source patterns. Pearson's correlation spatial maps between solutions guide the final reconstruction, in which the entire excitation source grid pattern is incorporated. This scheme is naïve to any a priori expectation of fluorescence localization.

The algorithm was tested on in vivo fluorescence tomography data whereby mice were injected with a fluorescent probes targeting orthotopically implanted tumors. In comparison of reconstructions with and without the coupling artifact reduction algorithm, the in vivo identified fluorescence source intensity disagreement is ~5%. The visibility of artifacts associated with the excitation source coupling to the imaging subject is greatly reduced, contributing to increased interpretability of the fluorescence tomography reconstruction.

Acknowledgements
The authors would like to thank Justin Jarrell, Ed Lim, and Sunetra Ray for the animal models.

PerkinElmer, Inc., 940 Winter Street, Waltham, MA USA (800) 762-4000 or (+1) 203 925-4602 www.perkinelmer.com